

Applicant  
Copy  
09/689,366  
2/18/04

RESULT 2  
PCT-US96-12860-5  
Sequence 5, Application PC/TUS9612860  
GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBACH, TEST, ALBRIGHTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08,512,946 & 08/569,749  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 55 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-5  
Query Match  
Best Local Similarity 100.0%; Score 307; DB 5; Length 55;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNKLGDSP 55  
DB 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNKLGDSP 55  
RESULT 3  
US-08-511-485-8  
Sequence 8, Application US/08511485  
Patent No. 5919912  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-511-485-8  
Query Match  
Best Local Similarity 100.0%; Score 307; DB 2; Length 618;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNKLGDSP 55  
DB 45 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNKLGDSP 99  
RESULT 4  
US-09-212-971-8  
Sequence 8, Application US/09212971B  
Patent No. 6107041  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
DISEASE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212,971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017,354  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-212-971-8  
Query Match  
Best Local Similarity 100.0%; Score 307; DB 3; Length 618;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNKLGDSP 55  
DB 45 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNKLGDSP 99  
RESULT 5  
US-08-800-929A-8

Applicant Copy  
09/689,366  
2/18/2004

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RESULT 2
PCT-US96-12860-7
Sequence 7, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TOLAR, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/12,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-7

Query Match          100.0%; Score 269; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.3e-28;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGTYIGPDVACFCGKLSNWEPRKDDAMSEHRRHPNCPF 46
DB 1 LARAGTYIGPDVACFCGKLSNWEPRKDDAMSEHRRHPNCPF 46

RESULT 3
US-08-511-485-23
Sequence 23, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-23

Query Match          100.0%; Score 269; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 6.4e-28;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGTYIGPDVACFCGKLSNWEPRKDDAMSEHRRHPNCPF 46
DB 21 LARAGTYIGPDVACFCGKLSNWEPRKDDAMSEHRRHPNCPF 66

RESULT 4
PCT-US95-05922A-2
Sequence 2, Application PC/TUS9505922A
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05922A
FILING DATE: 11 MAY 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-292
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-05922A-2
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Tue May 6 18:23:47 2003

US-08-569-749-2.ra1

09/689,366 8/18/04  
Examined, Search Page 1  
Notes

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 15:59:02 ; Search time 42.0069 seconds

(without alignments)  
432.865 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277

Sequence: 1 MHKTASQRLFPSPSYONIKS.....LNRCPICRGIIKGTFTFLS 618

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
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3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	3277	100.0	618	4	US-09-069-023-29
3	3277	100.0	618	5	PCT-US96-12860-2
4	3247	99.1	618	2	US-08-511-485-8
5	3247	99.1	618	3	US-09-212-971-8
6	3247	99.1	618	4	US-08-800-929A-8
7	3247	99.1	618	4	US-09-617-053A-4
8	2728	83.2	612	4	US-08-569-749-14
9	2728	83.2	612	5	PCT-US96-12860-14
10	2724	83.1	612	3	US-09-212-971-14
11	2724	83.1	612	4	US-08-800-929A-14
12	2724	83.1	612	4	US-09-617-053A-14
13	2353	71.8	604	4	US-08-569-749-4
14	2353	71.8	604	5	PCT-US96-12860-4
15	2332	71.2	604	2	US-08-511-485-6
16	2332	71.2	604	3	US-09-212-971-6
17	2332	71.2	604	4	US-08-800-929A-6
18	2332	71.2	604	4	US-09-617-053A-6
19	2326	71.0	438	5	PCT-US95-05922A-2
20	2172	66.3	600	3	US-09-212-971-12
21	2172	66.3	600	4	US-08-800-929A-12
22	2172	66.3	600	4	US-09-617-053A-12
23	909	27.7	497	2	US-08-511-485-4
24	909	27.7	497	3	US-09-212-971-4
25	909	27.7	497	4	US-08-800-929A-4
26	909	27.7	497	4	US-09-617-053A-4
27	874	26.7	496	2	US-08-511-485-10

28	874	26.7	496	3	US-09-212-971-10	Sequence 10, Appl
29	874	26.7	496	4	US-08-800-929A-10	Sequence 10, Appl
30	874	26.7	496	4	US-09-617-053A-10	Sequence 10, Appl
31	736.5	22.5	498	2	US-08-511-485-13	Sequence 13, Appl
32	513	15.7	268	3	US-08-836-134-22	Sequence 22, Appl
33	513	15.7	268	4	US-09-493-784-22	Sequence 22, Appl
34	492.5	15.0	236	4	US-08-836-134-23	Sequence 23, Appl
35	463	14.1	1151	3	US-08-836-134-23	Sequence 23, Appl
36	463	14.1	1151	4	US-09-493-784-23	Sequence 23, Appl
37	463	14.1	1232	3	US-08-836-134-2	Sequence 2, Appl
38	463	14.1	1232	4	US-09-493-784-2	Sequence 2, Appl
39	461	14.1	275	2	US-08-511-485-12	Sequence 12, Appl
40	461	14.1	275	3	US-08-836-134-21	Sequence 21, Appl
41	461	14.1	275	4	US-09-493-784-21	Sequence 21, Appl
42	458.5	14.0	236	4	US-09-121-979-4	Sequence 4, Appl
43	458.5	14.0	236	4	US-09-332-319-4	Sequence 4, Appl
44	458.5	14.0	236	4	US-09-239-867-2	Sequence 2, Appl
45	431	13.2	89	4	US-09-099-041A-32	Sequence 32, Appl

#### ALIGNMENTS

RESULT 1  
US-08-569-749-2  
Sequence 2, Application US/08569749  
Patent No. 6187557  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)386-3249  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-2  
Query Match 100.0%; Score 3277; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 3.4e-308; Indels 0; Gaps 0;  
Matches 618; Conservative 0; Mismatches 0;  
QY 1 MHKTASQRLFPSPSYONIKSIMESTIISDWTNSKKQKMYDFSCELYRMSTYFPAGV 60  
DB 1 MHKTASQRLFPSPSYONIKSIMESTIISDWTNSKKQKMYDFSCELYRMSTYFPAGV 60  
QY 61 PVSERSLARAGFYITGVNDKVCFCGGLMDNWKLGDSPIQKHQOLYSCSFQNTLVAS 120

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Db 61 PVERSLARAGFYITGVNCKVCCGGLMDNNKLGDEPQKHKQLYPSCSFQNLVSAS 120
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Db 121 LGSTSKNTSPMRNSFAHSISPTLHSSLSFGSYSSLSPPNLNSRAVEDISSSTNPYSYA 180
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Db 181 MSTEEARFLTYHMMPLTFPLSPSELARAGFYIIGPGRVACFACGGLSNMPEPDDAMSEH 240
QY 241 RRHFPNCPLENSLETFLRFSSISMLSMQTHAARMRTFMYPPSSVPVPEOLASAGFYVGR 300
Db 241 RRHFPNCPLENSLETFLRFSSISMLSMQTHAARMRTFMYPPSSVPVPEOLASAGFYVGR 300
QY 301 NDDVKCFCCDGLRCWESGDDPWEHAKMFPCEFLIRKGOEFVEIGRPHLEQLL 360
Db 301 NDDVKCFCCDGLRCWESGDDPWEHAKMFPCEFLIRKGOEFVEIGRPHLEQLL 360
QY 361 STSDTGEENADPPIIHFGGESSSEDVAMMNTPVYKSALEMGNLDVQKQVSKILTT 420
Db 361 STSDTGEENADPPIIHFGGESSSEDVAMMNTPVYKSALEMGNLDVQKQVSKILTT 420
QY 421 GENYKTVNDIVSALLNAEDEKREEEKQAEEASDLSLIRNRNALFCQLTCVPIID 480
Db 421 GENYKTVNDIVSALLNAEDEKREEEKQAEEASDLSLIRNRNALFCQLTCVPIID 480
QY 481 NLKANVINKEHDIKOKTOIPLQARELIDTLVKGNAANIFKCKLEIDSTLYKNLF 540
Db 481 NLKANVINKEHDIKOKTOIPLQARELIDTLVKGNAANIFKCKLEIDSTLYKNLF 540
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Db 541 VDKNMKIPTEDVSGLSLEQLRLQEBERTCKYCMDEKVSVPFPGHLVVOCECAPSLR 600
QY 601 KCPICRGIIKGTVRTFLS 618
Db 601 KCPICRGIIKGTVRTFLS 618

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## RESULT 2

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US-09-069-023-29
; Sequence 29, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Inohara, Gabriel
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-29

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Query Match 100.0%; Score 3277; DB 4; Length 618;
Best Local Similarity 100.0%; Pred. No. 3,4e-308;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MHTASGRLLPPGSPYONKISIMEDSTLSMTWTSNKKMKYDPSCELYRMTSTYTPPAGV 60
QY 61 PVERSLARAGFYITGVNCKVCCGGLMDNNKLGDEPQKHKQLYPSCSFQNLVSAS 120
Db 61 PVERSLARAGFYITGVNCKVCCGGLMDNNKLGDEPQKHKQLYPSCSFQNLVSAS 120

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QY 121 LGSTSKNTSPMRNSFAHSISPTLHSSLSFGSYSSLSPPNLNSRAVEDISSSTNPYSYA 180
Db 121 LGSTSKNTSPMRNSFAHSISPTLHSSLSFGSYSSLSPPNLNSRAVEDISSSTNPYSYA 180
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QY 241 RRHFPNCPLENSLETFLRFSSISMLSMQTHAARMRTFMYPPSSVPVPEOLASAGFYVGR 300
Db 241 RRHFPNCPLENSLETFLRFSSISMLSMQTHAARMRTFMYPPSSVPVPEOLASAGFYVGR 300
QY 301 NDDVKCFCCDGLRCWESGDDPWEHAKMFPCEFLIRKGOEFVEIGRPHLEQLL 360
Db 301 NDDVKCFCCDGLRCWESGDDPWEHAKMFPCEFLIRKGOEFVEIGRPHLEQLL 360
QY 361 STSDTGEENADPPIIHFGGESSSEDVAMMNTPVYKSALEMGNLDVQKQVSKILTT 420
Db 361 STSDTGEENADPPIIHFGGESSSEDVAMMNTPVYKSALEMGNLDVQKQVSKILTT 420
QY 421 GENYKTVNDIVSALLNAEDEKREEEKQAEEASDLSLIRNRNALFCQLTCVPIID 480
Db 421 GENYKTVNDIVSALLNAEDEKREEEKQAEEASDLSLIRNRNALFCQLTCVPIID 480
QY 481 NLKANVINKEHDIKOKTOIPLQARELIDTLVKGNAANIFKCKLEIDSTLYKNLF 540
Db 481 NLKANVINKEHDIKOKTOIPLQARELIDTLVKGNAANIFKCKLEIDSTLYKNLF 540
QY 541 VDKNMKIPTEDVSGLSLEQLRLQEBERTCKYCMDEKVSVPFPGHLVVOCECAPSLR 600
Db 541 VDKNMKIPTEDVSGLSLEQLRLQEBERTCKYCMDEKVSVPFPGHLVVOCECAPSLR 600
QY 601 KCPICRGIIKGTVRTFLS 618
Db 601 KCPICRGIIKGTVRTFLS 618

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## RESULT 3

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PCT-US96-12860-2

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; Sequence 2, Application /PC/TUS9612860
; GENERAL INFORMATION:

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; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:

```

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; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids

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TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-2

Query Match 100.0%; Score 3277; DB 5; Length 618;  
Best Local Similarity 100.0%; Pred. No. 3,46-308;  
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MHKTSORLFPSPSYONIKSIMEDSTIISDWTNSNKKKKYFSCELYMSTYSPFAGY 60
DB 1 MHKTSORLFPSPSYONIKSIMEDSTIISDWTNSNKKKKYFSCELYMSTYSPFAGY 60
QY 61 PVSESLARAGYYGVNDKVCFCGGLMDNMKLGDSPIQKHOLYPCSFIONLVAS 120
DB 61 PVSESLARAGYYGVNDKVCFCGGLMDNMKLGDSPIQKHOLYPCSFIONLVAS 120
QY 121 LGSTKNTSPMNSFAHSLSPLEHSLFSGSYSLSPNLSRAVEDISSRTNPSYA 180
DB 121 LGSTKNTSPMNSFAHSLSPLEHSLFSGSYSLSPNLSRAVEDISSRTNPSYA 180
QY 181 MSTERARFLTYMMPLTFLSPSELARAGYYIGPDRAVACFCGGLSWEPKDDAMSEH 240
DB 181 MSTERARFLTYMMPLTFLSPSELARAGYYIGPDRAVACFCGGLSWEPKDDAMSEH 240
QY 241 RHHFNCPLFENSLFTLRFSISNLSMOTHAARMRTFMWPSVPOEQLASAGFYVGR 300
DB 241 RHHFNCPLFENSLFTLRFSISNLSMOTHAARMRTFMWPSVPOEQLASAGFYVGR 300
QY 301 NDVVCFCGCGDLRCWESGDDPWVEHAKWPRCEFLIRKKGDFVDEIOGRPHLEQL 360
DB 301 NDVVCFCGCGDLRCWESGDDPWVEHAKWPRCEFLIRKKGDFVDEIOGRPHLEQL 360
QY 361 STSDTGEENADPPIIHGPGSSSEDVAMMTPVYKSLFNGFNDLYKOVOSKILTT 420
DB 361 STSDTGEENADPPIIHGPGSSSEDVAMMTPVYKSLFNGFNDLYKOVOSKILTT 420
QY 421 GENYTVNDIVSALLNAEDEKREKEKOAEMASDLSLIRKNMALFOQLTCLPLID 480
DB 421 GENYTVNDIVSALLNAEDEKREKEKOAEMASDLSLIRKNMALFOQLTCLPLID 480
QY 481 NLLKANVINKOEHDIKOKTOIPLQARELIDTILVGNNAANIFNCKLEIDSTLYKNLF 540
DB 481 NLLKANVINKOEHDIKOKTOIPLQARELIDTILVGNNAANIFNCKLEIDSTLYKNLF 540
QY 541 VDKNNKIYPTEDVSGLSLEQLRLQEBERTCKVCKDKESVVFICGHLVYQECAPSIR 600
DB 541 VDKNNKIYPTEDVSGLSLEQLRLQEBERTCKVCKDKESVVFICGHLVYQECAPSIR 600
QY 601 KPCICGIIKGTVRTFLS 618
DB 601 KPCICGIIKGTVRTFLS 618

```

RESULT 4  
US-08-511-485-8  
Sequence 8, Application US/08511485  
Patent No. 5919912

GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
PROBES, AND DETECTION METHODS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-511-485-8

Query Match 99.1%; Score 3247; DB 2; Length 515;  
Best Local Similarity 99.4%; Pred. No. 2,76-305;  
Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MHKTSORLFPSPSYONIKSIMEDSTIISDWTNSNKKKKYFSCELYMSTYSPFAGY 60
DB 1 MHKTSORLFPSPSYONIKSIMEDSTIISDWTNSNKKKKYFSCELYMSTYSPFAGY 60
QY 61 PVSESLARAGYYGVNDKVCFCGGLMDNMKLGDSPIQKHOLYPCSFIONLVAS 120
DB 61 PVSESLARAGYYGVNDKVCFCGGLMDNMKLGDSPIQKHOLYPCSFIONLVAS 120
QY 121 LGSTKNTSPMNSFAHSLSPLEHSLFSGSYSLSPNLSRAVEDISSRTNPSYA 180
DB 121 LGSTKNTSPMNSFAHSLSPLEHSLFSGSYSLSPNLSRAVEDISSRTNPSYA 180
QY 181 MSTERARFLTYMMPLTFLSPSELARAGYYIGPDRAVACFCGGLSWEPKDDAMSEH 240
DB 181 MSTERARFLTYMMPLTFLSPSELARAGYYIGPDRAVACFCGGLSWEPKDDAMSEH 240
QY 241 RHHFNCPLFENSLFTLRFSISNLSMOTHAARMRTFMWPSVPOEQLASAGFYVGR 300
DB 241 RHHFNCPLFENSLFTLRFSISNLSMOTHAARMRTFMWPSVPOEQLASAGFYVGR 300
QY 301 NDVVCFCGCGDLRCWESGDDPWVEHAKWPRCEFLIRKKGDFVDEIOGRPHLEQL 360
DB 301 NDVVCFCGCGDLRCWESGDDPWVEHAKWPRCEFLIRKKGDFVDEIOGRPHLEQL 360
QY 361 STSDTGEENADPPIIHGPGSSSEDVAMMTPVYKSLFNGFNDLYKOVOSKILTT 420
DB 361 STSDTGEENADPPIIHGPGSSSEDVAMMTPVYKSLFNGFNDLYKOVOSKILTT 420
QY 421 GENYTVNDIVSALLNAEDEKREKEKOAEMASDLSLIRKNMALFOQLTCLPLID 480
DB 421 GENYTVNDIVSALLNAEDEKREKEKOAEMASDLSLIRKNMALFOQLTCLPLID 480
QY 481 NLLKANVINKOEHDIKOKTOIPLQARELIDTILVGNNAANIFNCKLEIDSTLYKNLF 540
DB 481 NLLKANVINKOEHDIKOKTOIPLQARELIDTILVGNNAANIFNCKLEIDSTLYKNLF 540
QY 541 VDKNNKIYPTEDVSGLSLEQLRLQEBERTCKVCKDKESVVFICGHLVYQECAPSIR 600
DB 541 VDKNNKIYPTEDVSGLSLEQLRLQEBERTCKVCKDKESVVFICGHLVYQECAPSIR 600
QY 601 KPCICGIIKGTVRTFLS 618
DB 601 KPCICGIIKGTVRTFLS 618

```

## RESULT 5

US-09-212-971-8  
Sequence 8, Application US/09212971B  
Patent No. 6107041  
GENERAL INFORMATION:  
APPLICANT: Korneiluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212,971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017,354  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-212-971-8

Query Match 99.1%; Score 3247; DB 3; Length 618;  
Best Local Similarity 99.4%; Pred. No. 2.7e-305;

Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHKTAQRLEPPGSPYONKINSIMEDSTLLSDWTNSNKKMKYDFSCELYRMSTYSTEPAGY 60  
DB 1 MHKTAQRLEPPGSPYONKINSIMEDSTLLSDWTNSNKKMKYDFSCELYRMSTYSTEPAGY 60  
QY 61 PVSESLARAGFYTYGVNDKVKCFCCGLMDNKKLGDSPLOKHOLYPCSCFIONLVAS 120  
DB 61 PVSESLARAGFYTYGVNDKVKCFCCGLMDNKKLGDSPLOKHOLYPCSCFIONLVAS 120  
QY 121 LGSTSKTSPMRNSFAHSLPTLEHSSLFSGSYSLSPNPLNSRAVDISSRTNPYSYA 180  
DB 121 LGSTSKTSPMRNSFAHSLPTLEHSSLFSGSYSLSPNPLNSRAVDISSRTNPYSYA 180  
QY 181 MSTEERAFLLYHMWPLTFLSPSELARAGFYTYGPGDRVACFACGGLSMNEPRDDAMSEH 240  
DB 181 MSTEERAFLLYHMWPLTFLSPSELARAGFYTYGPGDRVACFACGGLSMNEPRDDAMSEH 240  
QY 241 RRHFPNCPLENSLETRESISNLSMOTHAARKTFMYWSSYPVOEQLASAGFYTYGR 300  
DB 241 RRHFPNCPLENSLETRESISNLSMOTHAARKTFMYWSSYPVOEQLASAGFYTYGR 300  
QY 241 RRHFPNCPLENSLETRESISNLSMOTHAARKTFMYWSSYPVOEQLASAGFYTYGR 300  
DB 241 RRHFPNCPLENSLETRESISNLSMOTHAARKTFMYWSSYPVOEQLASAGFYTYGR 300  
QY 301 NDVKKCFCCGGLRCWESGDDPVYERAKWPCFELIRMGGEFVDETOGRYHLLLEQL 360  
DB 301 NDVKKCFCCGGLRCWESGDDPVYERAKWPCFELIRMGGEFVDETOGRYHLLLEQL 360  
QY 361 STDDTTEENADPPIIFGGESESSDEDAVAMNTPYVKSALEMGFNRDLVQVQOSKILTT 420  
DB 361 STDDTTEENADPPIIFGGESESSDEDAVAMNTPYVKSALEMGFNRDLVQVQOSKILTT 420  
QY 421 GENTKYNDIVSALLNADEKREBEKQAEEMASDDLSTIRNRMALEFOQLCVLPILD 480  
DB 421 GENTKYNDIVSALLNADEKREBEKQAEEMASDDLSTIRNRMALEFOQLCVLPILD 480  
QY 481 NLKANYINKEHDIKOKTOIPLQARELIDTILVNGNAANITFKNCKEITDSTLYKNLF 540  
DB 481 NLKANYINKEHDIKOKTOIPLQARELIDTILVNGNAANITFKNCKEITDSTLYKNLF 540

QY 541 YDKNMKTIPEVDYSGSLSEQLRLQERCKYCMKREYSVYIPCGHLVQCECAPSLR 600  
DB 541 YDKNMKTIPEVDYSGSLSEQLRLQERCKYCMKREYSVYIPCGHLVQCECAPSLR 600  
QY 601 KCPICRGIIKGYRTFLS 618  
DB 601 KCPICRGIIKGYRTFLS 618

## RESULT 6

US-08-800-929A-8  
Sequence 8, Application US/08800929A  
Patent No. 6133437  
GENERAL INFORMATION:  
APPLICANT: Korneiluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF  
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,929A

FILING DATE: 13-FEB-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/030,590

FILING DATE: 14-NOV-1996

APPLICATION NUMBER: 60/017,354

FILING DATE: 26-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bieker-Brady, Kristina

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 07891/009001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-428-0200

TELEFAX: 617-428-7045

TELEX:

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 618 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-800-929A-8

Query Match 99.1%; Score 3247; DB 4; Length 618;  
Best Local Similarity 99.4%; Pred. No. 2.7e-305;

Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHKTAQRLEPPGSPYONKINSIMEDSTLLSDWTNSNKKMKYDFSCELYRMSTYSTEPAGY 60  
DB 1 MHKTAQRLEPPGSPYONKINSIMEDSTLLSDWTNSNKKMKYDFSCELYRMSTYSTEPAGY 60  
QY 61 PVSESLARAGFYTYGVNDKVKCFCCGLMDNKKLGDSPLOKHOLYPCSCFIONLVAS 120  
DB 61 PVSESLARAGFYTYGVNDKVKCFCCGLMDNKKLGDSPLOKHOLYPCSCFIONLVAS 120

QY 121 LGSTSKNTSPMRNSFAHSLSPTEHSLFSGSYSSLFENPLNSRAVEDISSRTNPYSYA 180  
DB 121 LGSTSKNTSPMRNSFAHSLSPTEHSLFSGSYSSLFENPLNSRAVEDISSRTNPYSYA 180  
QY 181 MSTEEARFLTYHMMPLTFPLSPSELARAGFYIIGPGRVACFACGKLSNMPEDDAMSEH 240  
DB 181 MSTEEARFLTYHMMPLTFPLSPSELARAGFYIIGPGRVACFACGKLSNMPEDDAMSEH 240  
QY 241 RRHFPCPLENSLETLRFESISNLSMOTHAARMRTMYPPSSVPVPEOLASAGFYVGR 300  
DB 241 RRHFPCPLENSLETLRFESISNLSMOTHAARMRTMYPPSSVPVPEOLASAGFYVGR 300  
QY 301 NDDVKCFCCDGLRCWESGDDPVEHAKMPPCEFLIRMGQEFVDEIOGRYPHLEOLL 360  
DB 301 NDDVKCFCCDGLRCWESGDDPVEHAKMPPCEFLIRMGQEFVDEIOGRYPHLEOLL 360  
QY 361 STSDTTEENADPPIIHFGGESSSEDVAMMNTPVKSALEMGNLDVQVQSKILTT 420  
DB 361 STSDTTEENADPPIIHFGGESSSEDVAMMNTPVKSALEMGNLDVQVQSKILTT 420  
QY 421 GENYKTVNDIVSALLNAEDEKREKEKQAEASDLSLRKRNALFQOLTCVPIID 480  
DB 421 GENYKTVNDIVSALLNAEDEKREKEKQAEASDLSLRKRNALFQOLTCVPIID 480  
QY 481 NLKANVINKOEHDIIKOKTQIPLQARELIDTILVGNAAANIFKNCLEIDSTLYKNLF 540  
DB 481 NLKANVINKOEHDIIKOKTQIPLQARELIDTILVGNAAANIFKNCLEIDSTLYKNLF 540  
QY 541 VDKNMKYIPTEDVSGLSLEQLRLQOEERTCKYCMDEKSVFIPCGHLVCOECAPSIR 600  
DB 541 VDKNMKYIPTEDVSGLSLEQLRLQOEERTCKYCMDEKSVFIPCGHLVCOECAPSIR 600  
QY 601 KCPICRGIIKGTVRTFLS 618  
DB 601 KCPICRGIIKGTVRTFLS 618

RESULT 7  
US-09-617-053A-8  
; Sequence 8, Application US/09617053A  
; Patent No. 6300492  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; FILE REFERENCE: 07891/009003  
; CURRENT APPLICATION NUMBER: US/09/617,053A  
; CURRENT FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/800,929  
; PRIOR FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 618  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-09-617-053A-8

Query Match 99.1%; Score 3247; DB 4; Length 618;  
Best Local Similarity 99.4%; Pred. No. 2,7e-305;  
Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MHKTAORLPFGPSYQIKSIMEDSTLSMTNNSKOKMYDSCELYRSTSTSTPAGV 60  
DB 1 MHKTAORLPFGPSYQIKSIMEDSTLSMTNNSKOKMYDSCELYRSTSTSTPAGV 60

QY 61 PVSESLARAGFYITGVNDKVCFCGGLMDNKKLDDSPIQKHQOLYPSCSFQUNVSAS 120  
DB 61 PVSESLARAGFYITGVNDKVCFCGGLMDNKKLDDSPIQKHQOLYPSCSFQUNVSAS 120  
QY 121 LGSTSKNTSPMRNSFAHSLSPTEHSLFSGSYSSLFENPLNSRAVEDISSRTNPYSYA 180  
DB 121 LGSTSKNTSPMRNSFAHSLSPTEHSLFSGSYSSLFENPLNSRAVEDISSRTNPYSYA 180  
QY 181 MSTEEARFLTYHMMPLTFPLSPSELARAGFYIIGPGRVACFACGKLSNMPEDDAMSEH 240  
DB 181 MSTEEARFLTYHMMPLTFPLSPSELARAGFYIIGPGRVACFACGKLSNMPEDDAMSEH 240  
QY 241 RRHFPCPLENSLETLRFESISNLSMOTHAARMRTMYPPSSVPVPEOLASAGFYVGR 300  
DB 241 RRHFPCPLENSLETLRFESISNLSMOTHAARMRTMYPPSSVPVPEOLASAGFYVGR 300  
QY 301 NDDVKCFCCDGLRCWESGDDPVEHAKMPPCEFLIRMGQEFVDEIOGRYPHLEOLL 360  
DB 301 NDDVKCFCCDGLRCWESGDDPVEHAKMPPCEFLIRMGQEFVDEIOGRYPHLEOLL 360  
QY 361 STSDTTEENADPPIIHFGGESSSEDVAMMNTPVKSALEMGNLDVQVQSKILTT 420  
DB 361 STSDTTEENADPPIIHFGGESSSEDVAMMNTPVKSALEMGNLDVQVQSKILTT 420  
QY 421 GENYKTVNDIVSALLNAEDEKREKEKQAEASDLSLRKRNALFQOLTCVPIID 480  
DB 421 GENYKTVNDIVSALLNAEDEKREKEKQAEASDLSLRKRNALFQOLTCVPIID 480  
QY 481 NLKANVINKOEHDIIKOKTQIPLQARELIDTILVGNAAANIFKNCLEIDSTLYKNLF 540  
DB 481 NLKANVINKOEHDIIKOKTQIPLQARELIDTILVGNAAANIFKNCLEIDSTLYKNLF 540  
QY 541 VDKNMKYIPTEDVSGLSLEQLRLQOEERTCKYCMDEKSVFIPCGHLVCOECAPSIR 600  
DB 541 VDKNMKYIPTEDVSGLSLEQLRLQOEERTCKYCMDEKSVFIPCGHLVCOECAPSIR 600  
QY 601 KCPICRGIIKGTVRTFLS 618  
DB 601 KCPICRGIIKGTVRTFLS 618

RESULT 8  
US-08-569-749-14  
; Sequence 14, Application US/08569749  
; Patent No. 618757  
; GENERAL INFORMATION:  
; APPLICANT: Rothe, Mike  
; APPLICANT: Goeddel, David V  
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brezner, David J.  
; REGISTRATION NUMBER: 24,774  
; REFERENCE/DOCKET NUMBER: A-62464/DJB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)781-1989  
; TELEFAX: (415)398-3249

; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 612 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-569-749-14

Query Match 83.2% Score 2728; DB 4; Length 612;  
 Best Local Similarity 83.4%; Pred. No. 4.5e-255;  
 Matches 517; Conservative 45; Mismatches 48; Indels 10; Gaps 6;

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QY 1 MHKTAQRLLPFGPGYONIKSIMESTILSDWTNSNKKMKYDSCCELYRMSTYSPAGV 60
DB 1 MDKTVSQRLOGGTLHQKLRIMEKSTILSNWTKESEKMFDSCELYRMSTYSAFPGV 60
QY 61 PVSESLARAGFYTYGVNDKVKCCCGGLMDNMKLGDSPIQKHQOLYPCSCFTONLVAS 120
DB 61 PVSESLARAGFYTYGVNDKVKCCCGGLMDNMKOGDSFVEKHQFPCSCFVOILLAS 120
QY 121 LGSTSKTSPMRNSPFAHSLSTLEHSSLFSGYSLSLSPNLSRAVEDISSRTNPYSYA 180
DB 121 LQSPSKMSPVKSRAHSP-SP-LEP---GGIHSNLCSPLNSRAVEDF--SSRMDPCSYA 173
QY 181 MSTEAREFLTYHMPPLFLSPSELARAGFYTYIGPDVACFACGKLSNMEPKDDAMSEH 240
DB 174 MSTEAREFLTYHMPPLFLSPSELARAGFYTYIGPDVACFACGKLSNMEPKDDAMSEH 233
QY 241 RRHPNCPFLNLSLETLEFSLISNLSMOTHAARMRTFMTWPSVPVQPEQLASAGFYVGR 300
DB 234 RRHPNCPFLNLSLETLEFSLISNLSMOTHAARMRTFMTWPSVPVQPEQLASAGFYVDR 293
QY 301 NDDVKCFCCDGGGLKMCWEGDDPWYEHAKWPRCEFLIRMGQEFVDEIQGRYHLLQQL 360
DB 294 NDDVKCFCCDGGGLKMCWEGDDPWYEHAKWPRCEFLIRMGQEFVDEIQGRYHLLQQL 353
QY 361 STSDTTEENADP--PIIHFGPGSSSEDAVMNTPVYKSALEMGFNLDYKQTVOSKIL 418
DB 354 STSDTTEENADPTEYVYHFGPG--SEEDVYMMSTPVYKALEMGFSLSLVQVQOIL 412
QY 419 TTGENYKTVNDIYVALLNADEKREBEKEQAEMASDDLILIRKNMALFOOLLTVLP 478
DB 413 ATGENYKTVNDIYVALLNADEKREBEKEQAEMASDDLILIRKNMALFOOLLTVLP 472
QY 479 LDNLKANKVINKOEHDIIRKTOIPIQARLIDITLVKGAANAIFPNCKLEIDSTLYKN 538
DB 473 LDNLKANKVINKOEHDIIRKTOIPIQARLIDITLVKGAANAIFPNCKLEIDSTLYKN 532
QY 539 LFVDKNNKIYPTEDVSGLSLEEQRLRLQEBRTCKVCKDKESVYVIFPCGHLVYVQCECAPS 598
DB 533 LFVEKNNKIYPTEDVSGLSLEEQRLRLQEBRTCKVCKDKESVYVIFPCGHLVYVQCECAPS 592
QY 599 LRKPCICRGITIKGTVPFFLS 618
DB 593 LRKPCICRGITIKGTVPFFLS 612
  
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## RESULT 9

PCT-US96-12860-14

; Sequence 14, Application PC/TUS9612860  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TULARIK, INC.  
 ; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
 ; STREET: 4 Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US96/12860  
 ; FILING DATE: 06 AUG 1996  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Brezner, David J.  
 ; REGISTRATION NUMBER: 24,774  
 ; REFERENCE/DOCKET NUMBER: A-62464/DOB  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415)781-1989  
 ; TELEFAX: (415)398-3249  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 612 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; PCT-US96-12860-14

Query Match 83.2% Score 2728; DB 5; Length 612;  
 Best Local Similarity 83.4%; Pred. No. 4.5e-255;  
 Matches 517; Conservative 45; Mismatches 48; Indels 10; Gaps 6;

```

QY 1 MHKTAQRLLPFGPGYONIKSIMESTILSDWTNSNKKMKYDSCCELYRMSTYSPAGV 60
DB 1 MDKTVSQRLOGGTLHQKLRIMEKSTILSNWTKESEKMFDSCELYRMSTYSAFPGV 60
QY 61 PVSESLARAGFYTYGVNDKVKCCCGGLMDNMKLGDSPIQKHQOLYPCSCFTONLVAS 120
DB 61 PVSESLARAGFYTYGVNDKVKCCCGGLMDNMKOGDSFVEKHQFPCSCFVOILLAS 120
QY 121 LGSTSKTSPMRNSPFAHSLSTLEHSSLFSGYSLSLSPNLSRAVEDISSRTNPYSYA 180
DB 121 LQSPSKMSPVKSRAHSP-SP-LEP---GGIHSNLCSPLNSRAVEDF--SSRMDPCSYA 173
QY 181 MSTEAREFLTYHMPPLFLSPSELARAGFYTYIGPDVACFACGKLSNMEPKDDAMSEH 240
DB 174 MSTEAREFLTYHMPPLFLSPSELARAGFYTYIGPDVACFACGKLSNMEPKDDAMSEH 233
QY 241 RRHPNCPFLNLSLETLEFSLISNLSMOTHAARMRTFMTWPSVPVQPEQLASAGFYVGR 300
DB 234 RRHPNCPFLNLSLETLEFSLISNLSMOTHAARMRTFMTWPSVPVQPEQLASAGFYVDR 293
QY 301 NDDVKCFCCDGGGLKMCWEGDDPWYEHAKWPRCEFLIRMGQEFVDEIQGRYHLLQQL 360
DB 294 NDDVKCFCCDGGGLKMCWEGDDPWYEHAKWPRCEFLIRMGQEFVDEIQGRYHLLQQL 353
QY 361 STSDTTEENADP--PIIHFGPGSSSEDAVMNTPVYKSALEMGFNLDYKQTVOSKIL 418
DB 354 STSDTTEENADPTEYVYHFGPG--SEEDVYMMSTPVYKALEMGFSLSLVQVQOIL 412
QY 419 TTGENYKTVNDIYVALLNADEKREBEKEQAEMASDDLILIRKNMALFOOLLTVLP 478
DB 413 ATGENYKTVNDIYVALLNADEKREBEKEQAEMASDDLILIRKNMALFOOLLTVLP 472
QY 479 LDNLKANKVINKOEHDIIRKTOIPIQARLIDITLVKGAANAIFPNCKLEIDSTLYKN 538
DB 473 LDNLKANKVINKOEHDIIRKTOIPIQARLIDITLVKGAANAIFPNCKLEIDSTLYKN 532
QY 539 LFVDKNNKIYPTEDVSGLSLEEQRLRLQEBRTCKVCKDKESVYVIFPCGHLVYVQCECAPS 598
DB 533 LFVEKNNKIYPTEDVSGLSLEEQRLRLQEBRTCKVCKDKESVYVIFPCGHLVYVQCECAPS 592
QY 599 LRKPCICRGITIKGTVPFFLS 618
DB 593 LRKPCICRGITIKGTVPFFLS 618
  
```

Db 593 LRKPCIRGRTKGTVRTPLS 612

RESULT 10

US-09-212-971-14

Sequence 14, Application US/09212971B

Patent No. 6107041

GENERAL INFORMATION:

APPLICANT: Korneiluk, Robert G

APPLICANT: Mackenzie, Alexander E

APPLICANT: Liston, Peter

APPLICANT: Baird, Stephen

APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND

TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

FILE REFERENCE: 07891/009002

CURRENT FILING DATE: US/09/212, 971B

EARLIER FILING DATE: 1998-12-16

EARLIER FILING DATE: 1996-04-26

EARLIER FILING DATE: 1996-04-26

EARLIER FILING DATE: 1996-11-14

EARLIER FILING DATE: 1997-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14

LENGTH: 612

TYPE: PRT

ORGANISM: Mus musculus

US-09-212-971-14

Query Match

Best Local Similarity 83.1%; Score 2724; DB 3; Length 612;

Matches 516; Conservative 46; Mismatches 48; Indels 10; Gaps 6;

Db 593 LRKPCIRGRTKGTVRTPLS 612

1 MHHTASORLEPPGSSYONIKSIMEDSTLSPTWTSNOKMYDSCELYRSTSTPAGV 60

1 MDVTTSORLGQGLHOLKRIKSTILSWTSESEKMFDFSCELYRSTSTPAGV 60

61 PVSESLARAGFYTYGVNDVKCFCCGLMDNKLGDSP1QKHOLYPPSCFIONTSAS 120

61 PVSESLARAGFYTYGVNDVKCFCCGLMDNKLGDSP1QKHOLYPPSCFIONTSAS 120

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

Db 593 LRKPCIRGRTKGTVRTPLS 612

RESULT 11

US-08-800-929A-14

Sequence 14, Application US/08800929A

Patent No. 6133437

GENERAL INFORMATION:

APPLICANT: Korneiluk, Robert G

APPLICANT: Mackenzie, Alexander E

APPLICANT: Liston, Peter

APPLICANT: Baird, Stephen

APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF

TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Ebling LLP

STREET: 176 Federal Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800, 929A

FILING DATE: 13-Feb-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/030, 590

FILING DATE: 14-Nov-1996

APPLICATION NUMBER: 60/017, 354

FILING DATE: 26-Apr-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bleker-Brady, Kristina

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 07891/009001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-428-0200

TELEFAX: 617-428-7045

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 612 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-800-929A-14

Query Match

Best Local Similarity 83.1%; Score 2724; DB 4; Length 612;

Matches 516; Conservative 46; Mismatches 48; Indels 10; Gaps 6;

Db 593 LRKPCIRGRTKGTVRTPLS 612

1 MHHTASORLEPPGSSYONIKSIMEDSTLSPTWTSNOKMYDSCELYRSTSTPAGV 60

1 MDVTTSORLGQGLHOLKRIKSTILSWTSESEKMFDFSCELYRSTSTPAGV 60

61 PVSESLARAGFYTYGVNDVKCFCCGLMDNKLGDSP1QKHOLYPPSCFIONTSAS 120

61 PVSESLARAGFYTYGVNDVKCFCCGLMDNKLGDSP1QKHOLYPPSCFIONTSAS 120

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

121 LGSTSKTSPMRNSFAHSLSPLEHSSLFSGYSVSLSPNPLNSRAVEDISSRTNPSYA 180

Db 61 PVSESLARAGFYTYGVNDKVKCFCCGMLDMNKQGD:PYEKHRQFPPSCSFVOTLLSAS 120  
QY 121 LGSTSKTSPMRNSFAHSLPTLEHSSLFGSYSSLSINPLNSRAVEDISSRNPYSYA 180  
Db 121 LOSPSKMSVYKSRFAHS-SP-LEH---GSHSNLCSPLNSRAVEDF--SSRMDPCSYA 173  
QY 181 MSTEAFRLTYHMPPLTFLSPSELARAGFYTYIGPDRVACFACGKLSNNEPKDDAMSEH 240  
Db 174 MSTEAFRLTYHMPPLTFLSPSELARAGFYTYIGPDRVACFACGKLSNNEPKDDAMSEH 233  
QY 241 RRHPNCPFLNLSLETIRFSISNLSMOTHAARMFTMYWSSVPVPOEOLASAGFYTYGR 300  
Db 234 RRHPNCPFLNLSLETIRFSISNLSMOTHAARMFTMYWSSVPVPOEOLASAGFYTYDR 293  
QY 301 NDDVKCCCGGGLRCMESGDDPWVHAKMPPRCFELIRMGQEVDEIQRYPHLLBOLL 360  
Db 294 NDDVKCCCGGGLRCMESGDDPWVHAKMPPRCFELIRMGQEVDEIQRYPHLLBOLL 353  
QY 361 STSDTJGEENADP--PIIHFGPGESESDAVMMNTPVYKSALEMGFNRLVKOTVOSKIL 418  
Db 354 STSDTJGEENADPPEYVYHFGPGE--SSKDYVMNSTPVYKSALEMGFNRLVKOTVOSKIL 412  
QY 419 TTGENTYVNDIVSALINAEDEREEREKQAEEMASDDLSLRKNMALFQOLTHVLP1 478  
Db 413 ATGENTYVNDIVSALINAEDEREEREKQAEEMASDDLSLRKNMALFQOLTHVLP1 472  
QY 479 LDNLKANVINKOEHDIKOKTOIPLQARELIDITLVKGNAAANIFNCKLEIDSTLYKN 538  
Db 473 LDNLKANVINKOEHDIKOKTOIPLQARELIDITLVKGNAAANIFNCKLEIDSTLYKN 532  
QY 539 LFVDKMKKIYPTEDVSGLSLEBQLRLQERTCKVCMDKEVSVYFPCGHLVYVOCQCAPS 598  
Db 533 LFVEKNMKKIYPTEDVSGLSLEBQLRLQERTCKVCMDKEVSVYFPCGHLVYVOCQCAPS 592  
QY 599 LRKPCIGRTIKGTVPRTFLS 618  
Db 593 LRKPCIGRTIKGTVPRTFLS 612

RESULT 12  
US-09-617-053A-14  
; Sequence 14, Application US/09617053A  
; Patent No. 6300492  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: DISEASE  
; FILE REFERENCE: 07891/009003  
; CURRENT APPLICATION NUMBER: US/09/617, 053A  
; CURRENT FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/800,929  
; PRIOR FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 612  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-617-053A-14

Query Match 83.18; Score 2724; DB 4; Length 612;  
Best Local Similarity 83.2%; Pred. No. 1,1e-254;  
Matches 516; Conservative 46; Mismatches 48; Indels 10; Gaps 6;

QY 1 MHRASORLPGPSPYKINSIMEDSTILSPMTNSKOKMKYD:SCELYRSTVSTPAGV 60  
Db 1 MDTVSRQLRGGITLQKLRIMEKSTILSNWTKSEKMKFDSCELYRSTVSTPAGV 60

QY 61 PVSESLARAGFYTYGVNDKVKCFCCGMLDMNKLGSDP1OKHKOQLPSCSFIONLYSAS 120  
Db 61 PVSESLARAGFYTYGVNDKVKCFCCGMLDMNKQGDSPYEKHRQFPPSCSFVOTLLSAS 120  
QY 121 LGSTSKTSPMRNSFAHSLPTLEHSSLFGSYSSLSINPLNSRAVEDISSRNPYSYA 180  
Db 121 LOSPSKMSVYKSRFAHS-SP-LEH---GSHSNLCSPLNSRAVEDF--SSRMDPCSYA 173  
QY 181 MSTEAFRLTYHMPPLTFLSPSELARAGFYTYIGPDRVACFACGKLSNNEPKDDAMSEH 240  
Db 174 MSTEAFRLTYHMPPLTFLSPSELARAGFYTYIGPDRVACFACGKLSNNEPKDDAMSEH 233  
QY 241 RRHPNCPFLNLSLETIRFSISNLSMOTHAARMFTMYWSSVPVPOEOLASAGFYTYGR 300  
Db 234 RRHPNCPFLNLSLETIRFSISNLSMOTHAARMFTMYWSSVPVPOEOLASAGFYTYDR 293  
QY 301 NDDVKCCCGGGLRCMESGDDPWVHAKMPPRCFELIRMGQEVDEIQRYPHLLBOLL 360  
Db 294 NDDVKCCCGGGLRCMESGDDPWVHAKMPPRCFELIRMGQEVDEIQRYPHLLBOLL 353  
QY 361 STSDTJGEENADP--PIIHFGPGESESDAVMMNTPVYKSALEMGFNRLVKOTVOSKIL 418  
Db 354 STSDTJGEENADPPEYVYHFGPGE--SSKDYVMNSTPVYKSALEMGFNRLVKOTVOSKIL 412  
QY 419 TTGENTYVNDIVSALINAEDEREEREKQAEEMASDDLSLRKNMALFQOLTHVLP1 478  
Db 413 ATGENTYVNDIVSALINAEDEREEREKQAEEMASDDLSLRKNMALFQOLTHVLP1 472  
QY 479 LDNLKANVINKOEHDIKOKTOIPLQARELIDITLVKGNAAANIFNCKLEIDSTLYKN 538  
Db 473 LDNLKANVINKOEHDIKOKTOIPLQARELIDITLVKGNAAANIFNCKLEIDSTLYKN 532  
QY 539 LFVDKMKKIYPTEDVSGLSLEBQLRLQERTCKVCMDKEVSVYFPCGHLVYVOCQCAPS 598  
Db 533 LFVEKNMKKIYPTEDVSGLSLEBQLRLQERTCKVCMDKEVSVYFPCGHLVYVOCQCAPS 592  
QY 599 LRKPCIGRTIKGTVPRTFLS 618  
Db 593 LRKPCIGRTIKGTVPRTFLS 612

RESULT 13  
US-08-569-749-4  
; Sequence 4, Application US/08569749  
; Patent No. 6187557  
; GENERAL INFORMATION:  
; APPLICANT: Rothe, Mike  
; APPLICANT: Goeddel, David V  
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLHR, HOBBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/569,749  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brezner, David J.  
; REGISTRATION NUMBER: 24,774  
; REFERENCE/DOCKET NUMBER: A-62464/DJB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)781-1989

TELEFAX: (415)398-3249  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 604 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-569-749-4

Query Match 71.8%; Score 2353; DI 4; Length 604;  
 Best Local Similarity 72.8%; Pred. No. 8.5e-219;  
 Matches 440; Conservative 71; Mismatches 87; Indels 6; Gaps 5;

20 STMEDSTIISDWTNS-NKOKMYDFSCELYRMSTYTFPAGVPSERSLARAGFYTGYN 78  
 2 NIYENSIFLSNLMKSAFTELKYLDSCELYRMSTYTFPAGVPSERSLARAGFYTGYN 61  
 79 DKYKCCGGLMDNMLGSPDIOKHQOLYPCSFQIONLYSA-SLGSTSKNTSP--MRNSF 135  
 62 DKYKCCGGLMDNMLGSPDIOKHQOLYPCSFQIONLYSA-SLGSTSKNTSP--MRNSF 120  
 136 AHSLSPTLEHSSLSFGSYSLSPNPLNSRAVEDISSRTNPSYAMSTEAREFLTYHMP 195  
 121 THSLPGETENSGYFRGSYSNSPNPNNSRANODFSALMSSYHCANNENARLLTFQTMP 180  
 196 LTFPLSESLARAGFYITIGQDRVACFACGKLSNMEPKDAMSEHRRHPNCPFLNSL- 254  
 181 LTFPLSESLARAGFYITIGQDRVACFACGKLSNMEPKDAMSEHRRHPNCPFLNSL- 240  
 255 ETLRFISNLSMOTHAARKTEFMWPSVYPVOEOLASAGFYVGNNDVKKCCDGGGLR 314  
 241 DTSRYTVSNLSMOTHAARKTEFMWPSVYPVOEOLASAGFYVGNNDVKKCCDGGGLR 300  
 315 CWESGDDPWEHAKEPPEFLIRMGQFVDEIOGRYPHLLEQLLSTSDTTEENADPP 374  
 301 CWESGDDPWEHAKEPPEFLIRMGQFVDEIOGRYPHLLEQLLSTSDTTEENADPP 360  
 375 IIFHGGESESDAVMANTPVVKSALMGFNRLDVQVOSKILTTGENYKTVNDIVSL 434  
 361 IIFHGGESESDAVMANTPVVKSALMGFNRLDVQVOSKILTTGENYKTVNDIVSL 420  
 435 LNAEDEREERERATREESNDLLIRKRRALFQHLVCVPIIDSLTAGIINQEH 494  
 421 LNAEDEREERERATREESNDLLIRKRRALFQHLVCVPIIDSLTAGIINQEH 480  
 495 IIRKQIPLQARELIDITLVKGNAAANIFKNCLEIDSTLYKNTLVDRNMKXIPTEDEVS 554  
 481 VIKOKTQTSLOARELIDITLVKGNAAANIFKNCLEIDSTLYKNTLVDRNMKXIPTEDEVS 540  
 555 GJLSLEQLRLQERCKVKCMKEVSIVIFPCGHLVYVCECAPSLKPCICRSTIKGTVR 614  
 541 DLPVEQLRLQERCKVKCMKEVSIVIFPCGHLVYVCECAPSLKPCICRSTIKGTVR 600  
 615 TFLS 618  
 601 TFLS 604

RESULT 14  
 PCT-US96-12860-4  
 Sequence 4, Application PC/TUS9612860  
 GENERAL INFORMATION:  
 APPLICANT: TOLARIK, INC.  
 TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FLIER, HOBACH, TEST, ALBRITTON & HERBERT  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/12860  
 FILING DATE: 06 AUG 1996  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brezner, David J.  
 REGISTRATION NUMBER: 24,774  
 REFERENCE/DOCKET NUMBER: A-62464/DJB  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415)781-1989  
 TELEFAX: (415)398-3249  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 604 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US96-12860-4

Query Match 71.8%; Score 2353; DI 5; Length 604;  
 Best Local Similarity 72.8%; Pred. No. 8.5e-219;  
 Matches 440; Conservative 71; Mismatches 87; Indels 6; Gaps 5;

20 STMEDSTIISDWTNS-NKOKMYDFSCELYRMSTYTFPAGVPSERSLARAGFYTGYN 78  
 2 NIYENSIFLSNLMKSAFTELKYLDSCELYRMSTYTFPAGVPSERSLARAGFYTGYN 61  
 79 DKYKCCGGLMDNMLGSPDIOKHQOLYPCSFQIONLYSA-SLGSTSKNTSP--MRNSF 135  
 62 DKYKCCGGLMDNMLGSPDIOKHQOLYPCSFQIONLYSA-SLGSTSKNTSP--MRNSF 120  
 136 AHSLSPTLEHSSLSFGSYSLSPNPLNSRAVEDISSRTNPSYAMSTEAREFLTYHMP 195  
 121 THSLPGETENSGYFRGSYSNSPNPNNSRANODFSALMSSYHCANNENARLLTFQTMP 180  
 196 LTFPLSESLARAGFYITIGQDRVACFACGKLSNMEPKDAMSEHRRHPNCPFLNSL- 254  
 181 LTFPLSESLARAGFYITIGQDRVACFACGKLSNMEPKDAMSEHRRHPNCPFLNSL- 240  
 255 ETLRFISNLSMOTHAARKTEFMWPSVYPVOEOLASAGFYVGNNDVKKCCDGGGLR 314  
 241 DTSRYTVSNLSMOTHAARKTEFMWPSVYPVOEOLASAGFYVGNNDVKKCCDGGGLR 300  
 315 CWESGDDPWEHAKEPPEFLIRMGQFVDEIOGRYPHLLEQLLSTSDTTEENADPP 374  
 301 CWESGDDPWEHAKEPPEFLIRMGQFVDEIOGRYPHLLEQLLSTSDTTEENADPP 360  
 375 IIFHGGESESDAVMANTPVVKSALMGFNRLDVQVOSKILTTGENYKTVNDIVSL 434  
 361 IIFHGGESESDAVMANTPVVKSALMGFNRLDVQVOSKILTTGENYKTVNDIVSL 420  
 435 LNAEDEREERERATREESNDLLIRKRRALFQHLVCVPIIDSLTAGIINQEH 494  
 421 LNAEDEREERERATREESNDLLIRKRRALFQHLVCVPIIDSLTAGIINQEH 480  
 495 IIRKQIPLQARELIDITLVKGNAAANIFKNCLEIDSTLYKNTLVDRNMKXIPTEDEVS 554  
 481 VIKOKTQTSLOARELIDITLVKGNAAANIFKNCLEIDSTLYKNTLVDRNMKXIPTEDEVS 540  
 555 GJLSLEQLRLQERCKVKCMKEVSIVIFPCGHLVYVCECAPSLKPCICRSTIKGTVR 614  
 541 DLPVEQLRLQERCKVKCMKEVSIVIFPCGHLVYVCECAPSLKPCICRSTIKGTVR 600  
 615 TFLS 618

DB 601 FLS 604

RESULT 15  
US-08-511-485-6  
Sequence 6, Application US/08511485  
Patent No. 5919912  
GENERAL INFORMATION:  
APPLICANT: Kornejuk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ. ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 604 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-511-485-6

Query Match 71.2%; Score 2332; DB 2: Length 604;  
Best Local Similarity 72.1%; Pred. No. 9, 2e-217;  
Matches 435; Conservative 72; Mismatches 93; Indels 4; Gaps 4;

QY 20 SIMEDSTILSDWTNS--NKOKMKYDFSGCELYRMSTYSFPAGVPSERSLARAGFYTGYN 78  
DB 2 NIVENSFTLSNLMKSAWTEFLKTYDLSCELYRMSTYSFPAGVPSERSLARAGFYTGYN 61  
QY 79 DKVCECCGMLDNWKLKGSPIQKHQOLYPCSCFIONLYSA-SLGSTSKNTSPMRNSFA-136  
DB 62 DKVCECCGMLDNWKLKGSPIQKHQOLYPCSCFIONLYSA-SLGSTSKNTSPMRNSFA-136  
QY 137 HSLSPLEHSLFSGSSLSFNPFLNSRAVEDISSRTNPFYAMSTEARFLTYHMKPL 196  
DB 122 HSLSPLEHSLFSGSSLSFNPFLNSRAVEDISSRTNPFYAMSTEARFLTYHMKPL 196  
QY 197 TFLSPSELARAGFYTGPGGRVACFACGGKLSNMEPPDAMSDHRRHFPNCPLENSTL-E 255  
DB 182 TFLSPSELARAGFYTGPGGRVACFACGGKLSNMEPPDAMSDHRRHFPNCPLENSTL-E 255  
QY 256 TLRFSISNLSMOTHAARMRTFTMTWPSVPYQPOLASAGFYTYGRNDVYCFCCDGLRC 315  
DB 242 TLRFSISNLSMOTHAARMRTFTMTWPSVPYQPOLASAGFYTYGRNDVYCFCCDGLRC 301  
QY 316 WESGDDPWVHAHAKWPRCEFLIMKGOEYVDEIQGRYPHLEQLLSTSDTGGENADPPI 375

DB 302 WESGDDPWVHAHAKWPRCEFLIMKGOEYVDEIQGRYPHLEQLLSTSDTGGENADPPI 361  
QY 376 IHEPGESSEDVAMNTPVYKSALEMGFNRDYVKOTVOSKILTTGENYKTVNDIVSALL 435  
DB 362 IHEPGESSEDVAMNTPVYKSALEMGFNRDYVKOTVOSKILTTGENYKTVNDIVSALL 421  
QY 436 NADDEREEREKQAEEMASDDLSLRKNMALFOQLTCVPLDNLKRVNINKQEHDI 495  
DB 422 NADDEREEREKQAEEMASDDLSLRKNMALFOQLTCVPLDNLKRVNINKQEHDI 481  
QY 496 IKOKTOIPLQARELIDPILVKGNAANIPFNCKEIDSTLYKMLFVGNKMYTPEDVSG 555  
DB 482 IKOKTOIPLQARELIDPILVKGNAANIPFNCKEIDSTLYKMLFVGNKMYTPEDVSG 541  
QY 556 LSLBQRLRLQEBRTCKVCMKKEVSVFIPCGHLVYVQCBAPSIRKCPICRGITKGTVT 615  
DB 542 LSLBQRLRLQEBRTCKVCMKKEVSVFIPCGHLVYVQCBAPSIRKCPICRGITKGTVT 601  
QY 616 FLS 618  
DB 602 FLS 604

Search completed: May 5, 2003, 16:09:08  
Job time: 44.0069 secs



GenCore version 5.1.4-D5\_4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:50:57 ; Search time 121.749 Seconds

(without alignments)  
676.383 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277  
Sequence: 1 MKRTASQRLPFGPSYQNIKS.....LKKPCICGKITKTVRTFLS 618

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: A.Geneseq.101002:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	3277	100.0	618	AAW19746	Human Inhibitor of
2	3277	100.0	618	AAW13545	Human c-IAP1. Hom
3	3277	100.0	618	AAV33998	Human cellular inh
4	3247	99.1	618	AAW19583	Human apoptosis in
5	3247	99.1	618	AAW69296	Human HIAP-2 prote
6	3247	99.1	618	ABG55665	Human inhibitor of
7	2728	83.2	612	AAW13555	Murine c-IAP. Mus
8	2724	83.1	612	AAW69299	Murine HIAP-2 prot
9	2654	81.0	591	AAW19586	Mouse apoptosis in
10	2654	81.0	591	ABG55668	Mouse inhibitor of

11	2353	71.8	604	18	AAW19747	Human Inhibitor of
12	2353	71.8	604	18	AAW13546	Human c-IAP2. Hom
13	2353	71.8	604	20	AAV52703	Human cellular inh
14	2353	71.8	604	20	AAV33997	Human cellular inh
15	2332	71.2	604	18	AAW19582	Human apoptosis in
16	2332	71.2	604	19	AAW69295	Human HIAP-1 prote
17	2332	71.2	604	23	ABG55664	Human inhibitor of
18	2326	71.0	438	17	AAW04583	Human Inhibitor of
19	2172	66.3	600	19	AAW69298	Murine HIAP-1 prot
20	2152	65.7	602	23	ABG55667	Mouse inhibitor of
21	2148	65.5	602	18	AAW19585	Mouse apoptosis in
22	1678	51.2	1140	22	AAU97837	Human cysteine pro
23	1678	51.2	1141	22	ABG50694	Human APR2-MIF chl
24	1593	48.6	306	22	AAU02925	Angiotensin conver
25	910	27.8	496	18	AAW19745	Mouse inhibitor of
26	909	27.7	497	19	AAW19581	Human apoptosis in
27	909	27.7	497	19	AAW69294	Human XIAP protein
28	909	27.7	497	21	AAV99985	Human X-linked inh
29	909	27.7	497	23	ABG55663	Human inhibitor of
30	908	27.7	497	21	AAV59451	Human XIAP protein
31	874	26.7	496	18	AAW19584	Human apoptosis in
32	874	26.7	496	19	AAW69297	Murine XIAP protei
33	874	26.7	496	23	ABG55666	Mouse inhibitor of
34	760.5	23.2	464	23	AAU75747	Human inhibitor of
35	737.5	22.5	498	22	ABG52863	Drosophila melanog
36	735.5	22.4	498	18	AAW19748	Drosophila inhibit
37	539	16.4	108	22	AAE10158	Caspase recruitment
38	533.5	16.3	278	23	AAO20511	Protein of APP rel
39	494	15.1	438	22	AAW48189	Drosophila mutant
40	490.5	15.0	438	22	AAW48190	Drosophila mutant
41	490	15.0	438	22	ABG51858	Drosophila melanog
42	490	15.0	438	22	ABG57347	Drosophila melanog
43	490	15.0	438	22	AAW48188	Drosophila wild-ty
44	490	15.0	438	22	AAW48192	Drosophila mutant
45	484	14.8	438	22	AAW48191	Drosophila mutant

#### ALIGNMENTS

RESULT 1	AAW19746	AAW19746 standard; Protein: 618 AA.
ID	AAW19746	
AC	AAW19746;	
XX		
DT	16-SEP-1997 (first entry)	
XX		
DE	Human Inhibitor of apoptosis protein homologue MIHB.	
XX		
KW	Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHB;	
KW	degenerative disease; infectious disease; autoimmune disease;	
KW	cancer; therapy; diagnosis.	
XX		
OS	Homo sapiens.	
XX		
EH		
FT	Key	Location/Qualifiers
FT	Region	46..113
FT	Region	/label- BIR
FT	Region	184..250
FT	Region	/label- BIR
FT	Region	269..337
FT	Region	/label- BIR
FT	Region	569..606
FT	Region	/label- RING_finger
XX		
XX	W09723501-A1.	
XX		
XX	03-JUL-1997.	
PD		
XX		
XX	20-DEC-1996;	96W0-AU00827.
XX		
XX	22-DEC-1995;	95AU-0007275.

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XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX Vaux DL.
XX WPI. 1997-350966/32.
XX N-PSDB; AAT72711.
XX Isolated protein homologues of viral inhibitors of apoptosis - used
XX to modulate apoptosis for treatment of degenerative, infectious or
XX autoimmune diseases and cancer
XX Claim 8; Page 51-54; 136pp; English.
XX
XX Mammalian IAP homologue B (MIIB) (AAW19746) is a human homologue of
XX baculovirus inhibitor of apoptosis protein (IAP). Its amino acid
XX sequence was deduced from a cDNA clone (see also AAT72711) isolated
XX from a human foetal liver cDNA library using primers based on
XX human EST sequences that resembled the BIR repeats of Orygia
XX pseudotsuguta polyhedrosis virus IAP. IAP homologues (see also
XX AAW19745 and AAW19747-52) and their derivatives and chemical analogues
XX can be used in methods for modulating apoptosis in animal cells,
XX specifically for treatment, by inhibition, of degenerative and
XX infectious disease or, by promotion, of cancer and autoimmune
XX disease.
XX
XX Sequence 618 AA:
SQ
Query Match 100.0%; Score 3277; DB 18; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.4e-284;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHKTSQRLEPGPSYONIKSIMEDSTILSDWTNSNKKKKYDFSCELYRMSTYTFPAGV 60
DB 1 MHKTSQRLEPGPSYONIKSIMEDSTILSDWTNSNKKKKYDFSCELYRMSTYTFPAGV 60
QY 61 PVSESLAAGAGYTYGVNDKVKCFCCGMLDNWKLGDSPIQKHQOLYPCSFQNLVSA 120
DB 61 PVSESLAAGAGYTYGVNDKVKCFCCGMLDNWKLGDSPIQKHQOLYPCSFQNLVSA 120
QY 121 LGSTSKNTSPMKNFSFAHSIPTLEHSLFSGSYSLSPRLNSRAVEDISSRTNYSYA 180
DB 121 LGSTSKNTSPMKNFSFAHSIPTLEHSLFSGSYSLSPRLNSRAVEDISSRTNYSYA 180
QY 181 MSTEARPLTYIMMPITFISPELARAAGFYTGPGDRAVACFACGKLSNWEPRKDAMSEH 240
DB 181 MSTEARPLTYIMMPITFISPELARAAGFYTGPGDRAVACFACGKLSNWEPRKDAMSEH 240
QY 241 RRRFPKPLENSLETLRESISNLSMOTHAARMTFMYPSVPPVQPEQLASNGFYVGR 300
DB 241 RRRFPKPLENSLETLRESISNLSMOTHAARMTFMYPSVPPVQPEQLASNGFYVGR 300
QY 301 NDDVKKCFCCDGLRCWESGDDPVEHAKEFPRCEFLIRKKGQEFVDEIGRPYHLEQL 360
DB 301 NDDVKKCFCCDGLRCWESGDDPVEHAKEFPRCEFLIRKKGQEFVDEIGRPYHLEQL 360
QY 361 STSDTTEENADPPIIHFGPGSSSEDVAMNTPVYKSALEKMFNDLVKQTVQSKILTT 420
DB 361 STSDTTEENADPPIIHFGPGSSSEDVAMNTPVYKSALEKMFNDLVKQTVQSKILTT 420
QY 421 GSNYKTVNDIVSALLNADEKREKEKAEEMASDDLSLIRKRRALVQQLTCLVPIID 480
DB 421 GSNYKTVNDIVSALLNADEKREKEKAEEMASDDLSLIRKRRALVQQLTCLVPIID 480
QY 481 NLLKANVINKOEHDIKQKQIPLQARELIDTILVGNAAANIFKNCLEIDISTLYKNLF 540
DB 481 NLLKANVINKOEHDIKQKQIPLQARELIDTILVGNAAANIFKNCLEIDISTLYKNLF 540
QY 541 VDKNMKYIPTEDVSGISLEQLRLQDEERTCYVCMDEKVSVEFTPCGHLVVOQECAPSLR 600
DB 541 VDKNMKYIPTEDVSGISLEQLRLQDEERTCYVCMDEKVSVEFTPCGHLVVOQECAPSLR 600
QY 601 KCPICGIIKGIYTRFELS 618

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DB 601 KCPICGIIKGIYTRFELS 618
XXXXXXXXXXXXXXXXXXXX
RESULT 2
AAW13545
ID AAW13545 standard; Protein; 618 AA.
XX
XX AAW13545;
AC 22-JUL-1997 (first entry)
XX
XX Human c-IAP1.
DE
XX
XX IAP, inhibitor; apoptosis; RING finger domain; restinosis;
KM myocardial infarction; nephritis; HIV.
XX
XX Homo sapiens.
OS
XX WO9706182-A1.
PN
XX 20-FEB-1997.
PD
XX 06-AUG-1996; 96WO-US12860.
PF
XX 08-DEC-1995; 95US-0569749.
PR 08-AUG-1995; 95US-0512946.
XX
XX (TUDA-) TUDARIC INC.
PA
XX Goeddel DV, Rothe M;
XX
XX WPI. 1997-154209/14.
DR N-PSDB; AAT61590.
XX
XX Nucleic acids encoding cellular inhibitor of apoptosis proteins
PT useful for apoptosis regulation in cells to reduce or increase
XX apoptosis and for pharmacological screening
XX
XX Disclosure; Page 18-20; 35pp; English.
XX
XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
XX AAT61590/761591) comprise a series of defined structural domain
XX repeats and/or a RING finger domain; in particular, at least two of
XX a first domain repeat (AAW13547 or AAW13548), a second domain repeat
XX (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
XX and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
XX sequence derived from these human genes.
XX The nucleic acid is used for recombinant prodn. of human cellular
XX inhibitor of apoptosis protein which modulates apoptosis
XX regulation. The nucleic acids are useful in therapies where
XX increased cell-specific apoptosis is desired, e.g. in restinosis,
XX inflammatory disease states, myocardial infarction, glomerular
XX nephritis, transplant rejection and infectious diseases, e.g. HIV.
XX They can also be used in conditions requiring a reduction in
XX apoptosis.
XX
XX Sequence 618 AA:
SQ
Query Match 100.0%; Score 3277; DB 18; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.4e-284;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHKTSQRLEPGPSYONIKSIMEDSTILSDWTNSNKKKKYDFSCELYRMSTYTFPAGV 60
DB 1 MHKTSQRLEPGPSYONIKSIMEDSTILSDWTNSNKKKKYDFSCELYRMSTYTFPAGV 60
QY 61 PVSESLAAGAGYTYGVNDKVKCFCCGMLDNWKLGDSPIQKHQOLYPCSFQNLVSA 120
DB 61 PVSESLAAGAGYTYGVNDKVKCFCCGMLDNWKLGDSPIQKHQOLYPCSFQNLVSA 120
QY 121 LGSTSKNTSPMKNFSFAHSIPTLEHSLFSGSYSLSPRLNSRAVEDISSRTNYSYA 180

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Db 121 LGSTSKNTSPMRNSFAHSLSPLEHSSLFSGSYSLSPNPLNSRAVEDISSRTNPYSYA 180
QY 181 MSTERARFLTYHMPDLTFLSPSELARAGFYIIGPDRAVACFACGKLSNWEKDDAMSEH 240
Db 181 MSTERARFLTYHMPDLTFLSPSELARAGFYIIGPDRAVACFACGKLSNWEKDDAMSEH 240
QY 241 RRRHFNCFLENSLETFLFSTISNLSMOTHAARMFTFMTWPSVPVQPOLASAGFYVGR 300
Db 241 RRRHFNCFLENSLETFLFSTISNLSMOTHAARMFTFMTWPSVPVQPOLASAGFYVGR 300
QY 301 NDDVACFCDCDGLRCWESGDDPWVEHAKMPFCEFLIRMGQEFVDEIOGRYPHLEQL 360
Db 301 NDDVACFCDCDGLRCWESGDDPWVEHAKMPFCEFLIRMGQEFVDEIOGRYPHLEQL 360
QY 361 STSDTGEENADPPIIHGPGESSEDAVMNMTPVKSALEMGFNRDLVKOTVOSKILTT 420
Db 361 STSDTGEENADPPIIHGPGESSEDAVMNMTPVKSALEMGFNRDLVKOTVOSKILTT 420
QY 421 GENKTVDIYASALNADDEREEREKQAEEMASDLSLRKNMALFOOLTVCVPLTD 480
Db 421 GENKTVDIYASALNADDEREEREKQAEEMASDLSLRKNMALFOOLTVCVPLTD 480
QY 481 NLKANVINKEHDIIRKOTQIPIQARELIDTILVKGNAANIFKNCLEIDSTLYKNLF 540
Db 481 NLKANVINKEHDIIRKOTQIPIQARELIDTILVKGNAANIFKNCLEIDSTLYKNLF 540
QY 541 VDKNMKXIPTEDVSGLSLEQLRLQEBERTCKVCMDKEVSVEFIPCGHLVVOCECAPSLR 600
Db 541 VDKNMKXIPTEDVSGLSLEQLRLQEBERTCKVCMDKEVSVEFIPCGHLVVOCECAPSLR 600
QY 601 KCPICRGIIKGTVRTFLS 618
Db 601 KCPICRGIIKGTVRTFLS 618

RESULT 3
AAY33998
ID AAY33998 standard; Protein: 618 AA.
AC AAY33998;
AA 26-NOV-1999 (first entry)
DE Human cellular inhibitor of apoptosis-1 sequence.
KW Cellular inhibitor of Apoptosis-1; antisense; diagnostic; therapeutic;
KW c-IAP-1; prophylaxis; infection; inflammation; tumor formation.
XX Homo sapiens.
OS
XX US5958772-A.
PN 28-SEP-1999.
XX
PD 03-DEC-1998; 98US-0205204.
XX
PE 03-DEC-1998; 98US-0205204.
XX
PR 03-DEC-1998; 98US-0205204.
XX
PA (ISIS-) ISIS PHARM INC.
PI Bennett CF, Cowsett LM, Ackermann EJ;
XX
XX WPI, 1999-561047/47.
XX
XX N-PSDB; AA22143.
XX
XX Antisense compounds complementary to Cellular inhibitor of Apoptosis-1
XX useful for e.g. diagnostics, therapeutics, and as research reagents.
XX
XX Example 13; Columns 41-46; 32pp; English.
XX
XX The invention provides antisense compounds of 8-30 nucleotides that
XX inhibit the expression of human Cellular inhibitor of Apoptosis-1
XX (c-IAP-1). The antisense compounds may be used for diagnostics,
XX

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CC therapeutics (for modulating the expression of c-IAP-1), prophylaxis
CC (e.g. to prevent or delay infection, inflammation, or tumor formation),
CC as research reagents (e.g. to distinguish between members of a biological
CC pathway) and in kits. The present sequence represents the human cellular
CC inhibitor of apoptosis-1.
XX
XX Sequence 618 AA;
SQ
Query Match 100.0%; Score 3277; DB 20; Length 618;
Best Local Similarity 100.0%; Pred. No. 1,4e-284;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHKTASQRLFPGPSYQNTKISIMEDSTILSDTNSKQKMYDFSCELYRMSTYSFFPAGV 60
Db 1 MHKTASQRLFPGPSYQNTKISIMEDSTILSDTNSKQKMYDFSCELYRMSTYSFFPAGV 60
QY 61 PVSESLARAGFYIIGVNDKVCFCGGLMDNMKIGDSPIQKHQOLYSCSTIOMLVASAS 120
Db 61 PVSESLARAGFYIIGVNDKVCFCGGLMDNMKIGDSPIQKHQOLYSCSTIOMLVASAS 120
QY 121 LGSTSKNTSPMRNSFAHSLSPLEHSSLFSGSYSLSPNPLNSRAVEDISSRTNPYSYA 180
Db 121 LGSTSKNTSPMRNSFAHSLSPLEHSSLFSGSYSLSPNPLNSRAVEDISSRTNPYSYA 180
QY 181 MSTERARFLTYHMPDLTFLSPSELARAGFYIIGPDRAVACFACGKLSNWEKDDAMSEH 240
Db 181 MSTERARFLTYHMPDLTFLSPSELARAGFYIIGPDRAVACFACGKLSNWEKDDAMSEH 240
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Db 241 RRRHFNCFLENSLETFLFSTISNLSMOTHAARMFTFMTWPSVPVQPOLASAGFYVGR 300
QY 301 NDDVACFCDCDGLRCWESGDDPWVEHAKMPFCEFLIRMGQEFVDEIOGRYPHLEQL 360
Db 301 NDDVACFCDCDGLRCWESGDDPWVEHAKMPFCEFLIRMGQEFVDEIOGRYPHLEQL 360
QY 361 STSDTGEENADPPIIHGPGESSEDAVMNMTPVKSALEMGFNRDLVKOTVOSKILTT 420
Db 361 STSDTGEENADPPIIHGPGESSEDAVMNMTPVKSALEMGFNRDLVKOTVOSKILTT 420
QY 421 GENKTVDIYASALNADDEREEREKQAEEMASDLSLRKNMALFOOLTVCVPLTD 480
Db 421 GENKTVDIYASALNADDEREEREKQAEEMASDLSLRKNMALFOOLTVCVPLTD 480
QY 481 NLKANVINKEHDIIRKOTQIPIQARELIDTILVKGNAANIFKNCLEIDSTLYKNLF 540
Db 481 NLKANVINKEHDIIRKOTQIPIQARELIDTILVKGNAANIFKNCLEIDSTLYKNLF 540
QY 541 VDKNMKXIPTEDVSGLSLEQLRLQEBERTCKVCMDKEVSVEFIPCGHLVVOCECAPSLR 600
Db 541 VDKNMKXIPTEDVSGLSLEQLRLQEBERTCKVCMDKEVSVEFIPCGHLVVOCECAPSLR 600
QY 601 KCPICRGIIKGTVRTFLS 618
Db 601 KCPICRGIIKGTVRTFLS 618

RESULT 4
AAW19583
ID AAW19583 standard; Protein: 618 AA.
AC AAW19583;
AA 02-SEP-1997 (first entry)
DE Human apoptosis inhibitor HIAP-2.
KW Apoptosis inhibitor; HIAP-2; HIV; AIDS; neurodegeneration;
KW myelodysplastic syndrome; ischemia; myocardial infarction; stroke;
KW reperfusion injury; toxin-induced liver disease; gene therapy;
KW diagnosis.
XX
XX Homo sapiens.
OS

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XX Key Location/Qualifiers
FH Domain 46..113
FT Domain /label= BIR-1
FT Domain 184...250
FT Domain /label= BIR-2
FT Domain 269...336
FT Domain /label= BIR-3
FT Domain 560..605
FT Domain /label= Ring_zinc_finger
PPN WO9706255-A2.
XX 20-FEB-1997.
XX 05-AUG-1996; 96WO-1B01022.
XX 22-DEC-1995; 95US-0576956.
XX 04-AUG-1995; 95US-0511485.
XX (UYOT-) UNIV OTTAWA.
XX PA
XX PI Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX DR WPI; 1997-154262/14.
XX DR N-PSDB; AAT70838.
XX PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
XX PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
XX PT of susceptibility to apoptotic disease
XX PS
XX PS Claim 27; Page 75-77; 219pp; English.
CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC are inhibitors of apoptosis (IAP) and which are characterised by
CC the presence of a ring zinc finger domain (see also AAW19587) and at
CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC The IAP amino acid sequences were deduced from cDNA clones (AAT70837
CC and AAT70838) from a human liver library. IAP polypeptides can be
CC expressed in host cells (in vitro or in vivo) and used in methods
CC for treating diseases and disorders involving apoptosis, esp. in a
CC human diagnosed as HIV-positive or as having AIDS, a
CC neurodegenerative disease, a myelodysplastic syndrome or an
CC ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease.
XX CC
XX SQ Sequence 618 AA:
Query Match 99.1%; Score 3247; DB 16; Length 618;
Best Local Similarity 99.4%; Pred. No. 6.8e-282;
Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 MHKTAQRLPFGPSYONIKSIMEDSTILSDWTNSNKKKYPSCELYRMSTYSPAGV 60
DB 1 MHKTAQRLPFGPSYONIKSIMEDSTILSDWTNSNKKKYPSCELYRMSTYSPAGV 60
QY 61 PYSEERLARAAGFYTYGVNKKVCFCCGMLDMNKKLDSPIQRIKOLYPCSFYQNIYSAS 120
DB 61 PYSEERLARAAGFYTYGVNKKVCFCCGMLDMNKKLDSPIQRIKOLYPCSFYQNIYSAS 120
QY 121 LGSTSNTPMRNSFAHSPLTEHSSLPFGSYSSSPNPLNRAVEDISSRTNPSYA 180
DB 121 LGSTSNTPMRNSFAHSPLTEHSSLPFGSYSSSPNPLNRAVEDISSRTNPSYA 180
QY 181 MSTEARFLTYHAMPLTFLSPSELARAGFYTYGPGRVACFCAGKLSMWEPRKDMASER 240
DB 181 MSTEARFLTYHAMPLTFLSPSELARAGFYTYGPGRVACFCAGKLSMWEPRKDMASER 240
QY 241 RRHFPACPLENSLETLRSISLMSOTHAARMRTMYPSSVPVPEOLASGFFYYGR 300
DB 241 RRHFPACPLENSLETLRSISLMSOTHAARMRTMYPSSVPVPEOLASGFFYYGR 300

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QY 301 NDVYKCFCCDGLRCWESGDDPWVHAKWPRCEFLIRKKGEPVDEIGRRPHLLPOLL 360
DB 301 NDVYKCFCCDGLRCWESGDDPWVHAKWPRCEFLIRKKGEPVDEIGRRPHLLPOLL 360
QY 361 STSDTTGEENADPPIIHFGPSSSEDVAMNTPVYKSALEMGFNNDLYKOTVQSKILTT 420
DB 361 STSDTTGEENADPPIIHFGPSSSEDVAMNTPVYKSALEMGFNNDLYKOTVQSKILTT 420
QY 421 GENYTVNDIVSALLNAEDEKREERKEKQAEEMASDLSLIRKNMALPQOLTCLVPLID 480
DB 421 GENYTVNDIVSALLNAEDEKREERKEKQAEEMASDLSLIRKNMALPQOLTCLVPLID 480
QY 481 NLKANVINKQKHDIITKOTQIPLOARELIDITLYKGNAAAFNCKLEIDSTLYKNLF 540
DB 481 NLKANVINKQKHDIITKOTQIPLOARELIDITLYKGNAAAFNCKLEIDSTLYKNLF 540
QY 541 VDKNNKIPTEDVSGLSLEQLRRLQERTCYCKDKESVVFIFCGHLVWQECAPSIR 600
DB 541 VDKNNKIPTEDVSGLSLEQLRRLQERTCYCKDKESVVFIFCGHLVWQECAPSIR 600
QY 601 KCPICRGIIKGTVPRTPLS 618
DB 601 KCPICRGIIKGTVPRTPLS 618

```

RESULT 5  
AAW69296  
ID AAW69296 standard; Protein: 618 AA.

AAW69296;

13-NOV-1998 (first entry)

Human HIAP-2 protein.

Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
proliferative disease; IAP; therapy; cancer; human; HIAP-2 protein.

Homo sapiens.

WO9835693-A2;

20-AUG-1998;

13-FEB-1998; 98WO-1B00781.

13-FEB-1997; 97US-0800929.

(UYOT-) UNIV OTTAWA.

Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;

Tsang B;

WPI; 1998-467164/40.

N-PSDB; AAW55040.

Inducing apoptosis in proliferative mammalian cells with inhibitor  
of IAP or NAIP polypeptide - also methods for prognosis based on  
presence of IAP and NAIP, specifically applied to cancers involving  
p53 mutations

Disclosure; Fig 3; 147pp; English.

This sequence is the human HIAP-2 protein, which is a inhibitor of  
apoptosis protein (IAP), and can be used in the method of the invention.  
The method is for enhancing apoptosis in cells from a mammal with  
proliferative disease by treatment with a compound that inhibits  
biological activity of an IAP or NAIP polypeptide. The inhibitory  
compounds are used to treat proliferative diseases, specially cancers of  
ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
liver, nasopharynx, thyroid, central nervous system, prostate, colon,  
rectum, cervix or endometrium, particularly to increase their sensitivity  
to chemotherapeutic agents. High levels of the IAP or NAIP proteins are

CC detected in many cancers and are associated with poor prognosis.  
 CC resistance to chemotherapeutic agents and mutations in p53 (it is  
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIAP  
 CC genes). Transgenic animals are used for testing the effects of antisense  
 CC oligonucleotides and for screening for the inhibitors.

XX Sequence 618 AA:

Query Match 99.1%; Score 3247; DB 19; Length 618;  
 Best Local Similarity 99.4%; Pred. No. 6,8e-282;  
 Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHKTSQRLFPGPSTONIKSIMEDSTIISDMTNSKOKKKYFSCELYMSTYTFPACV 60  
 DB 1 MHKTSQRLFPGPSTONIKSIMEDSTIISDMTNSKOKKKYFSCELYMSTYTFPACV 60  
 QY 61 PVSERSIARAGFYTGVDKVKCFCCGLMDNMKLDSP1QKHOKLPSCSTIONLVAS 120  
 DB 61 PVSERSIARAGFYTGVDKVKCFCCGLMDNMKLDSP1QKHOKLPSCSTIONLVAS 120  
 QY 121 LGSTSKNTSPMNSFAHSLSPLEHSLFSGSYSLSPNPLMSRAVEDISSRTNPYSYA 180  
 DB 121 LGSTSKNTSPMNSFAHSLSPLEHSLFSGSYSLSPNPLMSRAVEDISSRTNPYSYA 180  
 QY 181 MSTEERARFLTYHMPPLTFSPSELARAGFYTGPDGRVACFCAGGKLSMWEKDDAMSPH 240  
 DB 181 MSTEERARFLTYHMPPLTFSPSELARAGFYTGPDGRVACFCAGGKLSMWEKDDAMSPH 240  
 QY 241 RHHFPCPLENSLETLRFSISNLSMOTHAARMRTFMWPSVVPQPEOLASAGFYVGR 300  
 DB 241 RHHFPCPLENSLETLRFSISNLSMOTHAARMRTFMWPSVVPQPEOLASAGFYVGR 300  
 QY 301 NNDVACFCGDDGLRCWESGDDPWVEHAKWPRCEFLIRMGGEFVDEIGRYPHLEQLL 360  
 DB 301 NNDVACFCGDDGLRCWESGDDPWVEHAKWPRCEFLIRMGGEFVDEIGRYPHLEQLL 360  
 QY 361 STSDTGEENAPPIIHFEFGESSEDVAMNTPVKSALEMGFNDDYKOTVQSKILTT 420  
 DB 361 STSDTGEENAPPIIHFEFGESSEDVAMNTPVKSALEMGFNDDYKOTVQSKILTT 420  
 QY 421 GENYKTVNDIVALLNAEDEKREKEKQAEEMASDLSLIRKRMALFOOLTVCVPLID 480  
 DB 421 GENYKTVNDIVALLNAEDEKREKEKQAEEMASDLSLIRKRMALFOOLTVCVPLID 480  
 QY 481 NLKANVINKOEHDIKOKTOIPLQARELIDTIVKGNAAITFKCKLEIDSTLYKNLF 540  
 DB 481 NLKANVINKOEHDIKOKTOIPLQARELIDTIVKGNAAITFKCKLEIDSTLYKNLF 540  
 QY 541 YDKNMKYIPTEDVSGLSLEQLRLQERTCKYCMDEKESVVFPCGHLVWCOECAPSIR 600  
 DB 541 YDKNMKYIPTEDVSGLSLEQLRLQERTCKYCMDEKESVVFPCGHLVWCOECAPSIR 600  
 QY 601 KPCICRGIIKGTVPFELS 618  
 DB 601 KPCICRGIIKGTVPFELS 618

RESULT 6

ABG65665  
 ID ABG65665 standard; Protein; 618 AA.

AC ABG65665;

DT 26-AUG-2002 (first entry)

DE Human inhibitor of apoptosis, HIAp2.

KM Human: antisense; inhibitor of apoptosis; HIAp1; HIAp2; XIAP;

KM cytosolic cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;

KM pancreatic cancer; embryonic development; viral pathogenesis;

KM autoimmune disorder; neurodegenerative disease; multiple sclerosis;

KM lupus erythematosus; herpes virus infection; pox virus infection;

KM adenovirus infection; proliferative disease.

XX OS Homo sapiens.  
 XX WO200226968-A2.  
 XX 04-APR-2002.  
 XX 27-SEP-2001; 2001WO-CA01379.  
 XX 28-SEP-2000; 2000US-0672717.  
 XX (UNOT-) UNIV OTTAWA.  
 XX (ABGE-) ABGERA THERAPEUTICS INC.  
 XX Korneiluk RG, Lacasse E, Baird S, Holcik M, Young S,  
 XX WPI: 2002-479562/51.  
 XX N-PSDB: ABK93871.  
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for  
 XX enhancing apoptosis in a cell, for treating cancer and other  
 XX proliferative diseases  
 XX PS Disclosure: Fig 3; 135pp; English.  
 XX The invention relates to an inhibitor of apoptosis (IAP) antisense  
 XX nucleic acid (I) that inhibits IAP biological activity, regardless of  
 XX length of the antisense nucleic acid, the IAP proteins may be mouse  
 XX or human XIAP, HIAp1 or HIAp2. Also included are a pharmaceutical  
 XX composition comprising a mammalian IAP antisense molecule and a method of  
 XX enhancing apoptosis in a cell, comprising administering a negative  
 XX regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 XX antisense inhibitor is useful for enhancing apoptosis in a cell in a  
 XX mammal diagnosed with a proliferative disease. The method is useful for  
 XX treating a patient diagnosed with a proliferative disease like cancer.  
 XX The IAP antisense molecule is useful to treat, ameliorate, improve,  
 XX sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 XX adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
 XX conditions where apoptosis is involved or implicated (e.g. embryonic  
 XX development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 XX diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
 XX virus, pox virus and adenovirus). The present sequence is a human IAP  
 XX protein sequence.  
 XX Sequence 618 AA:

Query Match 99.1%; Score 3247; DB 23; Length 618;  
 Best Local Similarity 99.4%; Pred. No. 6,8e-282;  
 Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHKTSQRLFPGPSTONIKSIMEDSTIISDMTNSKOKKKYFSCELYMSTYTFPACV 60  
 DB 1 MHKTSQRLFPGPSTONIKSIMEDSTIISDMTNSKOKKKYFSCELYMSTYTFPACV 60  
 QY 61 PVSERSIARAGFYTGVDKVKCFCCGLMDNMKLDSP1QKHOKLPSCSTIONLVAS 120  
 DB 61 PVSERSIARAGFYTGVDKVKCFCCGLMDNMKLDSP1QKHOKLPSCSTIONLVAS 120  
 QY 121 LGSTSKNTSPMNSFAHSLSPLEHSLFSGSYSLSPNPLMSRAVEDISSRTNPYSYA 180  
 DB 121 LGSTSKNTSPMNSFAHSLSPLEHSLFSGSYSLSPNPLMSRAVEDISSRTNPYSYA 180  
 QY 181 MSTEERARFLTYHMPPLTFSPSELARAGFYTGPDGRVACFCAGGKLSMWEKDDAMSPH 240  
 DB 181 MSTEERARFLTYHMPPLTFSPSELARAGFYTGPDGRVACFCAGGKLSMWEKDDAMSPH 240  
 QY 241 RHHFPCPLENSLETLRFSISNLSMOTHAARMRTFMWPSVVPQPEOLASAGFYVGR 300  
 DB 241 RHHFPCPLENSLETLRFSISNLSMOTHAARMRTFMWPSVVPQPEOLASAGFYVGR 300  
 QY 301 NNDVACFCGDDGLRCWESGDDPWVEHAKWPRCEFLIRMGGEFVDEIGRYPHLEQLL 360  
 DB 301 NNDVACFCGDDGLRCWESGDDPWVEHAKWPRCEFLIRMGGEFVDEIGRYPHLEQLL 360

QY 361 STSDTGEENADPPIHFGGSSSEDVAMNTPVYKSALEMGNRLVQTVQSKILTT 420  
 DB 361 STSDTGEENADPPIHFGGSSSEDVAMNTPVYKSALEMGNRLVQTVQSKILTT 420  
 QY 421 GENTKTVDIVSALLNADEREKREKEKQAEEMASDDLSTLRKRMALFOQLCVLPILD 480  
 DB 421 GENTKTVDIVSALLNADEREKREKEKQAEEMASDDLSTLRKRMALFOQLCVLPILD 480  
 QY 481 NLKANVINKEHDIKOKTOIPLQARELIDTILVKGNAANIFKNCLEIDSTLYKNLF 540  
 DB 481 NLKANVINKEHDIKOKTOIPLQARELIDTILVKGNAANIFKNCLEIDSTLYKNLF 540  
 QY 541 VDNMKKIPTEDVSGLSLEBQLRLQERCTCKVCMDEKVSVPFPCGHLVQCECAPSLR 600  
 DB 541 VDNMKKIPTEDVSGLSLEBQLRLQERCTCKVCMDEKVSVPFPCGHLVQCECAPSLR 600  
 QY 601 KCPICRGIIKGTVPFLS 618  
 DB 601 KCPICRGIIKGTVPFLS 618

## RESULT 7

AAW13555 standard; Protein; 612 AA.

AAW13555;

22-JUL-1997 (first entry)

Murine c-IAP.

IAP; Inhibitor; apoptosis; RING finger domain; restinosis;

myocardial infarction; nephritis; HIV.

Mus musculus.

WO9706182-A1.

20-FEB-1997.

06-AUG-1996; 96WO-0512860.

08-DEC-1995; 95US-0569749.

08-AUG-1995; 95US-0512946.

(TULA-) TULARIK INC.

Goeddel DV, Rothe M;

WPI; 1997-154209/14.

N-PSDB; AAT61592.

Nucleic acids encoding cellular inhibitor of apoptosis proteins

useful for apoptosis regulation in cells to reduce or increase

apoptosis and for pharmacological screening

Disclosure; Page 28-29; 35pp; English.

The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -

AAW61590/761591) comprise a series of defined structural domain

repeats and/or a RING finger domain; in particular, at least two of

a first domain repeat (AAW13547 or AAW13548), a second domain repeat

(AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)

and/or a RING finger domain (AAW13553 or AAW13554), or a consensus

sequences derived from these human genes.

The nucleic acid is used for recombinant prodn. of human cellular

inhibitor of apoptosis protein which modulates apoptosis

regulation. The nucleic acids are useful in therapies where

increased cell-specific apoptosis is desired, e.g. in restinosis,

inflammatory disease states, myocardial infarction, glomerular

nephritis, transplant rejection and infectious diseases, e.g. HIV.

They can also be used in conditions requiring a reduction in

CC apoptosis.

Sequence 612 AA;

Query Match 83.2%; Score 2728; DB 18; Length 612;

Best Local Similarity 83.4%; Pred. No. 2.3e-235;

Matches 517; Conservative 45; Mismatches 48; Indels 10; Gaps 6;

1 MKRTASQRLFPGPSYONIKSIMEDSTILSDWTSNKKOKMYDFSCELYRMSTYTPAGY 60

1 MDRTVSQRLGQGLHOKTKRKIMEKSTILSNWTESEKMFDFSCELYRMSTYTPAGY 60

61 PVSESLARAGFYTYGVNDKVCFCGGLMDNKLDSPLQKOKYLPSCSFYONIVSAS 120

61 PVSESLARAGFYTYGVNDKVCFCGGLMDNKKGGSPKPKRQPTPSCSFYOTILSAS 120

121 LGSTSKNTSPMRNSFAHSLSPTLHSSLSFGSYSLSPNPLNSRAVEDISSSTPNYSYA 180

121 LGSPSKNMSPVKSRFAHS-SP-LEP---GSHSNLCSSPLNSRAVEDF-SSRQDPCSYA 173

181 MSTEARFLTYHMPLTFLSPSELARAGFYTYGPRVACFACGGLSNWEPDAMSEH 240

174 MSTEARFLTYSMWPLSFSPSELARAGFYTYGPRVACFACGGLSNWEPDAMSEH 233

241 RRHFPNCPLENSLETLRFSISNLSMOTHAARMRTFMWPPSSVQPEOLASGFYVGR 300

234 RRHFPNCPLENSLETLRFSISNLSMOTHAARMRTFMWPPSSVQPEOLASGFYVDR 293

301 NDDVCFCCDGGGLRCWESGDDPWEHAKEPCEFLIRKGOEFVDEIOGRYPHLEOLL 360

294 NDDVCFCCDGGGLRCWEPGDDPWIEHAKEPCEFLIRKGOEFVDEIOGRYPHLEOLL 353

361 STSDTGEENADP-PIHFGGSSSEDVAMNTPVYKSALEMGNRLVQTVQSKIL 418

354 STSDTGEENADPTEVYVHGPGE-SEEDVVMSTVVAALMGFSRSLSVQTVQRL 412

419 TTGENTKTVDIVSALLNADEREKREKEKQAEEMASDDLSTLRKRMALFOQLCVLP 478

413 ATGENTKTVDIVSALLNADEREKREKEKQAEEMASDDLSTLRKRMALFOQLCVLP 472

479 LDNLKANVINKEHDIKOKTOIPLQARELIDTILVKGNAANIFKNCLEIDSTLYKN 538

473 LDNLKASVYTKOEHDIKOKTOIPLQARELIDTILVKGNAANIFKNCLEIDSTLYKN 532

539 LFVDMKMKYIPTEDVSGLSLEBQLRLQERCTCKVCMDEKVSVPFPCGHLVQCECAPS 598

533 LFVEKMKKIPTEDVSGLSLEBQLRLQERCTCKVCMDEKVSVPFPCGHLVQCECAPS 592

599 LKCPICRGIIKGTVPFLS 618

593 LKCPICRGIIKGTVPFLS 612

RESULT 8

AAW69299

AAW69299 standard; Protein; 612 AA.

AAW69299;

13-NOV-1998 (first entry)

Murine HIAP-2 protein.

Inhibitor of apoptosis protein; apoptosis enhancer; NADP polypeptide;

proliferative disease; IAP; therapy; cancer; mouse; HIAP-2 protein.

Mus sp.

WO9835693-A2.

20-AUG-1998.

13-FEB-1998; 98WO-IB00781.

XX 13-FEB-1997; 97US-0800929.  
 PR (UYOT-) UNIV OTTAWA.  
 XX  
 PA  
 XX  
 PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;  
 PI Tsang B;  
 XX WPI: 1998-467164/40.  
 DR N-PSDB; AAV55043.  
 XX  
 PT Inducing apoptosis in proliferative mammalian cells with inhibitor  
 PT of IAP or NAIP polypeptide - also methods for prognosis based on  
 PT presence of IAP and NAIP, specifically applied to cancers involving  
 PT p53 mutations  
 PS  
 PS Disclosure: Fig 6; 147pp; English.  
 XX  
 CC This sequence is the murine HIAP-2 protein, which is a inhibitor of  
 CC apoptosis protein (IAP), and can be used in the method of the invention.  
 CC The method is for enhancing apoptosis in cells from a mammal with  
 CC proliferative disease by treatment with a compound that inhibits  
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
 CC compounds are used to treat proliferative diseases, specially cancers of  
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
 CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,  
 CC rectum, cervix or endometrium, particularly to increase their sensitivity  
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
 CC detected in many cancers and are associated with poor prognosis.  
 CC resistance to chemotherapeutic agents and mutations in p53 (it is  
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
 CC genes). Transgenic animals are used for testing the effects of antisense  
 CC oligonucleotides and for screening for the inhibitors.  
 CC  
 SQ Sequence 612 AA:  
 Query Match 83.1%; Score 2724; DB 15; Length 612;  
 Best Local Similarity 83.2%; Pred. No. 5.2e-23;  
 Matches 516; Conservative 46; Mismatches 48; Indels 10; Gaps 6;  
 Oy 1 MHKTSORLFPQSPYONKSIEMEDSTIISDMTNSKQKKYFSCELYRMTSTFFPAGV 60  
 Db 1 MDKTSORLGGTGHQKLRIMEKSTIISNWKESSEKMKPFSCELYRMTSTFFPAGV 60  
 Oy 61 PYSESLARAGYYTGVNDKVKFCFCGLMDNWKLGSDPIOKHQLYPCSEFIQNVSNAS 120  
 Db 61 PYSESLARAGYYTGVNDKVKFCFCGLMDNWKQSDSPVEKHQRFYSCSFVQLLSAS 120  
 Oy 121 LGSTSKNTSPMNSFAHSLSPLEHSLFSGSYSLSPNPLNRAVEDISSRTPIYSYA 180  
 Db 121 LQSPKNNSPKSRPAHS-SP-LEP---GGIHSNLCSSPLNSRAVEDF-SSRMDPCSYA 173  
 Oy 181 MSTEAREFLTYHMPLETLSPSELARAGYYTIGPDRAVACFGKLSMWEKDKDAMSEH 240  
 Db 174 MSTEAREFLTYHMPLETLSPSELARAGYYTIGPDRAVACFGKLSMWEKDKDAMSEH 233  
 Oy 241 RHHFNCPELNSLTLRFSISNLSMOTHAMRFTMTSSVVPQPOLASAGYYVGR 300  
 Db 234 RHHFNCPELNSLTLRFSISNLSMOTHAMRFTMTSSVVPQPOLASAGYYVGR 293  
 Oy 301 NDDVACFCDDGRLCMESGDDPWEHAKWFPCEFLIRKKGGEIVDELOGRYPHILEQL 360  
 Db 294 NDDVACFCDDGRLCMESGDDPWEHAKWFPCEFLIRKKGGEIVDELOGRYPHILEQL 353  
 Oy 361 STSDTTEGENADP--PIIHFGPSESSSDAVMMNPVYKSALENGFNRLDYKQVOSKIL 418  
 Db 354 STSDPGEENADPTEFVYHFGPE--SKRDVMMSTPVYKAALENGFSRLVQYQOROL 412  
 Oy 419 TTGENYKYNDIVSALLNADEKREKEKQAEASDDLIRNRNALFOQLTCVLP 478  
 Db 413 AGENYRTVNDIVSALLNADEKREKEKQAEASDDLIRNRNALFOQLTCVLP 472  
 Oy 479 LDNLKANYINQOEHDIIKQTOIPLQARELIDTILVGNMAANIFKNLKRKIDSTIVKN 538

Db 473 LDNLLEASVITKOEHDIIKQTOIPLQARELIDTILVGNMAANIFKNLKRKIDSTIVKN 532  
 Oy 539 LEVDKMKYITPEVYSGLSLEOLRLLOEERCKYCMDESVYFPCGHLVYCOECAPS 598  
 Db 533 LEVEKMKYITPEVYSGLSLEOLRLLOEERCKYCMDESVYFPCGHLVYCOECAPS 592  
 Oy 599 LRKPCIRGIIKGVTRFELS 618  
 Db 593 LRKPCIRGIIKGVTRFELS 612  
 RESULT 9  
 AAW19586  
 ID AAW19586 standard; Protein: 591 AA.  
 AC AAW19586;  
 XX  
 DT 02-SEP-1997 (first entry)  
 XX  
 DE Mouse apoptosis inhibitor M-HIAP-2.  
 XX  
 KW Apoptosis inhibitor; M-HIAP-2; HIV; AIDS; neurodegeneration;  
 KW myelodysplastic syndrome; ischaemia; myocardial infarction; stroke;  
 KW reperfusion injury; toxin-induced liver disease; gene therapy;  
 KW diagnosis.  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 25..92  
 FT Domain /label- BIR-1  
 FT Domain 156..222  
 FT Domain /label- BIR-2  
 FT Domain 241..308  
 FT Domain /label- BIR-3  
 FT Domain 541..578  
 FT Domain /label- Ring\_zinc\_finger  
 FT  
 XX  
 XX WO9706255-A2.  
 PD 20-FEB-1997.  
 XX  
 PF 05-AUG-1996; 96WO-IB01022.  
 XX  
 PR 22-DEC-1995; 95US-0576956.  
 PR 04-AUG-1995; 95US-0511485.  
 XX  
 PA (UYOT-) UNIV OTTAWA.  
 XX  
 PI Baird S, Korneluk RG, Liston P, Mackenzie AE;  
 DR WPI: 1997-154262/74.  
 DR N-PSDB; AAT70841.  
 XX  
 PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used  
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection  
 PT of susceptibility to apoptotic disease  
 PS  
 PS Claim 30; Page 100-102; 219pp; English.  
 CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and  
 CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that  
 CC are inhibitors of apoptosis (IAP) and which are characterized by  
 CC the presence of a ring zinc finger domain (see also AAW19587) and at  
 CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).  
 CC The M-HIAP amino acid sequences were deduced from isolated m-hiap  
 CC cDNA clones (AAT70840-41). IAP polypeptides can be expressed in host  
 CC cells (in vitro or in vivo) and used in methods for treating  
 CC diseases and disorders involving apoptosis, esp. in a human  
 CC diagnosed as HIV-positive or as having AIDS, a neurodegenerative  
 CC disease, a myelodysplastic syndrome or an ischemic injury, selected  
 CC from myocardial infarction, stroke, reperfusion injury, or a toxin-





QY 500 TQPIQARLIDITLVKGNAAANIFKNCLEIDSTLYKMLFVDKMKYIPTEDVSGLSLE 559  
 DB 473 TQPIQARLIDITLVKGNAAANIFKNSLKGIDSTLYENLFYEKNKKYIPTEDVSGLSLE 532  
 QY 560 EOLRLQERTCKVCMDEKVSIVFPCGHLVYCOBCAPSLRKCPCITGRIKGVRFELS 618  
 DB 533 EOLRLQERTCKVCMDEKVSIVFPCGHLVYCOBCAPSLRKCPCITGRIKGVRFELS 591

## RESULT 11

AAW19747  
 ID AAW19747 standard: Protein; 604 AA.

AC AAW19747;  
 DT 16-SEP-1997 (first entry)  
 DE Human inhibitor of apoptosis protein homologue MHC.  
 KM Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MHC;  
 KW degenerative disease; infectious disease; autoimmune disease;  
 cancer; therapy; diagnosis.  
 OS Homo sapiens.

Key Location/Qualifiers  
 FH Region 29..97  
 FT /label= BIR  
 FT 169..236  
 FT /label= BIR  
 FT 255..323  
 FT /label= BIR  
 FT 556..593  
 FT /label= RING\_finger

PN MO9723501-A1.  
 PD 03-JUL-1997.  
 PF 20-DEC-1996; 96WO-AU00827.  
 PR 22-DEC-1995; 95AU-0007275.  
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 PI Vaux DL;

DR MPI; 1997-350966/32.  
 DR N-PSDB; AAT72712.  
 PT Isolated protein homologues of viral inhibitors of apoptosis - used  
 PT to modulate apoptosis for treatment of degenerative, infectious or  
 PT autoimmune diseases and cancer  
 PS Claim 9; Page 58-62; 136pp; English.

CC Mammalian IAP homologue C (MHC) (AAW19747) is a human homologue of  
 CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid  
 CC sequence was deduced from a cDNA clone (see also AAT72712) isolated  
 CC from a human foetal liver cDNA library using primers based on  
 CC human EST sequences that resembled the BIR repeats of Orygia  
 CC pseudotsuguta polyhedrosis virus IAP. IAP homologues (see also  
 CC AAW19745-46 and AAW19748-52) and their derivatives and chemical  
 CC analogues can be used in methods for modulating apoptosis in animal  
 CC cells, specifically for treatment, by inhibition, of degenerative  
 CC and infectious disease or, by promotion, of cancer and autoimmune  
 CC disease.

SO Sequence 604 AA;

Query Match 71.8%; Score 2353; DB 18; Length 604;  
 Best Local Similarity 72.8%; Pred. No. 9.4e-202;

Matches 440; Conservative 71; Mismatches 87; Indels 6; Gaps 5;  
 QY 20 SIMEDSTLSDWTNS-NKQMKRYDESCLELYRMSTYSPAGVPSERSLRAGFYTYGVN 78  
 DB 2 NIVENSIFLSNLMKSAANTFELKYLDSCELYRMSTYSTPAGVPSERSLRAGFYTYGVN 61  
 QY 79 DRYKFCGCCGLMDNNKLGDSPIQKQLYPSCSFIONLYSA-SLGSTSKNTSP--NRNF 135  
 DB 62 DRYKFCGCCGLMDNNKLGDSPIQKQLYPSCSFIONLYSA-SLGSTSKNTSP--NRNF 120  
 QY 136 AHSLSPTLHSSLSFGSSVSLSPNPLNSRAVEDISSRTNPYSYANSTAEARFLRYHMP 195  
 DB 121 THSLPTEENSGYFRGSIYNSPNSRANODFSALMSSTHCANNANARLLFTQTP 180  
 QY 196 LTFLSPEELARAGFYIIGPDRVACFACGKLSNNEPKDAMSEHRHPNCPFLSNL- 254  
 DB 181 LTFLSPTDLAKAGFYIIGPDRVACFACGKLSNNEPKDAMSEHRHPNCPFLSNL- 240  
 QY 255 ETLRFSISNLSMOTHAARKRTMYPPSSVYPVQPEOLASAGFYTYGVNDRNDYKFCDCGGLR 314  
 DB 241 DTSRYTVSNLSMOTHAARKRTMYPPSSVYPVQPEOLASAGFYTYGVNDRNDYKFCDCGGLR 300  
 QY 315 CWESGDDPWEHAKMPPRCFLIRKKGDFVDEIOGRYPHLEOLLSTSDTGEENADPP 374  
 DB 301 CWESGDDPWEHAKMPPRCFLIRKKGDFVDEIOGRYPHLEOLLSTSDTGEENADPP 360  
 QY 375 IIFGPGESSSEDVAMNTPVYKSALEMGFNLDVQKQVQSKILTGENYKTVNDIVSAL 434  
 DB 361 IIFGPGESSSEDVAMNTPVYKSALEMGFNLDVQKQVQSKILTGENYKTVNDIVSAL 420  
 QY 435 LNADEKREERKQAEASDLSLRKRNALCOQLCVPIIDNLKAVINKEOHD 494  
 DB 421 LNADEKREERKQAEASDLSLRKRNALCOQLCVPIIDNLKAVINKEOHD 480  
 QY 495 IIKQKQIPLQARELIDITLVKGNAAANIFKNCLEIDSTLYKMLFVDKMKYIPTEDVS 554  
 DB 481 VKQKQIPLQARELIDITLVKGNAAANIFKNCLEIDSTLYKMLFVDKMKYIPTEDVS 540  
 QY 555 GLSLEQRLRLQERTCKVCMDEKVSIVFPCGHLVYCOBCAPSLRKCPCITGRIKGV 614  
 DB 541 GLSLEQRLRLQERTCKVCMDEKVSIVFPCGHLVYCOBCAPSLRKCPCITGRIKGV 600  
 QY 615 TFLS 618  
 DB 601 TFLS 604

## RESULT 12

AAW13546  
 ID AAW13546 standard: Protein; 604 AA.

AC AAW13546;  
 DT 22-JUL-1997 (first entry)  
 DE Human c-IAP2.

KW IAP; inhibitor; apoptosis; RING finger domain; restinosis;  
 KW myocardial infarction; nephritis; HIV.

OS Homo sapiens.

PN WO9706182-A1.

PD 20-FEB-1997.

PF 06-AUG-1996; 96WO-US12860.

PR 08-DEC-1995; 95US-0569749.

PA (TULAR) TULARIK INC.



```

Db 2 NIVENSIFLSNLMKSNTELEKTDLSCELYRMSTYTFPAGVVSRSRLARAGFYTGVA 61
Qy 79 DKVCCFCGGLMDNMKLGDSPIQKHQOLYPCSCFIONLYSA-SLGSTSKNTSP--NRNSF 135
Db 62 DKVCCFCGGLMDNMKRGSPTEKHKKLYPCSCFYVSLNSVNNLEATSOQTFPSSVTNS- 120
Qy 136 AHSLSPTLEHSSLFSGSYSLSPNPLNSRAVEDISSRNPYSYAMSTEARLYTHMMP 195
Db 121 THSLPTGTEHSGYFSGSYSPSPNPNVSRANDOFSAIMRSSTYCANNNENARLLTFOQTP 180
Qy 196 LFLSPSELARAGFYIIGDPRVACFACGKLSNWEPKDAMSEHRHHPNCPFLNSU- 254
Db 181 LFLSPSELARAGFYIIGDPRVACFACGKLSNWEPKDAMSEHRHHPNCPFLNSU- 240
Qy 255 ETLRFISINLSMOTHAARMTEFMYMPSVYPVOEOLASAGFYVGRNDVCKCCDGLR 314
Db 241 DTSRYTVSNLSMOTHAARMTEFMYMPSVYPVOEOLASAGFYVGRNDVCKCCDGLR 300
Qy 315 CWSSGDDPVMVHAHAKMPFCEYLIRKGOEFVDEIQRYPHLEQLLSTSDTTEENADPP 374
Db 301 CWSSGDDPVMVHAHAKMPFCEYLIRKGOEFVDEIQRYPHLEQLLSTSDTTEENADPP 360
Qy 375 IIFHGGESESSDVAVMANTPVVKSALMGFNRDLVQVOSKLTITGENTKYNDIVSAL 434
Db 361 IIFHGGESESSDVAVMANTPVVKSALMGFNRDLVQVOSKLTITGENTKYNDIVSAL 420
Qy 435 LNADEKREERKEKQAEEMASDLSLRKRMALFOQLTCVPLIDNLKAVYNKOEHD 494
Db 421 LNADEKREERKEKQAEEMASDLSLRKRMALFOQLTCVPLIDNLKAVYNKOEHD 480
Qy 495 IIFHGGESESSDVAVMANTPVVKSALMGFNRDLVQVOSKLTITGENTKYNDIVSAL 554
Db 481 IIFHGGESESSDVAVMANTPVVKSALMGFNRDLVQVOSKLTITGENTKYNDIVSAL 540
Qy 555 GLSLEBQLRLQERCKCKMCKEVSIVIFPCGHLVYVOCBAPSLKRCPIKCRITGTVA 614
Db 541 GLSLEBQLRLQERCKCKMCKEVSIVIFPCGHLVYVOCBAPSLKRCPIKCRITGTVA 600
Qy 615 TFLS 618
Db 601 TFLS 604

```

RESULT 14  
AA19582  
ID AA19582 standard; Protein: 604 AA.  
XX  
AC AA19582;  
XX  
DT 26-NOV-1999 (first entry)  
XX  
DE Human cellular inhibitor of apoptosis-2 sequence.  
XX  
KW Cellular inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;  
KM c-IAP-2; prophylaxis; infection; inflammation; tumor formation.  
XX  
OS Homo sapiens.  
XX  
PN US5958771-A.  
XX  
PD 28-SEP-1999.  
XX  
PF 03-DEC-1998; 98US-0205144.  
XX  
PR 03-DEC-1998; 98US-0205144.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Bennett CF, Cowser LM, Ackermann EJ;  
XX  
DR WPI; 1999-561046/47.  
XX  
N-PSDB; AA222096.  
XX

```

Pt Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2
Xt useful for e.g. diagnostics, therapeutics, and as research reagents -
Xx Example 13; Columns 45-50; 33pp; English.
Cc The invention provides antisense compounds of 8-30 nucleotides that
Cc inhibit the expression of human Cellular Inhibitor of Apoptosis-2
Cc (c-IAP-2). The antisense compounds may be used for diagnostics,
Cc therapeutics (for modulating the expression of c-IAP-2), prophylaxis
Cc (e.g. to prevent or delay infection, inflammation, or tumor formation),
Cc as research reagents (e.g. to distinguish between members of a biological
Cc pathway) and in kits. The present sequence represents the human cellular
Cc inhibitor of apoptosis-2.
Xx
Sq Sequence 604 AA:
Query Match 71.8%; Score 2353; DB 20; Length 604;
Best Local Similarity 72.8%; Pred. No. 9,4e-202;
Matches 440; Conservative 71; Mismatches 87; Indels 6; Gaps 5;
Qy 20 SIMEDSTIISDWTNS-NKMKYDFSCELYRMSTYTFPAGVVSRSRLARAGFYTGVA 78
Db 2 NIVENSIFLSNLMKSNTELEKTDLSCELYRMSTYTFPAGVVSRSRLARAGFYTGVA 61
Qy 79 DKVCCFCGGLMDNMKLGDSPIQKHQOLYPCSCFIONLYSA-SLGSTSKNTSP--NRNSF 135
Db 62 DKVCCFCGGLMDNMKRGSPTEKHKKLYPCSCFYVSLNSVNNLEATSOQTFPSSVTNS- 120
Qy 136 AHSLSPTLEHSSLFSGSYSLSPNPLNSRAVEDISSRNPYSYAMSTEARLYTHMMP 195
Db 121 THSLPTGTEHSGYFSGSYSPSPNPNVSRANDOFSAIMRSSTYCANNNENARLLTFOQTP 180
Qy 196 LFLSPSELARAGFYIIGDPRVACFACGKLSNWEPKDAMSEHRHHPNCPFLNSU- 254
Db 181 LFLSPSELARAGFYIIGDPRVACFACGKLSNWEPKDAMSEHRHHPNCPFLNSU- 240
Qy 255 ETLRFISINLSMOTHAARMTEFMYMPSVYPVOEOLASAGFYVGRNDVCKCCDGLR 314
Db 241 DTSRYTVSNLSMOTHAARMTEFMYMPSVYPVOEOLASAGFYVGRNDVCKCCDGLR 300
Qy 315 CWSSGDDPVMVHAHAKMPFCEYLIRKGOEFVDEIQRYPHLEQLLSTSDTTEENADPP 374
Db 301 CWSSGDDPVMVHAHAKMPFCEYLIRKGOEFVDEIQRYPHLEQLLSTSDTTEENADPP 360
Qy 375 IIFHGGESESSDVAVMANTPVVKSALMGFNRDLVQVOSKLTITGENTKYNDIVSAL 434
Db 361 IIFHGGESESSDVAVMANTPVVKSALMGFNRDLVQVOSKLTITGENTKYNDIVSAL 420
Qy 435 LNADEKREERKEKQAEEMASDLSLRKRMALFOQLTCVPLIDNLKAVYNKOEHD 494
Db 421 LNADEKREERKEKQAEEMASDLSLRKRMALFOQLTCVPLIDNLKAVYNKOEHD 480
Qy 495 IIFHGGESESSDVAVMANTPVVKSALMGFNRDLVQVOSKLTITGENTKYNDIVSAL 554
Db 481 IIFHGGESESSDVAVMANTPVVKSALMGFNRDLVQVOSKLTITGENTKYNDIVSAL 540
Qy 555 GLSLEBQLRLQERCKCKMCKEVSIVIFPCGHLVYVOCBAPSLKRCPIKCRITGTVA 614
Db 541 GLSLEBQLRLQERCKCKMCKEVSIVIFPCGHLVYVOCBAPSLKRCPIKCRITGTVA 600
Qy 615 TFLS 618
Db 601 TFLS 604

```

RESULT 15  
AA19582  
ID AA19582 standard; Protein: 604 AA.  
XX  
AC AA19582;  
XX  
DT 02-SEP-1997 (first entry)  
XX



Gencore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:58:42 ; Search time 67.6382 Seconds

(without alignments)  
878.365 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277  
Sequence: 1 MHKTASQRLFPSPSYONIKS.....LAKPCICGIIKGVITPLS 618

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3247	99.1	618	2	S68450	apoptosis inhibitor
2	2332	71.2	604	2	S68449	apoptosis inhibitor
3	1332	46.8	358	2	JC5964	apoptosis inhibitor
4	908	27.7	497	2	S69544	apoptosis inhibitor
5	737	22.5	497	2	S69545	apoptosis inhibitor
6	723.5	22.1	496	2	S68452	apoptosis inhibitor
7	513	15.7	268	2	T10304	apoptosis inhibitor
8	513	15.7	268	2	A53989	apoptosis inhibitor
9	468	14.3	1447	2	T42628	apoptosis-inhibitor
10	463	14.1	1232	2	A53478	neutonal apoptosis
11	461	14.1	275	2	A45678	neutonal apoptosis
12	460.5	14.1	258	2	JC7568	inhibitor-of-apopt
13	240	7.3	292	2	T41772	kidney inhibitor c
14	237.5	7.2	997	2	T43523	IAP1 orf127 - Bomby
15	235.5	7.2	286	2	D36828	cut17 protein - Au
16	223.5	6.8	275	2	T10310	apoptosis-inhibiti
17	194	5.9	4845	2	T13067	BIR repeat contain
18	186.5	5.7	316	2	T33259	hypothetical prote
19	181.5	5.5	711	2	C84767	hypothetical prote
20	175.5	5.4	208	2	T03183	probable apoptosi
21	169	5.2	150	2	T28409	ORF MSY248 probabl
22	165	5.0	943	2	S68824	rns protein, cyto
23	161	4.9	155	2	T30489	apoptosis inhibitor
24	156	4.8	823	2	D86165	protein f15K9.3 [1
25	152	4.6	234	2	T30427	probable apoptosi
26	152	4.6	304	2	T04751	hypothetical prote
27	146	4.5	870	2	G86450	F5D14.31 protein -
28	144	4.4	249	2	H72858	apoptosis inhibitor
29	142	4.3	249	2	T41814	IAP2 orf71 - Bomby

30	140.5	4.3	785	2	T00474 hypothetical prote
31	138	4.2	372	2	C96631 hypothetical prote
32	137.5	4.2	236	2	T10343 inhibitor of apopt
33	137	4.2	614	2	S42526 finger protein unk
34	136.5	4.2	864	2	T01393 apoptos inhibitor
35	131.5	4.0	899	2	D6594 unknown protein, 7
36	131	4.0	308	2	T37474 apoptos inhibitor
37	130	4.0	115	2	B96664 ORF MSY242 probabl
38	129.5	4.0	329	2	T28403 hypothetical prote
39	128	3.9	347	2	T01044 probable sensory t
40	128	3.9	1639	2	T50119 probable zinc fing
41	126	3.8	145	2	S77736 hypothetical prote
42	124.5	3.8	383	2	F96582 RING finger protei
43	124	3.8	433	2	JC7678 cytoxin L - Clos
44	122	3.7	2364	2	I40884 hypothetical prote
45	121.5	3.7	708	2	T00064

ALIGNMENTS

RESULT 1									
S68450 apoptos inhibitor hlap-2 - human									
C:Species: Homo sapiens (man)									
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000									
C:Accession: S68450									
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha									
Nature 379, 349-353, 1996									
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of									
A:Reference number: A58182; PMID:96149249; PMID:8552191									
A:Accession: S68450									
A:Status: nucleic acid sequence not shown									
A:Molecule type: mRNA									
A:Residues: 1-618 <LIS>									
A:Cross-references: EMBL:45879; NID:g1184317; PIDN:AC50372.1; FID:g1184318									
C:Function:									
A:Description: apoptotic suppressor									
C:Superfamily: RING finger homology									
C:Keywords: apoptos; zinc finger									
F:567-611/Domain: RING finger homology <RING>									
Query Match									
Best Local Similarity 99.1%; Score 3247; DB 2; Length 615;									
Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;									
QY	1	MHKTASQRLFPSPSYONIKSIMEDSTILSDWTNSNKKYDFSCELYRMYSTYRPAQY	60						
DB	1	MHKTASQRLFPSPSYONIKSIMEDSTILSDWTNSNKKYDFSCELYRMYSTYRPAQY	60						
QY	61	PYSERSLARAGFYTVGVNDKVCFCGGLMDNKKLGDSPIQKHQOLYPSCSFIQNLVSAS	120						
DB	61	PYSERSLARAGFYTVGVNDKVCFCGGLMDNKKLGDSPIQKHQOLYPSCSFIQNLVSAS	120						
QY	121	LGSTSNTPMNRNSFAHSLSPTLHSSLSFGSYSSLPPLNSRAVEDISSFTNPSYA	180						
DB	121	LGSTSNTPMNRNSFAHSLSPTLHSSLSFGSYSSLPPLNSRAVEDISSFTNPSYA	180						
QY	181	MSTEARFLTYHMMPLTFLSPSELARAGFYIIGPGRVACFCAGGKLSNMWEPDDAMSH	240						
DB	181	MSTEARFLTYHMMPLTFLSPSELARAGFYIIGPGRVACFCAGGKLSNMWEPDDAMSH	240						
QY	241	RRFPNCPFLNSLETLRHSISLMSQTHAARMTYMPSSVPVQPEOLAAGFYTVGR	300						
DB	241	RRFPNCPFLNSLETLRHSISLMSQTHAARMTYMPSSVPVQPEOLAAGFYTVGR	300						
QY	301	NDVVKFCDCDGLRCWESGDDPVEVHAKEPPECFILRMKGOFVDEIGRYPHLEQL	360						
DB	301	NDVVKFCDCDGLRCWESGDDPVEVHAKEPPECFILRMKGOFVDEIGRYPHLEQL	360						
QY	361	STSDTTEENADPPIIHFGPGSSSSSDAVMNTPVVKSALENGFNLDVKTQVQSKILT	420						
DB	361	STSDTTEENADPPIIHFGPGSSSSSDAVMNTPVVKSALENGFNLDVKTQVQSKILT	420						



C:Species: Homo sapiens (man)  
C:Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Nov-2000  
C:Accession: S69544; S68451  
R:Ducret, C.S.; Nava, V.E.; Gedlich, R.W.; Clem, R.J.; van Dongen, J.L.; Giffillan, M.C.  
EMBO J. 15, 2685-2694, 1996  
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and er  
A:Reference number: S69544; MUID:96256286; PMID:6654366  
A:Accession: S69544  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-497 <DUC>  
A:Cross-references: EMBL:U32974; NID:g1016687; PION:AAC50518.1; PID:g1016688  
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Chetton-Horvat, G.; Farhani,  
Nature 379, 349-353, 1996  
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP  
A:Reference number: A58182; MUID:96149249; PMID:8952191  
A:Accession: S68451  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>  
A:Cross-references: EMBL:U45860; NID:g1184319; PION:AAC50373.1; PID:g1184320  
C:Genetics:  
A:Gene: 11p  
C:Function:  
A:Description: apoptotic suppressor  
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology  
C:Keyword: apoptosis, zinc finger  
F:446-490/Domain: RING finger homology <RNR>

Query Match 27.7%; Score 908; DB 2; Length 497;  
Best Local Similarity 33.8%; Pred. No. 4.8e-55;  
Matches 205; Conservative 88; Mismatches 164; Indels 150; Gaps 14;

QY 35 NKKKMTDSCCLYRSTYSTFPAQVPSERSLARAGFYTYGVNDKVCFCGGLMDNMK 94  
DB 18 NKDE---EFVEENRRLKTFANFSGSEVSASTARAGFLTGEDVYRCFSCHAAVDWQ 74  
QY 95 LGSPLOKHOLYPCSFIONLVASIGSTSKTSPMRNSE-AHSLPTLHESLSGVS 153  
DB 75 YGSAVGRHKKVSPNCFIIGFLYENSATVSTINGOYKVENTLGSKHFDLPDS- 133  
QY 154 SLSPLNPLNSRAVEDISSRTNPYSYAMSTEARFLTYHWP-LTFLSPSELARAGFY 212  
DB 134 ETHADYLFRTGYVDSDT-IYPRNPAMYSEARLKSFOQWMPYAHILTPRELASAGLY 192  
QY 213 GPDRAVACFCGKLSNWEKDKDAMSEHRRHFPNCPFL-----EN 252  
DB 193 GIDDOVCCFCGCGKLNWEPDRAMSEHRRHFPNCFVILRLINRSESDAVSDRNFPN 252  
QY 253 SLETLRFSISNLMOGTHAARMTFMYPSVPQPOLASAGFYTYGVNDVGCFCDDG 312  
DB 253 STULPR---NPSMADTEARITFTGWTYS--VNKQLARAGFYALGEGDKVCFHCGGG 306  
QY 313 LRCMESGDDPWFVNAKMPFPCFELIRKGFYDEIQGRPHLEQ-LTSTSTGGENA 371  
DB 307 LTMKRSSEDPWEHAKWPCCKYLLDQKGEYINNI--HLTHLEBELVATTEKT----- 359  
QY 372 DPEIIFHFGESSEDAVMNTPYKSALEMGNRDLVKOTVOSKITLTGENTKYNDIV 431  
DB 360 -----PDLTRRIDDTIQNPVOEALIMGFSFKDIKIMEKIQISSNYSLEVL 411  
QY 432 SALLNADEDEREEKKQAEASDDLSLRKRMALFOQLTVLPILDLMLANVINYO 491  
DB 412 ADLVNAOKDSMPDE----- 425  
QY 492 EHDIIKOKTQIPLQARELIDTILVGNAAANIFKNCLEIDSTLYKNLFVDKMKYIPT 551  
DB 426 -----SSQTSIQ-----KEL----- 435  
QY 552 DVSGSLSEBQLRLOEBRTCKVCMDEKESVYVTPCGHLVVCQCAPSLRKCPICRGIT 611  
DB 436 -----STEEQLRLQEBKCKICMDRNIAIVFPCGHLVYCKOQAEAVDKCPMCYVIT 490

QY 612 TVRTPLS 618  
DB 491 KOKIFMS 497

RESULT 5

apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000

C:Accession: S69545

R:Ducret, C.S.; Nava, V.E.; Gedlich, R.W.; Clem, R.J.; van Dongen, J.L.; Giffillan,

EMBO J. 15, 2685-2694, 1996

A:Title: A conserved family of cellular genes related to the baculovirus iap gene and

A:Reference number: S69544; MUID:96256286; PMID:6654366

A:Accession: S69545

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-497 <DUC>

A:Cross-references: EMBL:U32373; NID:g1019116; PIDN:AAC47155.1; PID:g1019117

C:Genetics:  
A:Gene: 11p

C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology

F:446-490/Domain: RING finger homology <RNR>

Query Match 22.5%; Score 737; DB 2; Length 497;  
Best Local Similarity 30.6%; Pred. No. 3.2e-43;  
Matches 180; Conservative 82; Mismatches 212; Indels 114; Gaps 15;

QY 46 ELYRMSTYSPFPAQVPSERSLARAGFYTYGVNDKVCFCGGLMDNMK 105  
DB 9 ESVRLATFGEMPLNAPVSAEDLVANGFATGNMLEHCFCHVRIDRWEQDQVAAGHR 68  
QY 106 LYPSCSFIONLVASIGSTSKTSPMRNSEAHSLPTLHESLSGVSLSPLNSRA 165  
DB 69 SSPICSMV--LAPNHCGNVP-----SQESDNENGS-- 97  
QY 166 VEDISSRNTPYAMSTEARFLTYHMP-LTFLSPSELARAGFYTYGVNDKVCFCGGLMDNMK 225  
DB 98 VDSPSCSCP--DLLENRLVTRKDPNPNITPOLAKAGFYTLNRLDHYKVCWNG 154  
QY 226 KLSNWEKDKDAMSEHRRHFPNCPFL-----NSLETLRFSISNLMOGTH--AA 271  
DB 155 VIKWKEKNDAFEHHRFPQCPRYOMGLIERATGKNDELGIOTPLRLRKYACVDA 214  
QY 272 RMFTMYWSSVPVQ-EDLASAGFYTYGVNDVGCFCDDGGLRCWESGDDPWFVNAKMP 330  
DB 215 RLRTFTDWPIS-NIQASALAQAGLYOKIGDOVRCFHCNIGIRSWQKEDPEFEBAKWS 273  
QY 331 PREPFLIRKMGOFVDEIQGRPHLEQ-LTSTSTGGENADPPIIHFPGRESSSDAVM 390  
DB 274 PKQFVLLAKGPSYVEVLA-----TTAANASSPPAT--APAPTLQADVLM 317  
QY 391 MNPPVKSALFEMFNLDIKQVQSKILTGTENYKTVNDIVSALLNAEDEKREEKEKA 450  
DB 318 DEAP-AKELALGIDGAVRNALQRLKLSGCAFSTLDELHIFP----- 362  
QY 451 EENASDLSLRKRMALFOQLTVLPILDLMLANVINYOEHDIKOKTQIPLQAREL 510  
DB 363 DAGAGADWRCSREPSAPF-----IPEQATTSKA-----ASVPIPVADSI 403  
QY 511 DTLVGNAAANIFKNCLEIDSTLYKNLFVDKMKYIPTEDVSGSLSEBQLRLOEBRT 570  
DB 404 PAKPOAAEAANISK-----ITDEIQKRSVATPNGNISTLEENLOLDARL 449  
QY 571 CKVCMDEKESVYVTPCGHLVVCQCAPSLRKCPICGIIIGTVRTPLS 618  
DB 450 CKVCMDEKESVYVTPCGHLVVCQCAPSVANCMCADIKGIVRTPLS 497

RESULT 6  
S68452  
apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)

T10304  
inhibitor of apoptosis protein 3 - Orygia pseudotsugata nuclear polyhedrosis virus  
C/Species: Orygia pseudotsugata nuclear polyhedrosis virus, OPMNV  
C/Date: 16-Jul-1999 #sequence.revision 16-Jul-1999 #text.change 15-Sep-2000  
C/Accession: T10304  
R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.  
Virology 229, 381-399, 1997  
A>Title: The sequence of the Orygia pseudotsugata multinnucleocapsid nuclear polyhedro  
A/Reference number: Z17011; MUID:97271300; PMID:9126251  
A/Accession: T10304  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-268 <AHR>  
A:Cross-references: EMBL:U75930; NID:92934903; PID:AA59034.1; PID:91911281  
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology  
F:217-261/domain: RING finger homology <RRN>

Query Match 15.7%; Score 513; DB 2; Length 268;  
Best Local Similarity 24.1%; Pred.No. 4,26-28;  
Matches 107; Conservative 51; Mismatches 86; Indels 200; Gaps 4;

QY 181 MSTEARPLTHAMPPLTFLPSSELARAGFYITIGEDRVACFACGKSLNWEPKDAMSEH 240  
Db 15 MKNRAARGITATNMPVOFLPSRMAASGFYILRGDEVRCAFCCKEYILNWRGDDPETDH 74  
241 RRHFNPCEFLNSLE-----TLRFISNLSMOTHAARTRFMYWSSVVOPEOLAS 292  
QY 75 KRMAPQCCFVANNMADHTPHDRAPPARSAARQYATEARLRTFAEMVRGLKOREELAE 134  
293 AGFYVGNDDYKCFCCDGLRCWESGDDPWEHAKEWPFCEFLIRMGQEFVDEIGRY 352  
Db 135 AGFEYTGCGDGTWRCGCCDGLKDEWEPDAPMOOHARMYDRCEYVLVYVGRFVQK----- 189  
QY 353 PHLEQLLSTDTGTGEENADPTIHFPGESSSEDAVMMNPVYKSALEMGFNRLVKT 412  
Db 190 -----VTFEACVVR----- 198  
QY 413 VQSKLTGTGENYKTVINDIVASLALNADEKREEREKQAEASDDLILRRNMLFOOL 472  
Db 199 -----DADNEPHIERPAVEAE----- 214  
QY 473 TCVLPIDNLKAVYNKQEHDIIKQTOIPLQARELIDTILVKGNAANFNKCLKEID 532  
Db 215 ----- 214  
QY 533 STLYKNLFVDRNMKIPTEDVSGSLSEQLRLQDEERTCKYCKMKEVSEFIPGHLVVC 592  
Db 215 -----VADDRICKICLGAKEKTVCPGCHVAVAC 242  
QY 593 QECAPSLKRCPIKCIKIGIVRTF 616  
Db 243 GKCAAGVTTCPCVCRQGLDKAVRMY 266

RESULT 8  
A53989  
apoptosis-inhibiting protein - Orygia pseudotsugata multinnucleocapsid nuclear polyhedrosis  
C/Species: Orygia pseudotsugata multinnucleocapsid nuclear polyhedrosis virus, OPMNV  
C/Date: 15-Oct-1994 #sequence.revision 15-Oct-1994 #text.change 15-Sep-2000  
C/Accession: A53989  
R:Birnbaum, M.J.; Clem, R.J.; Miller, L.R.  
J. Virol. 68, 2521-2528, 1994  
A>Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a po  
A/Reference number: A53989; MUID:94187094; PMID:8139034  
A:Accession: A53989  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-268 <BIR>  
A:Cross-references: GB:U22564; NID:945611; PID:AA602610.1; PID:9456114  
A:Note: authors translated the codon TGG for residue 28 as Tyr, GAC for residue 50 as  
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology  
F:217-261/domain: RING finger homology <RRN>



Query Match 15.7%; Score 513; DB 2; Length 268;  
 Best Local Similarity 24.1%; Pred. No. 4.2e-28;  
 Matches 107; Conservative 51; Mismatches 86; Indels 200; Gaps 4;

181 MSTEEAFLLTYHMPPLFLSPSELARAGFYIGPDVACGAGKLSNMPKDDAMSEH 240  
 15 MKNAARLGTITMPPVQFLBPSRMAAGFYILRGDEVIKAFCKVEITMNVRODDPTDH 74  
 241 RRHFNCPLENSLE-----TLRFSINLSMOTHAAMKRTPTMPPSSVPPVQEBOLAS 292  
 75 KRMAPQCFEVRNNAHDTPHDRAPPARSAARPOYATEAARLRTFAEMPRGLKQPELAE 134  
 293 AGEFYVRANDVACFCFCCDGLKWESEGDPPVEHAKWFECEFLIRMGGEFVDEIGRY 352  
 135 AGEFYTGQGRKTRCCFCCDGLKWESEGDPPVEHAKWFECEFLIRMGGEFVDEIGRY 189  
 353 PHLEQLLSTSDTTEENADPPIIHFGPSSSEDAVMNTPVYKSALEMGFNRLVKQT 412  
 190 -----VMT3ACVVR----- 198  
 413 VQSKILTGENYKTVNDIVSALLNAEDEKREKEKQAEKASDLSLIRKRMALFQOL 472  
 199 -----DADNPHIERPAVEAE----- 214  
 473 TCVLPIIDNLKANVINKQEHDIKQTKQIPLARLIDPILVKGNAAMIFKNCKLEID 532  
 215 ----- 214  
 533 STLYKNLFDVKNMKYIPTEVDVSLGLEBOLRLQOEERTCVCMDEKVSYYVIFPGHLVVC 592  
 215 -----VADRLCKICIGAEKTVCFVPCGHVVC 242  
 593 QECAPSLRKPCPIRGITIKGYRTF 616  
 243 GKCAAGVTCTPCVCGQLDKAVRM 266

RESULT 9  
 T42628  
 neuronal apoptosis inhibitory protein 2 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000  
 C:Accession: T42628  
 R:Yaraghi, Z.; Diez, E.; Gros, P.; Mackenzie, A.  
 Mamm. Genome 10, 761-763, 1999  
 A:Title: CDNA cloning and the 5' genomic organization of Naip2, a candidate gene for murine  
 A:Reference number: Z22179; MIM:99315342; PMID:10384056  
 A:Accession: T42628  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 11447 <YAR>  
 A:Cross-references: EMBL:AF102871; NID:93860228; PID:93860229; PIDN:AAC73002.1  
 C:Genetics:  
 A:Gene: Naip2

Query Match 14.3%; Score 468; DB 2; Length 1447;  
 Best Local Similarity 25.9%; Pred. No. 6.5e-24;  
 Matches 147; Conservative 73; Mismatches 213; Indels 134; Gaps 19;

21 IMEDSTIL-----SDMTNSNKKMKYDFSC-----CELYRMSTYSTFPAGVPSER 65  
 20 VSELSTILRLDALSVLKROEDBDKTRMKKGFNSQMSREAKRLKTFEYIDKFRSTPQ 79  
 66 SLARAGFYTVGVNDKVCFCGGLMDNMKLGDSPIQKHOLYPSCSFTONLVASLIGSTS 125  
 80 EMAAGFYHGVKLVQVCFCCSLILFSTRKRLPIENHKRLRECECF--LLGQVGNIG 136  
 126 KNSPMNSNAHSLPTLEHSSLSFGSYSSLSNPLNSRAVEDISSRTNPIYAMSTEE 165  
 137 KYDIRVA-----SPEKM-----LRGDKAR--HEEE 160  
 186 ARFLTYHMPPLTF--LSPSELARAGFYIGPDVACGAGKLSNMPKDDAMSEHRRH 243

161 ARLESFEDMPEFYAHGTSPRVLSAAGFYETGKRDTVQCFSCGGCLGNMBEGDDPMKHAHV 220  
 244 FPMCPLEEN--SLPTLEFSINLSMOTHA----- 271  
 221 FPCFCEFLQSKSSPEELTQVQSEGLHYGEHFVNSWVRELPMYSAVNDVSFANEEL 280  
 272 RMTFTMPPSSVVPQBLASAGFYTVGRNDVCKPCCDGLKWESEGDPPVEHAKWFP 331  
 281 RMDTFKMPHESPGAVDALVAGLFTYGRKRDIVQCFSCGGMERKMGDNPTEDETFEP 340  
 332 RCEFLIRMKQ--EFVDEIQGR--YPHLEQLLSTSDTTEENAD-----PPIIHFGPGE 382  
 341 NCVFLOQLKSAEYIPALQSHCALPEAME-----TTSNNDHDAAAVSTYVDVSPSE 393  
 383 SSEDVAMNTPVYKSALEMGFNRLVKQTVQSKILTGTGNYTVNDIVSALLNAEDEKR 442  
 394 AOELPFA-----SSLVSVLCRDODHSEAOGCASGCTYLPSTDL-----GQSEAO 439  
 443 EEEKQAEEMASDLSLIRKRMALFQOLTCVLPIL-----DNLKANV--INKQEH 494  
 440 WLOEARSLOLRDPTT-----KATFRHMN--LPEVYSSLGTDHLSCDVSIIKHSIQ 491  
 495 IIRKQTIPLQARELIDTILVKGNAA 521  
 492 PVQGSILTFPEVFSNLSVMCBEAGS 518

RESULT 10  
 A55478  
 neuronal apoptosis inhibitory protein - human  
 N:Alternate names: NAIP  
 C:Species: Homo sapiens (man)  
 C:Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 02-Feb-2001  
 C:Accession: A55478  
 R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shuttler, G.; Yaraghi, Z.; Farahan, R.; Baird  
 d, T.O.; de Jong, P.J.; Suh, L.; Ikeda, J.E.; Kornelut, R.G.; Mackenzie, A.  
 Cell 80, 167-178, 1995  
 A:Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in 1  
 A:Reference number: A55478; MIM:95112344; PMID:7813013  
 A:Accession: A55478  
 A:Molecule type: mRNA  
 A:Residues: 1-1232 <ROY>  
 A:Cross-references: GB:U19251  
 C:Genetics:  
 A:Gene: GDB:SMA4; SMA  
 A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300  
 A:Map position: 5q12.2-5q13  
 A:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane p  
 F:94-110/Domain: transmembrane #status predicted <TM1>  
 F:470-477/Region: nucleotide-binding motif A (P-loop)  
 F:479-496/Domain: transmembrane #status predicted <TM2>  
 F:476/Binding site: ATP (lys) #status predicted  
 F:618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.1%; Score 463; DB 2; Length 1232;  
 Best Local Similarity 25.4%; Pred. No. 1.1e-23;  
 Matches 156; Conservative 90; Mismatches 221; Indels 146; Gaps 23;

28 LSDMTNSNKKMKYDFSC-----LYRMSTYSTFPAGVPSERSLARAGFYTVGVNDK 80  
 38 LEEDEQKERAKMKGYNSQMSREAKRLKTFEYIDKFRSTPQ 94  
 81 VKFCGGLMDNMKLGDSPIQKHOLYPSCSFTONLVASLIGSTSKNTSPMNSNAHSL 140  
 95 IOFCFCSLILFAGLRLPTEDHKRHPDGF--LLNKVGNIAVYDIRKN----- 144  
 141 PTLHSSLSFGSYSSLSNPLNSRAVEDISSRTNPIYAMSTEEARFLTYHMP--LTF 198  
 145 -----LKSRL-----RGKMY--QEEPARLASFRMPPRYVQ 175  
 199 LSPSELARAGFYIGPDVACGAGKLSNMPKDDAMSEHRRHPPNCPFL--ENSL 255  
 176 ISPCVLSAAGFYTVGKQDVTQVCFSCGGCLGNMBEGDDPMKHAHVPPKCEFLRSKSSSE 235

QY 256 TLRFIS-----NLSTOT-----HARMTFMTSPSSVPO 286  
 Db 236 ITQYISGKGVDTIGHEFVNSWORELPASAYCNDISIFAYEELRLDSFQDMPRESAVG 295  
 QY 287 PEOLASAGFYVGRNDVYKCCDGLRCWESGDDPWVSHAKWPRCEFLIRMGQ--EFV 345  
 Db 296 VAALAKAGLFYTGIDYVQFCSCGCKLEKQEGDDPLD)HRCFPCNCFILNMSSAENV 355  
 QY 346 DEIGRPHLEQLSTSDTGTGEEN--ADPPIIHFGPGSS--SEDAVMMNTPV----- 395  
 Db 356 PDLOS--GELCELETETSESLMEDSIAVGPVPEMAQGIAMQFQAKMLNEQLRAAYTA 414  
 QY 396 -----VKSLE-----MGFNRLVQKQVOSKI---LTGEMVKTVDIVSALLNED 439  
 Db 415 SFRHMSLDISDLDLHLCGLDLSIAKHSKYPQEPVLPPEVFGNLSVWCVGEAGS 474  
 QY 440 EKREBEKQAEWASDLSIRKRMALFOQLTCVLP-----IDLNLK----- 484  
 Db 475 KGTVLK-KIAFLWASGCCPLNRFQVFLSLSTRDEGLASIDQLLEKGSVTEM 533  
 QY 485 --ANVNNQEHDI-----KQKQIPLQARELD-----TILYKMAANI--FK 525  
 Db 534 CMRNIIQQLKNOVFLLDYDEICISIPQVIGKLIQKNHL:RTCLLIATVNRARDIRRYL 593  
 QY 526 NCLKEIDSTLYKN 538  
 Db 594 ETILEIQAFPPYN 606

## RESULT 11

A45679  
 Inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV  
 C:Species: Cydia pomonella granulosis virus CpGV  
 C>Date: 21-Sep-1993 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000  
 C:Accession: A45679  
 R: Crook, N.E.; Clem, R.J.; Miller, L.K.  
 J. Virol. 67, 2168-2174, 1993  
 A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.  
 A:Reference number: A45679; MUID:93188168; PMID:8445726  
 A:Accession: A45679  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-275 <CRO>  
 A:Cross-references: GB:105494; NID:9289583; PIDN:AAA43835.1; PID:9289584  
 A:Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBIPI:127015)  
 C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 14.18; Score 461; DB 2; Length 275;  
 Best Local Similarity 22.68; Pred. No. 1,7e-24;  
 Matches 103; Conservative 62; Mismatches 84; Indels 206; Gaps 9;

QY 184 EEARFLTYHMPPLTFELSPSELARAGFYIGSDVACAGCKSKSNMPEKDMASEHRRH 243  
 Db 7 EEARLNTFEKPVSPFLSEYAKNGFYLLGRSDEYCAFCVKEILRMWEGEDPADHKKW 66  
 QY 244 FPNCFLE-----SLETLRFISNLSMOTH-----AARMTFMTSPSSVP 284  
 Db 67 APQCFVGVGIDVCSYITN-NIGNT--THDTIIGRAHPKYAHEAARVYKSFHMPRCMK 123  
 QY 285 VQPOLASAGFYVGRNDVYKCCDGLRCWESGDDPWVSHAKWPRCEFLIRMGQEF 344  
 Db 124 QRPQMDAGFFYTGIDYVQFCSCGCKLEKQEGDDPLD)HRCFPCNCFILNMSSAENV 355  
 QY 345 VDEIGRPHLEQLSTSDTGTGEENADPPIIHFGPGSS--SEDAVMMNTPVVSALEM 403  
 Db 184 VQK-----LTEACVL-----PGNTTVSTAAVSEPIPTK-- 216  
 QY 404 FNRDLVQKQVOSKIITGENTKYNDIVSALLNAEDEKREBEKQAEWASDLSIRK 463  
 Db 217 -----EKEPYE----- 223  
 QY 464 NRMLFOQLTCVLPILDNLKANYINQEHDIKQKQIPLQARELDITILYKMAANI 523

Db 224 ----- 223  
 QY 524 FKNCLEIDSTLYKNLFVDKMKYIPEDVSGLSLEBQLRLQBERCKYCMDEKVSVP 583  
 Db 224 -----DSKICKICYVECIYCF 240  
 QY 584 IPCGHLYVCCAPSLKRCPCRCGIIIGTVTFIS 618  
 Db 241 VPCGHVACACALSVKCPKCRKRIYTSVLKYPS 275

## RESULT 12

JC7568  
 kidney inhibitor of apoptosis protein - human  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001  
 C:Accession: JC7568  
 R:Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.  
 Biochem. Biophys. Res. Commun. 279, 820-831, 2000  
 A:Title: KIAIP, a novel member of the inhibitor of apoptosis protein family.  
 A:Reference number: JC7568; MUID: 21092523; PMID:11162435  
 A:Contents: Fetal kidney  
 A:Accession: JC7568  
 A:Molecule type: mRNA  
 A:Residues: 1-298 <LIN>  
 C:Comment: This protein, a new member of the inhibitor of apoptosis protein family, is

C:Genetics:  
 A:Gene: KIAIP  
 A:Map position: 20q13.3  
 C:Keywords: apoptosis

Query Match 14.18; Score 460.5; DB 2; Length 298;  
 Best Local Similarity 28.88; Pred. No. 2.1e-24;  
 Matches 126; Conservative 36; Mismatches 105; Indels 171; Gaps 13;

QY 212 IGPDRAVACFAGGKLSNMPEKDMASEHRRNP-----NC----- 247  
 Db 1 MGRPKDSAKLHGRQPSHMAAGDPPE--RCGRSLSGPVLGLDTCRANDVDGILQ 58  
 QY 248 --PLENSLE-----TLRFISNLSMOTHAARMTFMTSPSSVPOPOLASAGFYVGR 300  
 Db 59 LRPLTEEBEEGAGATLSRGPAFGMGSEELRLASFYDWPPLTAEPPELLAAGFFHTGH 118  
 QY 301 NDVYKCCDGLRCWESGDDPWVSHAKWPRCEFLIRMGQEVVDILOGVPHLLBOL 360  
 Db 119 QDKVRCFCYGGLOSWMKRGDDPWTEHAKWPPSCQFLLSKGRDVSQVETH--SOL 174  
 QY 361 STSDTGEENADPPIIHFGPGSSSEDAVMMNTPVVSALEMGNRLVQKQVOSKIT 420  
 Db 175 GSWD-----PWE-BPDA--APVAVSVAQVPE-----LPT 203  
 QY 421 GENKYNDIVSALLNAEDEKREBEKQAEWASDLSIRKRMALFOQLTCVLPILD 480  
 Db 204 -----PREVQSESAQEPGVS----- 220  
 QY 481 NLKANYINQEHDIKQKQIPLQARELDITILYKMAANIKNCLKEIDSTLYKNLF 540  
 Db 221 -----PAEQR----- 226  
 QY 541 VDKMKYIPEDVSGLSLEBQLRLQBERCKYCMDEKVSVPFPCGHLVQCCAPSLR 600  
 Db 227 -----AMWLEFPARVDAQRLQBERCKYCLDRAVSVIVPCGHL--VCAECAGIQ 280  
 QY 601 KPCIGIIGTVTFIS 618  
 Db 281 LCPICRAVRSRVTFIS 298

## RESULT 13

T41772  
 IAP1orf27 - Bombyx mori nuclear polyhedrosis virus (isolate T3)

C:Species: Bombyx mori nuclear polyhedrosis virus; BMSNPV  
A:Variety: isolate T3  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 15-Sep-2000  
C:Accession: T41772  
R:Gomi, S.; Majima, K.; Maeda, S.  
J. Gen. Virol. 80, 1323-1337, 1999  
A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.  
A:Reference number: 222020; MID:99281911; PMID:10355780  
A:Accession: T41772  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-292 <RAM>  
A:Cross-references: EMBL:L33180; NID:g3745835; PIDN:AAC63701.1; PID:g3745854  
A:Experimental source: isolate T3  
C:Genetics:  
A:Note: 1ap1  
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 7.3%; Score 240; DB 2; Length 292;  
Best Local Similarity 18.0%; Pred. No. 3.7e-09;  
Matches 78; Conservative 41; Mismatches 96; Indels 218; Gaps 9;

QY 208 GFYVIGPGDRVACFACGKLSNMEPKDDAMSEHRRHFPNCPLENSLETLEFS----- 260  
DB 54 GFYVNDHVDHVCCEAEIKNSEDCEIEYAVTISPICAYANKIAEHESFGDNTITNA 113  
QY 261 -----ISNLSQTHAANRFTFM-YWSSVVPVQPEOLASAGFYVGRDDYK 305  
DB 114 VLVKGRPKVCYKCMSNLQ-----SRMDTFVNPMPALRMITINIAEAGLFTYGRGDETV 168  
QY 306 CFCCDGLRCWESGDDPWVHAHWPFRCEFLIMKGOEFLVETQGRYPHLLBLLSTSDP 365  
DB 169 CFCCDCCVCRDMHINEDAMORHATENPQCFVLSVKGKEFCQ----- 209  
QY 366 TGEENADPPIHGPESSEDAVMNTPVYKSALEKGFNDLVKQTVOSKILITGENYK 425  
DB 210 ----- 209  
QY 426 TVNDIYSALLNADDEREKEKEQAEMASDDSLIRKRNMAFLQOLTCVPLILDNLKA 485  
DB 210 -----NATATVHDKRDD-----DDD-----DNNLNE 232  
QY 486 NVINKOEHDIIKQTOIPIQARELIDTILVKGNAANIFKNCLEIDSTLYKNLFDYKNA 545  
DB 233 NV-----DDDI----- 238  
QY 546 KYPTEDVSGLSLEQLRLQERTCKVCMKEVSVPFPCGHLVYQCECAPSL-RKCP 604  
DB 239 -----EERYECKVCLERQDAVLMPCIRHFCVQCYCFGLDQKCP 278  
QY 605 CRGIINGIVATFL 617  
DB 279 CRQDVTDFTKIFV 291

RESULT 14  
T43523  
cut17 protein - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 02-Jun-2000  
C:Accession: T43523; T41649; T41700  
R:Morishita, J.; Matsusaka, T.; Yanagida, M.  
submitted to the EMBL Data Library, August 1999  
A:Description: Fission yeast cut17 is required for chromosome segregation.  
A:Reference number: 222536  
A:Accession: T43523  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-997 <MOR>  
A:Cross-references: EMBL:AB031034; PIDN:BAH83415.1  
R:Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, August 1998  
A:Reference number: 222007

A:Accession: T41649  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-997 <HAR>  
A:Cross-references: EMBL:AL031323; PIDN:CAA02434.1; GSPDB:GN00068; SPDB:SPCC962.02c  
A:Experimental source: strain 972b; cosmid c962  
R:Medler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1999  
A:Accession: T41700  
A:Reference number: 222010  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 932-997 <MED>  
A:Cross-references: EMBL:AL121859; PIDN:CAB58376.1; GSPDB:GN00068; SPDB:SPCC962.02c  
C:Genetics:  
A:Gene: cut17; SPCC962.02c; SPDB:SPCC31B10.10c  
A:Map position: 3L  
A:Introns: 43/3

Query Match 7.2%; Score 237.5; DB 2; Length 997;  
Best Local Similarity 23.1%; Pred. No. 3.3e-08;  
Matches 106; Conservative 63; Mismatches 196; Indels 93; Gaps 22;

QY 164 RAYEDISSRTNPSYAMSTEERFLTYH--MPLFLFSPSELARAGFY--IGPG----- 215  
DB 2 KPISSSKRWKRNFRREMCYSKRLDTFOKKMPRAKPPETATVGFYINPISSENSSE 61  
QY 216 --DRVACFACGKLSNMEPKDDAMSEHRRHFPNCPLENSLETLEFSISNLSQTHAA-- 271  
DB 62 RLDNVTCYMCYKSFYEMEDDDOPLKELHITHSPCPM-----ATLSSKNPNPNQAAAL 116  
QY 272 ---RMRTFM-YWP-----SSVPVQPEOLASAGFY--VGRDDYKCFCCDGLRCWESG 319  
DB 117 TKCREQTFVDKVPTNRPDYHCEPSVMAASGVVNPPTADAKPAACLCYDILHMEPD 176  
QY 320 DDPVWEHAKWFRCEFLIMKGOEFLVETQGRYPHLE-----QLSTSPDTGEE-NADPP 374  
DB 177 DDPYTEHKRRRADCVF-----FTWKDPNLSLPKLSFLSTSNIDPDLTEDNS 224  
QY 375 IIFHGPESSEDAVMN-TPVYKSALE-MGFNRDLVKQTVOSK-----IL 418  
DB 225 ILFVSPTRDSTKSHKTLNPSPSKNNMLNARPLTMSLYTWTSEKDSQPTKAPQSPKPYL 284  
QY 419 TTGENK-----TVNDIYSALLNADDEREKEKEQ--AEEMASDDSLIRKRNMA 467  
DB 285 LTAAPRRKNSPKKSPKPAVPRKPIFSDEDEDDDLTASQPFSGKICDSMOYAKRN--- 341  
QY 468 LFOQLTCVPLILDNLKAVINKEHDIIKQTOIPIQARELIDTILVKGNAANIFKNC 527  
DB 342 ----FTBEIPLKED-----EKDNLEH-LVSPATSVTTVSDINGHOSYVDESDFQ--NNC 390  
QY 528 LK-----EIDSTLYKNLFYDKNNKYIPTEDVSGLSLE 560  
DB 391 MSTPKRIETSKIEEISVYSKKEI-SSSVSSVSGKEQ 427

RESULT 15  
D36828  
orf13 protein - Autographa californica nuclear polyhedrosis virus  
C:Species: Autographa californica nuclear polyhedrosis virus; ACNMPV  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Nov-2000  
C:Accession: D36828; C72853  
R:Stranau, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.  
Virology 191, 1003-1008, 1992  
A:Title: Sequence, genomic organization of the EcoRI-A fragment of Autographa californica  
VP8 of rotavirus.  
A:Reference number: A44221; MID:93079853; PMID:1333113  
A:Accession: D36828  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-286 <BRA>  
A:Cross-references: GB:S52569  
R:Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.

Virology 202, 586-605, 1994

A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus

A:Reference number: A72850; MUID:94303173; PMID:8030224

A:Accession: C72853

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-199, 'L', 201-286 <AVR>

A:Cross-references: GB:L22858; NID:g510708; PIDN:AAA6657.1; PID:g559096

C:Genetics:

A:Gene: Ac-IAP1

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

#### Query Match

Best Local Similarity 7.2%; Score 235.5; DB 2; Length 286;

Matches 83; Conservative 47; Mismatches 112; Indels 229; Gaps 11;

```
QY 173 RTNPSTAMSTEARFLYHMP--TFLSPSLARAGFYIIGDVRVACFAGGRLSN 229
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18 RDNTAEHFVFDLIRHSFENYPIENTAFI--NSLIYGFKNQVDDHVCECEAEIKN 75
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 230 WEPRDDAMSEHRRHPNCPFLNSLETIRFS-----ISLSMOT 268
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 76 WSEDECIETAVTLSPYCAVANKIAERSEFGDNTITINAVLYKEGKPKVCYRCMSNLQ-- 132
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 269 HAAMRTFM-YMPSSVPVQPEQLASAGFYIYGRNDYKICCCDGLRCWESGDDPWVEHA 327
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 133 --SRMDTFVNFWPALDMTINIAAGLFTYRGDEYVCFDCCVARDWHTNEDTWORHA 190
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 328 KMFPRCEFLIMKGOEVDIEIGRYPHLLEQLSTSDTGEENADPPIHFGPSSSED 387
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 191 AENPQCYFVXSVKKGKFC----- 208
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 388 AVAMNTPVVKSALMGFNRDLYKOTVQSKILTGENYKTVNDIVSALLNADEKREEKE 447
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 209 -----ONSITVTHV-----DKRD-- 222
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 448 KQAEEMASDDLIRKRNMAFLFOQLTCVLPILDNLKANYINKOEHDIKOKTQIPLOAR 507
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 223 -----DNL-----NENADDI----- 232
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 508 ELIDTILYKGNAAANIRKNCLEIDSTLYKNLFYDKNMKYLPTEDVSGLSLEQLRLQE 567
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 233 -----EE 234
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 568 ERTCKVCMKREVSVPFLPCGHLVYCOCAPSL-RKCPICRGIIKGYRTFL 617
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 235 KYECKVCLERORDAVLMPCHRCVQCYFGLDQKCFPCRQDVYDFIKIFV 285
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: May 5, 2003, 16:08:04  
Job time : 71.6382 secs

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:51:32 ; Search time 25.6313 Seconds

(without alignments)  
1000.040 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277

Sequence: 1 MKKTASQRLFPSPSTQNIKS.....LKKPCIKGIIKGVTRFLS 618

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3277	100.0	618	1	BIR3_HUMAN
2	2728	83.2	612	1	BIR3_MOUSE
3	2353	71.8	604	1	BIR2_HUMAN
4	2233.5	66.2	611	1	BIR_CHICK
5	2172	66.3	600	1	BIR2_MOUSE
6	1532	46.8	358	1	PIAP_PIG
7	911	27.8	497	1	BIR4_HUMAN
8	910	27.8	496	1	BIR4_MOUSE
9	904.5	27.6	496	1	BIR4_RAT
10	744.5	22.7	498	1	IAP2_DROME
11	513	15.7	268	1	IAP3_NPVOP
12	506	15.4	1403	1	BIRE_MOUSE
13	499.5	15.2	1403	1	BIRE_MOUSE
14	498.5	15.2	1402	1	BIRG_MOUSE
15	484	14.8	438	1	IAP1_DROME
16	468.5	14.3	1403	1	BIRB_MOUSE
17	468	14.3	1447	1	BIRB_MOUSE
18	462	14.1	1403	1	BIR1_HUMAN
19	461	14.1	275	1	IAP_GVCP
20	460.5	14.1	298	1	BIR7_HUMAN
21	459.5	14.0	236	1	BIR8_GORGO
22	458.5	14.0	236	1	BIR8_HUMAN
23	457.5	14.0	236	1	BIR8_PANTR
24	238.5	7.3	286	1	IAP1_NPVAC
25	237.5	7.2	997	1	BIR1_SCHPO
26	223.5	6.8	275	1	IAP1_NPVOP
27	199.5	6.1	4829	1	BIR6_HUMAN
28	175.5	5.4	239	1	ZFP_IRV6
29	144	4.4	249	1	IAP2_NPVAC
30	141.5	4.3	142	1	BIR5_RAT
31	139	4.2	140	1	BIR5_MOUSE
32	137.5	4.2	236	1	IAP2_NPVOP
33	132.5	4.0	490	1	MDM4_HUMAN

34	131	4.0	142	1	BIR5_HUMAN	O15392 homo sapien
35	126	3.8	145	1	ZFP2_IRV6	P40629 chilo lride
36	124	3.8	433	1	RN26_HUMAN	O9D78 homo sapien
37	120.5	3.7	834	1	YNC4_CAEEL	P34537 caenorhabdi
38	120.5	3.7	954	1	BIR1_YEAST	P47134 saccharomyc
39	119.5	3.6	487	1	MDM2_CANFA	P56950 canis famli
40	119.5	3.6	735	1	YOD7_SCHPO	O10432 schizosach
41	119	3.6	619	1	PIA1_HELPY	O25149 hellicobacte
42	116.5	3.6	3418	1	BRC2_HUMAN	P51587 homo sapien
43	116	3.5	624	1	YMO8_YEAST	P54074 saccharomyc
44	115.5	3.5	491	1	MDM2_HUMAN	O00987 homo sapien
45	112.5	3.4	1075	1	PST2_SCHPO	O13919 schizosach

## ALIGNMENTS

RESULT 1  
ID BIR3\_HUMAN STANDARD: PRT; 618 AA.  
AC Q13490; Q16516;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis protein 2) (HIAP2) (HIAP-2) (C-IAP1) (TNFR2-TRAF signaling complex protein 2) (IAP homolog B).  
DE BIRC3 OR API2 OR IAP2 OR MIB.  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-96128127; PubMed-8548810;  
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel L.V.;  
RT "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";  
RL Cell 83:1243-1252(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-96149249; PubMed-8643514;  
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertton-Horvat G., Farhan R., McLean M., Ikeda J., Mackenzie A., Konecny R.G.;  
RT "Suppression of apoptosis in mammalian cells by NALP and a related family of IAP genes.";  
RL Nature 379:349-353(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-96209843; PubMed-8643514;  
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-96209843; PubMed-8643514;  
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
RN [5]  
RP STRUCTURE BY NMR OF 266-363.  
RX MEDLINE-99332054; PubMed-10404221;  
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;  
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP) repeat.";  
RL Nat. Struct. Biol. 6:648-651(1999).  
CC -I- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

```

CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
CC LEUCOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chromancer/genes/BIRC3ID39.html".
CC -----
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DR EMBL: LA9431; AAC1942.1; -
DR EMBL: U45879; AAC50372.1; -
DR EMBL: U37547; AAC50508.1; -
DR EMBL: BC016174; AAH16174.1; -
DR PDB: IOBH: 20-OCT-99.
DR GeneW: HGNC:590; BIRC2.
DR MIM: 601721; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR Pfam: PFO0097; zf-C3HC4; 1.
DR Pfam: PFO0619; CARD; 1..
DR Pfam: PFO0653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS0089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat; 3D-structure.
KW REPEAT 46 113 BIR 1.
FT REPEAT 184 250 BIR 2.
FT REPEAT 269 336 BIR 3.
FT DOMAIN 453 543 CARD.
FT ZN_RING 571 606 CARD.
FT CONFLICT 157 157 S -> P (IN REF. 2).
FT CONFLICT 308 308 C -> G (IN REF. 2).
FT CONFLICT 414 414 O -> L (IN REF. 2).
FT CONFLICT 514 514 L -> W (IN REF. 2).
SQ SEQUENCE 618 AA: 69899 MW: C1778D328063586E CRC64;
Query Match 100.0%; Score 3277; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 6.5e-209;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 MSTEERAFLLTYHMMPLFLSPSELARAGFYIIGDRAVACFAGCGKLSNNEPKDDAMSEH 240
Qy 241 RHHPNCPLENSLETRESISLUSMOTHAARKTEWYSPVPOEOLASAGFYTVGR 300
Db 241 RHHPNCPLENSLETRESISLUSMOTHAARKTEWYSPVPOEOLASAGFYTVGR 300
Qy 301 NDDVKCFCCGGGLRCWESSGDDPVEHAKMPRCEFLIRMGQEFVEIOGRYHLEOLL 360
Db 301 NDDVKCFCCGGGLRCWESSGDDPVEHAKMPRCEFLIRMGQEFVEIOGRYHLEOLL 360
Qy 361 STSDTGEENADPPIIHFGGESSSEDAVAMNPPVKSALMEGFNRDLYQVQSKILTT 420
Db 361 STSDTGEENADPPIIHFGGESSSEDAVAMNPPVKSALMEGFNRDLYQVQSKILTT 420
Qy 421 GENYKYNDIVSALLNADEKREERKQAEASDLSIRNRNALFOQLTCVPLILD 480
Db 421 GENYKYNDIVSALLNADEKREERKQAEASDLSIRNRNALFOQLTCVPLILD 480
Qy 481 NLKANVINQEHDIKOKQIPLQARELIDTILVGNMAANIFKNKLEISTLYKNLF 540
Db 481 NLKANVINQEHDIKOKQIPLQARELIDTILVGNMAANIFKNKLEISTLYKNLF 540
Qy 541 VDRNMKYIPTEDVSGLSLEBQLRLQERTCKVCMDEKSVFIPCGHLYVCECAPSLR 600
Db 541 VDRNMKYIPTEDVSGLSLEBQLRLQERTCKVCMDEKSVFIPCGHLYVCECAPSLR 600
Qy 601 KCPICGKITIGYVTRTSL 618
Db 601 KCPICGKITIGYVTRTSL 618

RESULT 2
BIR3_MOUSE
ID BIR3_MOUSE STANDARD: PRT: 612 AA.
AC 062210; 008864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
DE protein 2) (MARP2) (MARP-2).
GN BIRC3 OR AIP2 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes.";
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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CC -----
DR EMBL; L49433; AAC42078.1;
DR EMBL; U88909; AAC3532.1;
DR HSSP; 013490; 10BH.
DR MGD; MGI:1197009; BIRC3.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR Pfam; PF00097; zf-C3HC4.1.
DR Pfam; PF00619; CARD.1.
DR Pfam; PF00653; BIR.3.
DR SMART; SM00238; BIR.3.
DR SMART; SM00114; CARD.1.
DR SMART; SM00184; RING.1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS00209; CARD.1.
DR PROSITE; PS00518; zf_RING_1; FALSE_NEG.
DR PROSITE; PS00089; zf_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
DR REPEAT; 46; 113; BIR.1.
DR REPEAT; 177; 243; BIR.2.
DR REPEAT; 262; 329; BIR.3.
DR DOMAIN; 447; 537; CARD.
DR 2N_FING; 565; 600; CARD.
DR CONFLICT; 380; 380; E -> K (IN REF. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match      83.2%; Score 2728; DB 1; Length 612;
Best Local Similarity 83.4%; Pred. No. 1.1e-17;
Matches 517; Conservative 45; Mismatches 40; Indels 10; Gaps 6;

OY 1 MHRTASQRLFPGPSYONIKSIMEDSTILSDWTNSNKKKDYFSCELYMSTYSTFPAGV 60
DB 1 MDKTVSORLGQGTLHOKLKRIMEKSTILSNWTKSESEKKKFFSCELYMSTYSAPRRV 60
OY 61 PVSERSLARAGYTYGVNDKVCFCGGLMDWKLGDSTIQHKKIYSCSTIONIVSAS 120
DB 61 PVSERSLARAGYTYGVNDKVCFCGGLMDWKLGDSTIQHKKIYSCSTIONIVSAS 120
OY 121 LGSTKNTSPMNSFAHSLSPTEHSLFSGSYSLSPMLKSRAVEDISSRTPIYSYA 180
DB 121 LGSTKNTSPMNSFAHSLSPTEHSLFSGSYSLSPMLKSRAVEDISSRTPIYSYA 180
OY 122 LOSPSKNSPVASRFAHS-SP-LEH---GGIHSNLCSSPLNSRAVEDE-SSRMDPCSYA 173
DB 122 LOSPSKNSPVASRFAHS-SP-LEH---GGIHSNLCSSPLNSRAVEDE-SSRMDPCSYA 173
OY 181 MSTEERARFLTYHMPFLTELPSELARAGFYTYGPDRAVACFAKGGKLSNMEKXDAMSH 240
DB 181 MSTEERARFLTYHMPFLTELPSELARAGFYTYGPDRAVACFAKGGKLSNMEKXDAMSH 240
OY 174 MSTEERARFLTYHMPFLTELPSELARAGFYTYGPDRAVACFAKGGKLSNMEKXDAMSH 233
DB 174 MSTEERARFLTYHMPFLTELPSELARAGFYTYGPDRAVACFAKGGKLSNMEKXDAMSH 233
OY 241 RHHFPCNPLENSLETLRFSISNLSMOGTHAARMTFMTWSSVPVQPEQLASAGFYVGR 300
DB 241 RHHFPCNPLENSLETLRFSISNLSMOGTHAARMTFMTWSSVPVQPEQLASAGFYVGR 300
OY 234 RHHFPCNPLENSLETLRFSISNLSMOGTHAARMTFMTWSSVPVQPEQLASAGFYVGR 293
DB 234 RHHFPCNPLENSLETLRFSISNLSMOGTHAARMTFMTWSSVPVQPEQLASAGFYVGR 293
OY 301 NDDVACFCGCGGLRCMGESGDDPVVHAKWPRCEFLIRKKGEPFVDEIQARPHLEQL 360
DB 301 NDDVACFCGCGGLRCMGESGDDPVVHAKWPRCEFLIRKKGEPFVDEIQARPHLEQL 360
OY 294 NDDVACFCGCGGLRCMGESGDDPVVHAKWPRCEFLIRKKGEPFVDEIQARPHLEQL 353
DB 294 NDDVACFCGCGGLRCMGESGDDPVVHAKWPRCEFLIRKKGEPFVDEIQARPHLEQL 353
OY 361 STSDTGEENADP--PIIHFGPGESESDAVAMNTPVYKSALEMGFNRLVQVQSKIL 418
DB 361 STSDTGEENADP--PIIHFGPGESESDAVAMNTPVYKSALEMGFNRLVQVQSKIL 418
OY 354 STSDTGEENADPTEVVAHFGGE--SSEVYVAMSTPVYKAALEMGFSRLVQVQSKIL 412
DB 354 STSDTGEENADPTEVVAHFGGE--SSEVYVAMSTPVYKAALEMGFSRLVQVQSKIL 412
OY 419 TTGENYKTVNDIVSALLNADEKREERKEKQAEKASDLSLIRKRNALFOQLTCVLP 478
DB 419 TTGENYKTVNDIVSALLNADEKREERKEKQAEKASDLSLIRKRNALFOQLTCVLP 478
OY 413 ATGENYKTVNDIVSALLNADEKREERKEKQAEKASDLSLIRKRNALFOQLTCVLP 472
DB 413 ATGENYKTVNDIVSALLNADEKREERKEKQAEKASDLSLIRKRNALFOQLTCVLP 472
OY 479 LDNLKAVINQOEHDIIKQTOIPLQARELIDTILVGNMAANIFKNCIKRIDSTLYKN 538
DB 479 LDNLKAVINQOEHDIIKQTOIPLQARELIDTILVGNMAANIFKNCIKRIDSTLYKN 538

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DB 473 LDNLKAVINQOEHDIIKQTOIPLQARELIDTILVGNMAANIFKNCIKRIDSTLYKN 532
OY 539 LFVDMKMYTIPEDVSGSLERQLRLREERCCKMCKEVSVPVPGHVLVQCECAPS 598
DB 533 LFVDMKMYTIPEDVSGSLERQLRLREERCCKMCKEVSVPVPGHVLVQCECAPS 592
OY 599 LKPCICRGIINGKTVTFELS 618
DB 593 LKPCICRGIINGKTVTFELS 612

RESULT 3
BIR2_HUMAN STANDARD; PRT; 604 AA.
ID BIR2_HUMAN 013489; 016628; 09UP46; 09HC27;
AC 01-NOV-1997 (Rel. 35. Created)
DT 01-NOV-1997 (Rel. 35. Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1 (Inhibitor of apoptosis
DE protein 1) (H1AP1) (H1AP-1) (C-IAP2) (TNFR2-TRAF signalling complex
DE protein 1) (IAP homolog C).
GN BIRC2 OR APL1 OR IAP1 OR MHC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96128127; PubMed-8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signalling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins."
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-96149249; PubMed-8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAI1 and a related
RT family of IAP genes."
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-96209843; PubMed-8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-99252096; PubMed-10233894;
RA Horrevorts A.-J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
RA ten Cate J.W., Pannenkoek H.;
RT "Vascular endothelial genes that are responsive to tumor necrosis
RT factor-alpha in vitro are expressed in atherosclerotic lesions,
RT including inhibitor of apoptosis protein-1, stannin, and two novel
RT genes."
RL Blood 93:3418-3431(1999).
RN [5]
RP SEQUENCE OF 362-441 FROM N.A.
RX MEDLINE-20519161; PubMed-11066071;
RA Baens M., Steyls A., Dierlam J., De Wolf-Peters C., Marynen P.;
RT "Structure of the MIF gene and molecular characterization of the
RT genomic breakpoint junctions in the t(11;16)(q21;q21) of marginal zone
RT B-cell lymphomas of MALT type."
RL Genes Chromosomes Cancer 29:281-291(2000).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

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CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN
CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,
CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
CC -1- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid
CC tissue). This translocation is found in approximately 50% of
CC cytogenetically abnormal low-grade MALT lymphoma and involves
CC MAL1 and BIRC2.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
DR EMBL: L49432; AAC41943.1; -
DR EMBL: U45878; AAC50371.1; -
DR EMBL: U37546; AAC50507.1; -
DR EMBL: AF070674; AAC83232.1; -
DR EMBL: AF178945; AAG09369.1; -
DR HSSP: Q13490; 10BH.
DR GeneW: HGNC:591; BIRC3.
DR MIM: 601712; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR KIM: Apoptosis; Zinc-finger; Repeat; Chromosomal translocation.
FT REPEAT 29 96 BIR 1.
FT REPEAT 169 235 BIR 2.
FT REPEAT 255 322 BIR 3.
FT DOMAIN 439 529 CARD.
FT ZN_FING 557 592 RING-TYPE.
FT SITE 442 443 BREAKPOINT FOR TRANSLLOCATION TO FORM
FT BIRC2-MAL1.
FT CONFLICT 18 18 N -> Y (IN REF. 4).
FT CONFLICT 119 119 N -> H (IN REF. 2).
FT CONFLICT 153 153 D -> E (IN REF. 2).
FT CONFLICT 163 163 H -> P (IN REF. 2).
FT CONFLICT 165 165 A -> P (IN REF. 2).
FT CONFLICT 191 191 K -> R (IN REF. 2).
FT CONFLICT 191 191 F -> L (IN REF. 2).
FT CONFLICT 364 364 Q -> P (IN REF. 2).
FT CONFLICT 552 552 Q -> P (IN REF. 2).
SQ SEQUENCE 604 AA: 68371 MW: 8581A00BA9AAB4A7 CRC64;

Query Match 71.8%; Score 2353; DB 1; Length 604;
Best Local Similarity 72.8%; Pred. No. 5,9e-148;
Matches 440; Conservative 71; Mismatches 87; Indels 6; Gaps 5;
QY 20 SIEMDSTLLDNTNS-NKOKMDFSCETLRMSTYTFPAGVSVSESLARAGEYTTGVN 78
DB 2 NIYENSIFLSNLMKSNATFLKTDLSCELYRMSTYTFPAGVSVSESLARAGEYTTGVN 61

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QY 79 DKYKCCGGLMDNWKLGSPLOKHQOLYPSGCFIONLYSA-SLGSSTKNTSP--NRNSF 135
DB 62 DKYKCCGGLMDNWKLGSPLOKHQOLYPSGCFIONLYSA-SLGSSTKNTSP--NRNSF 120
QY 136 AHSLSPTLHSSLSFSSYSLSLSPNLSRAVEDISSRTNTPYSASTSEARLYTHMP 195
DB 121 THSLDPTENSQVFRSISYSPNPNSANDPFSALMSHYCAMNNENARLLTQTP 180
QY 196 LFLSPSELARAGEFYIYIGFDYVACFACGKLSNWEKPDAMSEHRHFPNCFLENSI- 254
DB 181 LFLSPTELDKAGFYIYIGFDYVACFACGKLSNWEKPDAMSEHRHFPNCFLENSI- 240
QY 255 ETLRFSTLSNLSMOTHAARRHTFMPSSVYPOEOLASAGFYVGNDDVKCCCGGR 314
DB 241 DSRITVSNLSMOTHAARRHTFMPSSVYPOEOLASAGFYVGNDDVKCCCGGR 300
QY 315 CWESGDDPWEVHAKEPCEFLIRMGQFVDEIQGRPHLLLEQLSTSDTGEENADPP 374
DB 301 CWESGDDPWEVHAKEPCEFLIRMGQFVDEIQGRPHLLLEQLSTSDTGEENADPP 360
QY 375 ITHFGGSSSEDAVAMNPPVYKSALEMGFNDLVQYQSKITLTGENYKYNDVSL 434
DB 361 ITHFGGSSSEDAVAMNPPVYKSALEMGFNDLVQYQSKITLTGENYKYNDVSL 420
QY 435 LNAEDKREERKEKQAEASDDSLIRKRMALFOQLCVLPIDNLTAKANYINQED 494
DB 421 LNAEDKREERKEKQAEASDDSLIRKRMALFOQLCVLPIDNLTAKANYINQED 480
QY 495 IIRKQTIPLQARELIDTLVKGNAANIFKNCLEIDSTLYKNLPVDRNMKXPTEDVS 554
DB 481 VIKQTIQTSIQARELIDTLVKGNAANIFKNCLEIDSTLYKNLPVDRNMKXPTEDVS 540
QY 555 GLSLEQLRLQERCKYCKMDEKSVVIFPGHLVYCGEAPSLKCIPIRCIIITGYR 614
DB 541 DLPEVEQLRLQERCKYCKMDEKSVVIFPGHLVYCGEAPSLKCIPIRCIIITGYR 600
QY 615 TFLS 618
DB 601 TFLS 604

RESULT 4
BIR_CHICK
ID BIR_CHICK STANDARD; PRT; 611 AA.
AC 090660;
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis
DE protein).
DE ITA.
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC [1] NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE= spleen; PubMed=8945639;
RX MEDLINE=97101112;
RA Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT "ITA, a vertebrate homologue of IAP that is expressed in T
RT lymphocytes."
RT Lymphocytes."
RL DNA Cell Biol. 15:981-988(1996).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.
CC -1- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN
CC BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.
CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF
CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.

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CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U27466; ABA8118.1;
DR HSSP: O13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Zn_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS0089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat; Nuclear protein.
KW REPEAT 30 97 BIR 1.
FT REPEAT 176 242 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 446 536 CARD.
FT ZN_FING 564 599 CARD.
SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;

Query Match 68.2%; Score 2233.5; DE 1; Length 611;
Best Local Similarity 69.2%; Pred. No. 4,6e-140;
Matches 424; Conservative 77; Mismatches 95; Indels 17; Gaps 8;

QY 20 STMEDSTLSDWTNSNKQ--KKKYDFSCELYRMSTYTFPAGVYVSERSLARAGFYTCV 77
DB 2 NIMDSPPLLASVKNANHGELKDYFSCELYRMSTFSTFPVNVYSERLARAGFYTCV 61
QY 78 NIKVCFCCGLMDWKKIGDSPLOKHKOYPCSFIONVSA-SIG-SF-----SKN 127
DB 62 QKRVKCFSGVLDMQPCDNAMEKHQYPCSFQNMLSNNGLSTHSAPSLVASN 121
QY 128 TSPMRNSFAHSLPTLHSSLSFGSYSLSPNPLNSRAVED:SSSRRTNYSYAMSTEER 187
DB 122 LSPSLRSM--TISPFEQYGYFSSGSFSPRPDPVTTTRAEDI:SHLSKILQNSMSTEER 179
QY 188 PLTYHMPILTLSPSELARAGFYTYIGPDRAVACAGCGKLSMWERKDMSEHRRHPNC 247
DB 180 LRTSHAMPILMCLMPAELVAAGAAGLDLGTADKVAACVNCVGLSNWEPEDNMSERRHPNC 239
QY 248 PRLNSL-ETLRFSTNSINSMOTHAARMFTWMPSSVPYQQLASAGTYTYGRDDVVC 306
DB 240 PVEVNLMRQPSFNWNSVNTMOTHEARVKTFEIMPTRIPIQPOLADAGTYTYGRDDVVC 299
QY 307 FCCDGLRCMESGDDPWVHAHAKFPRCEFLIMKGOEFYDEIGRYPHLL-DQLSTSDT 365
DB 300 FCCDGLRCMESGDDPWVHAHAKFPRCEFLIMKGOEFYDEIGRYPHLL-DQLSTSDT 359
QY 366 TEEENADPPIHFPGESSEDAVAMNTPYVKSALBMGNRDYVKQTVOSKILTTGENYK 425
DB 360 PVDEKND-PIHFPEGESEDEDAIMMNTPVYKAALMGFSRRILKQTVOSKILATEENYK 418
QY 426 TVNDIYSALLNDEKREKEKOEAMASDLSILRKRMALFOOLNVLILNLKA 485
DB 419 TVNDIYSALLNDEKREKEKOEAMASDLSILRKRMALFOOLNVLILNLKA 478
QY 486 NVINKEHDIKQTOIPLARELIDTILVKNAAANIFKNCIKETIDSTLYKNLEFVDKN 545
DB 479 KYTLEHDIKQTOIPLARELIDTILVKNAAANIFKNCIKETIDSTLYKNLEFVDKN 538

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QY 546 KYIPEDVSGLSLEQLRLQERCKVCMDEKESVVFIPCGHLVYCCQCAPSLRKCPTC 605
DB 539 KYVPEDVSGLSLEQLRLQERCKVCMDEKESVVFIPCGHLVYCCQCAPSLRKCPTC 598
QY 606 RGIKGTVPFPLS 618
DB 599 RGIKGTVPFPLS 611

RESULT 5
BIR2_MOUSE
ID BIR2_MOUSE STANDARD: PRT; 600 AA.
AC 008663;
DR 01-NOV-1997 (Rel. 35, Created)
DR 01-NOV-1997 (Rel. 35, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (inhibitor of apoptosis
DE protein 1) (MIAP1) (MIAP-1).
GN BIRC2 OR APL1 OR IAP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
CC -1- SUBUNIT: Interacts with SMAC and with PR55; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U88908; AAC53531.1;
DR HSSP: O13490; 10BH.
DR MGD: MGI:1197007; Birc2.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Zn_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS0089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
KW REPEAT 27 94 BIR 1.
FT REPEAT 167 233 BIR 2.
FT REPEAT 253 320 BIR 3.

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FT DOMAIN 436 525 CARD.  
 ZN\_RING 553 588 RING-TYPE.  
 SO SEQUENCE 600 AA: 67198 MW: AD7F736849317D1 CRC64;

Query Match 66.3%; Score 2172; DF 1; Length 600;  
 Best local similarity 66.7%; Pred. No. 5.1e-136;  
 Matches 406; Conservative 87; Mismatches 96; Indels 20; Gaps 7;

QY 21 IMDSITLISWMTS-NKOKKKYDFSCELYMTSTFPAGVPSSESLAAGFYTGVD 79  
 DB 1 MYDQSAFLAKMSADTFELKIDFSCELYRLSTYSAPRQVPSVSESLAAGFYTGVD 60.  
 QY 80 KVCFCGGLMDNMKLGDSPIQKHOLYPCSFYIOLVSA-----SLGSKTSTP 130  
 DB 61 KVCFCGGLMDNMKLGDSPIQKHOLYPCSFYIOLVSA-----SLGSKTSTP 120  
 QY 131 MRNSFAHSLPTLEHSLSESGYSISLPNLSRAVEDISSRTNPFYSYMSTEARFLT 190  
 DB 121 L--SFAS--EMTGYFSGYSISFPSPDVFNRANDCPALSTSPHFAMTEKARLLT 173  
 QY 191 YHMPPLTFELSPSELARAGFYIIGPDVACFAGCGKLSNRPDDAMSEHRRHPNCPFL 250  
 DB 174 YETWPLSLFSPAKAKAGFYIIGPDVACFAGCGKLSNRPDDAMSEHRRHPNCPFL 233  
 QY 251 EN-SLETLRESISNLSMOTHAARMTFMWPSVYVPOEOLASAGFYVGRNDVACFC 309  
 DB 234 KDQGSASRYTYSNLSMOTHAARMTFMWPSVYVPOEOLASAGFYVGRNDVACFC 293  
 QY 310 DGLRCWESDDPWVEHAKFPCEFLIRKKGFEVDEIGRYPHLEQLLSTDTGEE 369  
 DB 294 DGLRCWESDDPWVEHAKFPCEFLIRKKGFEVDEIGRYPHLEQLLSTDTGEE 353  
 QY 370 NADPPIHFGPGSSSDAYAMNTPVYKSALENGFNDDLYKOTYOSKILTTGENYK 429  
 DB 354 NADPPIHFGPGSSSDAYAMNTPVYKSALENGFNDDLYKOTYOSKILTTGENYK 412  
 QY 430 IYSALENADEKREKEKEKAEKASDLSLIRKNMALPQOLTCVPIIDNLKANVIN 489  
 DB 413 LVIGLDAEDMEKREKEKAEKASDLSLIRKNMALPQOLTCVPIIDNLKANVIN 472  
 QY 490 KOEHDIITKOTQIPLQARELIDTLVKGNAANIFKNCIKIDISTLYKNLFPVKNM 549  
 DB 473 KOEHDIITKOTQIPLQARELIDTLVKGNAANIFKNCIKIDISTLYKNLFPVKNM 531  
 QY 550 TEDVSGSLSEQLRLQERTCKYCKMDKEYSVYFPCGHLYVCOECPASRKPCIG 609  
 DB 532 TEDVSGSLSEQLRLQERTCKYCKMDKEYSVYFPCGHLYVCOECPASRKPCIG 591  
 QY 610 KGVVTRFLS 618  
 DB 592 KGVVTRFLS 600

RESULT 6  
 PIAP\_PIG STANDARD; PRT; 358 AA.  
 AC 062640;  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative inhibitor of apoptosis.  
 GN PIAP.  
 OS Sus scrofa (Pig); Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Cetartiodactyla; Suidae; Sus.  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 ON NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Aorta;  
 RX MEDLINE=98162622; Pubmed=9501011;  
 RA Stehlik C., de Martin R., Binder B.R., Lipp J.;  
 RT "Cytokine induced expression of porcine inhibitor of apoptosis  
 protein (Iap) family member is regulated by NF-kappa B.";

BL Biochem. Biophys. Res. Commun. 243:827-832(1998).  
 CC - SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC - SIMILARITY: CONTAINS 2 BIR REPEATS.  
 CC - SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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DR EMBL: U79142; AAC39171.1; -  
 DR HSRP: Q13490; 10BH.  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR001841; Znf\_Ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00653; BIR; 2.  
 DR SMART: SM00238; BIR; 2.  
 DR SMART: SM00114; CARD; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE: PS0143; BIR\_REPEAT\_2; 2.  
 DR PROSITE: PS0209; CARD; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE: PS00518; ZF\_RING\_2; 1.  
 DR Apoptosis; Zinc-finger; Repeat.  
 FT REPEAT 4 70 BIR 1.  
 FT REPEAT 90 157 BIR 2.  
 FT DOMAIN 193 283 CARD.  
 FT ZN\_RING 311 346 RING-TYPE.  
 SO SEQUENCE 358 AA: 40977 MW: EB226BFA9A6190A4 CRC64;

Query Match 46.8%; Score 1532; DB 1; Length 358;  
 Best local similarity 65.1%; Pred. No. 4.3e-94;  
 Matches 286; Conservative 38; Mismatches 33; Indels 82; Gaps 2;

QY 181 MSTEARFLTYHMPPLTFELSPSELARAGFYIIGPDVACFAGCGKLSNRPDDAMSEH 240  
 DB 1 MNTKEDRLTLTFQWPLTFELSPADLAKAGFYIIGPDVACFAGCGKLSNRPDDAMSEH 60  
 QY 241 RRHPNCPFLNLSL-ELTRPSISNLSMOTHAARMTFMWPSVYVPOEOLASAGFYTG 299  
 DB 61 LRHPNCPFLNLSL-ELTRPSISNLSMOTHAARMTFMWPSVYVPOEOLASAGFYTG 120  
 QY 300 RNDVACFCDDGGLRCWESDDPWVEHAKFPCEFLIRKKGFEVDEIGRYPHLEQL 359  
 DB 121 HSDVACFCDDGGLRCWESDDPWVEHAKFPCEFLIRKKGFEVDEIGRYPHLEQL 180  
 QY 360 LSTSDTTEENADPPIIHFGPGSSSDAYAMNTPVYKSALENGFNDDLYKOTYOSK 419  
 DB 181 LSTSDTTEENADPPIIHFGPGSSSDAYAMNTPVYKSALENGFNDDLYKOTYOSK 195  
 QY 420 TGENYKTVNDIYVALLNADEKREKEKEKAEKASDLSLIRKNMALPQOLTCVPII 479  
 DB 196 -----NDLSLIRKNMALPQOLTCVPII 219  
 QY 480 DNILKANVINKOEHDIITKOTQIPLQARELIDTLVKGNAANIFKNCIKIDISTLYKNL 539  
 DB 220 DNILKANVINKOEHDIITKOTQIPLQARELIDTLVKGNAANIFKNCIKIDISTLYKNL 279  
 QY 540 FVDKNMKYIPTEDVSGSLSEQLRLQERTCKYCKMDKEYSVYFPCGHLYVCOECPAS 599  
 DB 280 FVDKNMKYIPTEDVSGSLSEQLRLQERTCKYCKMDKEYSVYFPCGHLYVCOECPAS 339  
 QY 600 RKCPICGTLKGVTRFLS 618  
 DB 340 RKCPICGTLKGVTRFLS 358

RESULT 7			
BIR4_HUMAN	STANDARD:	PTT:	497 AA.
ID	BIR4_HUMAN		
AC	P96170; Q9NQ14;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis Protein) (X-linked IAP)		
DE	(IAP-like protein) (HILP).		
GN	BIRC4 OR API3 OR IAP3 OR XIAP.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Fetal brain;		
RX	MEDLINE=96149249; PubMed=8552191;		
RA	Liston P., Roy N., Tama K., LeFebvre C., Balnd S., Chertion-Horvat G.,		
RA	Farahani R., McLean M., Ikeda J., MacKenzie A., Korneluk R.G.;		
RT	"Suppression of apoptosis in mammalian cells by NAIP and a related		
RT	family of IAP genes.";		
RL	Nature 379:349-353(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Fetal heart;		
RX	MEDLINE=96256286; PubMed=8654366;		
RA	Duckett C.S., Nava V.B., Gedrich R.W., Clem R.J., van Dongen J.L.,		
RA	Gillfillian M.C., Shiels H., Hardwick J.M., Thompson C.B.;		
RT	"A conserved family of cellular genes related to the baculovirus IAP		
RT	gene and encoding apoptosis inhibitors.";		
RL	EMBO J. 15:2685-2694(1996).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Grafham D.;		
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	FUNCTION.		
RX	MEDLINE=97373959; PubMed=9230442;		
RA	Deveraux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;		
RT	"X-linked IAP is a direct inhibitor of cell-death proteases.";		
RL	Nature 388:300-304(1997).		
RN	[5]		
RP	MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.		
RX	MEDLINE=21654829; PubMed=11600410;		
RA	Verhegen A.M., Slike J., Eckert P.G., Pakusch M., Kaufmann H.,		
RA	Connolly L.M., Day C.L., Tikoo A., Burke R., Wrobel C., Moritz R.L.;		
RA	"HRA2 promotes cell death through its serine protease activity and		
RT	its ability to antagonize inhibitor of apoptosis proteins.";		
RL	J. Biol. Chem. 277:445-454(2002).		
RN	[6]		
RP	STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMA*.		
RX	MEDLINE=21020961; PubMed=11140637;		
RA	Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T.,		
RA	Herrmann J., Wu J.C., Fesik S.W.;		
RT	"Structural basis for binding of Smac/DIABLO to the XIAP BIR3		
RL	domain.";		
RL	Nature 408:1004-1008(2000).		
CC	-1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9.		
CC	-1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions		
CC	inhibit apoptotic suppressor activity.		
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.		
CC	-1- TISSUE SPECIFICITY: UBIQUITOUS, EXCEPT PERIPHERAL BLOOD		
CC	LEUCOCYTES.		
CC	-1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3		
CC	and -7, while the third BIR is involved in caspase-9 inhibition.		
CC	The interactions with SMAC and PRSS25 are mediated by the second		
CC	and third BIR domains.		
CC	-1- SIMILARITY: BELONGS TO THE IAP FAMILY.		
CC	-1- SIMILARITY: CONTAINS 3 BIR REPEATS.		

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CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U45880; AAC50373.1; -
CC DR EMBL; U32974; AAC50518.1; -
CC DR EMBL; AL121601; CAB95312.1; -
CC DR PDB; 1G3F; 10-JAN-01.
CC DR Genew; HGNC:592; BIRC4.
CC MIM; 300079; -
CC DR InterPro; IPR001370; BIR.
CC DR InterPro; IPR001841; Znf_fing.
CC DR Pfam; PF00097; Zf-C3HC4; 1.
CC DR Pfam; PF00653; BIR; 3.
CC DR SMART; SM00238; BIR; 3.
CC DR SMART; SM00184; RING; 1.
CC DR PROSITE; PS01282; BIR_REPEAT_1; 3.
CC DR PROSITE; PS01443; BIR_REPEAT_2; 3.
CC DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC DR PROSITE; PS50089; ZF_RING_2; 1.
CC DR Apoptosis; Zinc-finger; Repeat; Thiol protease inhibitor;
CC 3d-structure.
CC KW REPEAT 26 93 BIR 1.
CC FT REPEAT 163 230 BIR 2.
CC FT REPEAT 265 330 BIR 3.
CC FT ZN_FING 450 485 RING-TYPE.
CC FT MUTAGEN 214 214 D->S; REDUCED INTERACTION WITH PRSS25.
CC FT MUTAGEN 314 314 E->S; DECREASED INTERACTION WITH SMAC AND
CC WITH PRSS25.
CC FT CONFLICT 162 162 S -> C (IN REF. 1).
CC FT CONFLICT 423 423 Q -> P (IN REF. 2).
CC SQ SEQUENCE 497 AA; 56684 MW; 90394C16D45EB635 CRC64;
CC -----
Query Match 27.8%; Score 911; DB 1; Length 497;
Best Local Similarity 33.8%; Pred. No. 6.4e-53;
Matches 205; Conservative 89; Mismatches 163; Indels 150; Gaps 14;
CC -----
QY 35 NKKKKKYPSCELYIMSYTTPPAQVPVYSERSLARAGFYTVGVNDKVCFCGGLHDMNK 94
DB 18 NKEE--FEVEENLKEKFANFPSSPVASASTLARAGLYTEGTVRCFSCHAAVDRMQ 74
QY 95 LGSPIQHKDLPRSCSTIQLNLSASLSTSKNTSPMRNSF-AHSLSPIERSLSIFSQSY 153
DB 75 YGDSAVGHRHRYSPRCRINQNGFYLENSAQTSNGSIQNGYKVENYVLSGRHFALDRPS- 133
QY 154 SLSGPNPLNSRAVEDISSRINPYSYAMSTEARPLTYHMP-LTFPLSELARAGFYI 212
DB 134 ETHADYLLRTQVVDISDT-IYPRNPAYSEARLKSIFQMPDVAHLPRELASAGLYT 192
QY 213 GPGDVACFAGCGKSLNNEPKDASERRRHPNCPFL-----EN 252
DB 193 GIGDVOYQFCGCGKIKNNEPDRASERRRHPNCFYVLRNLNTRSESDAYSNDNFPN 252
QY 253 SLETLRFISNLKQTHAARMFTFYWPSSVVPQPDOLASAGFYVYGRNDYKFCQDCG 312
DB 253 STNLPK----NPSMADYEARITFTFTWYS--VNNEQLARAGFYALGEGDKYKFCGCG 306
QY 313 LRWSSGDDPVYEHAKMPPRCGFLIRMGQGFVEDEQRYPHLLDQ-LTSTDQTGEENA 371
DB 307 LTMKPSDDPWEQDAKMTPGCKYTLLEQKQETINN--HLHSLECLVRIETK----- 359
QY 372 DPEIIFHPGSSSSSDAYAMNTPVYKSALEMGFNLDVKQYQVSKILLTGENYKYTVNDIV 431
DB 360 -----PSLRRRIDDTILFQNPVQGAIRMGFSFKDIKKINEEKIQISGMYKSLVLY 411
QY 432 SALNADEKREKEKEQAEMASDLSILIKNRNALFOQLTCVPIIDNLKANYINQ 491

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Db 412 ADLVNAQKDSMODE-----425
Qy 492 EHDINKKTOPIQARELIPTLVKGNAAANIRKNCLEKIDSTLYKKNLFDVKNMKYTPTE 551
Db 426 -----SSQTSIQ-----KII-----435
Qy 552 DVSGLSLEOLRLQERTCKVCMDEKVSVPFPCGHLVYCOEAPSLRKCPCIOGRIING 611
Db 436 -----STEEDLRRLQERKCKICMDRNIATVFPDGHLYVCKQCAEAVDKPCMYITTF 490
Qy 612 TVRTFLS 618
Db 491 KOKIFMS 497

RESULT 8
BIR1_MOUSE STANDARD; PRT; 496 AA.
AC 060989; 008865;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bcl-2 viral IAP repeat-containing protein 4 (Inhibitor of apoptosis
  protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
  (IAP homolog A) (MIAP3) (MIAP-3).
GN BIRC4 OR API3 OR XIAP OR APIA OR MIHA.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  NCBI_TaxID=10090;
  [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uten A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT Cloning and expression of apoptosis inhibitory protein homologs that
  function to inhibit apoptosis and/or bind tumor necrosis factor
  receptor-associated factors."
  Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
  [2]
RN
RP SEQUENCE FROM N.A.
RA Paratani R., Lefevre C., Korneluk R.G., Mackenzie A.E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
  (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
  inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
  and -7, while the third BIR is involved in caspase-9 inhibition.
  The interactions with SMAC and PRS25 are mediated by the second
  and third BIR domains (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC
DR EMBL: U36842; AAC52594.1; -
DR EMBL: U88990; AAB58376.1; -
DR HSSP: Q13490; IQBH.
DR MGD: MGI:107572; Birc4.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; ZnF_Iing.
DR Pfam: PF00097; zf-C3HC4_1.
DR Pfam: PF00653; BIR_3.
DR SMART: SM00238; BIR_3.

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DR SMART: SM00184; RING_1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT 2N_RING 449 484 RING-TYPE.
FT CONFLICT 208 208 E -> K (IN REF. 2).
FT CONFLICT 317 317 E -> D (IN REF. 2).
FT CONFLICT 322 322 W -> C (IN REF. 2).
FT CONFLICT 346 346 S -> P (IN REF. 2).
FT CONFLICT 360 360 S -> P (IN REF. 2).
FT CONFLICT 388 388 I -> L (IN REF. 2).
FT CONFLICT 449 449 C -> S (IN REF. 2).
FT CONFLICT 462 462 V -> F (IN REF. 2).
FT CONFLICT 468 468 V -> A (IN REF. 2).
FT CONFLICT 490 490 K -> N (IN REF. 2).
SQ SEQUENCE 496 AA; 56079 MW; EC5FAE0799F2CDD8 CRC64;

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Query Match 27.8%; Score 910; DB 1; Length 496;
Best Local Similarity 32.5%; Pred. No. 7,4e-53;
Matches 203; Conservative 92; Mismatches 156; Indels 174; Gaps 14;

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Qy 27 ILSDWTNSKQKKKYPSCELYRMSTYTPPAQVPSERSLAAGYYGVNDKVCFC 86
Db 13 VLAD---TNKDE---FVEEFNRLKTFANPSSPVASATLARGLYGEGDTVCCFC 66
Qy 87 GLMDNMKLGDSPIQKHOKLYPSCSFIONLVASLSLSTSKNTSPMNSFASLPTLHS 146
Db 67 HAALDKQYDSDAVGRRRLSPICRI-----NGYFENGAAQSTNPGIOG 113
Qy 147 SLFS---GSYSLSPNP-----LNSRAVEDISSSTFNPYSAMSTEAREFLTYHM 193
Db 114 QYSEKNCVGNRNPADRPETHADYLRGQVYDISDT- IYRNPAMCSEAR- KSFQV 172
Qy 194 WP-LTSLPSBELARAFYYIGPDRAVACFACGCKLSNMEPKDAMEHRRHPCFEL- 250
Db 173 WPDYAHLPRELASAGLYTGGADDOVCCGCKLKNMEPCDAMSEHRRHPCFEL- 232
Qy 251 -----ENSLFLRPSISNLSMOTHAARKRTPMYPSPVQVPEOLASA 293
Db 233 RNVNVSSEGVSDRNFPNSTNSP-----NPAAEYEARLYVFGTWSS--VAKEDLARA 286
Qy 294 GFTYVGRNDVYKFCDDGLRCWESGDDPWEHAKNFPCEFTLRKGGFVDEIOGRYP 353
Db 287 GFYALGEGDVYKFCFGGGGLTDMKPSDEPWEQHAQVPCGKYLLDEKGOEYINNI- 341
Qy 354 HLEQLLSTSDTGEENADPPIIHFGPSSSDAMVMMTPVYKSLMEGFRNDLYKQYV 413
Db 342 HLHSLSEESIGRTAERT-----PSLTKKIDITIFONPVQEAIRNGFSKDKITM 392
Qy 414 OSKILTTGENTKVNQVNDIVSALNAEDEKREERKEKQAEEMASDLSLRKNRALEFOQLT 473
Db 393 EEKIQSGSSYLSLEVLINDIVSAQKNDNDE-----424
Qy 474 CVLPILDLNLKANVINKQEHDIKQTKQIPLQARELIDITLVKGNAAANIRKNCLEIDS 533
Db 425 -----SSQTSIQ-----431
Qy 534 TLTKNLFDVKNMKYITFEDVSGLSLEOLRLQERTCKVCMDEKVSVPFPCGHLVYCO 593
Db 432 -----KDISTEOLRLQERKCKICMDRNIATVFPDGHLYVCK 471
Qy 594 ECAPSLRKCPCIOGRIKGVRTFLS 618
Db 472 QCAEAVDKPCMYITTFKOKIFMS 496

RESULT 9
BIR1_RAT

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ID      BIR4.PAT      STANDARD:      PRT:      496 AA.
AC      Q9R016:
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE      protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE      (IAP homolog A) (RIAP3) (RIAP-3).
GN      BIR4 OR AIP3 OR XIAP.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_Taxid=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Saito N.;
RT      "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA.";
RL      Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
CC      -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC      (by similarity).
CC      -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC      inhibit apoptotic suppressor activity (by similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC      -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC      and -7, while the third BIR is involved in caspase-9 inhibition.
CC      The interactions with SMAC and PRSS25 are mediated by the second
CC      and third BIR domains (by similarity).
CC      -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC      -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC      -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC      -----
CC      This SMSS-PROT entry is copyright. It is produced through a collaboration
CC      the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: AB033366; BAA85304.1;
DR      HSSP: Q13450; IQBH.
DR      InterPro: IPR001370; BIR.
DR      InterPro: IPR001841; Znf_rlng.
DR      Pfam: PF000097; zf-C3HC4; 1.
DR      Pfam: PF00653; BIR; 3.
DR      SMART: SM00238; BIR; 3.
DR      SMART: SM00184; RING; 1.
DR      PROSITE: PS01282; BIR_REPEAT_1; 3.
DR      PROSITE: PS00143; BIR_REPEAT_2; 3.
DR      PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR      PROSITE: PS50089; ZF_RING_2; 1.
DR      PROSITE: PS50089; ZF_RING_2; 1.
KM      Apoptosis; Zinc-finger; Repeat.
FT      REPEAT 26 93
FT      REPEAT 163 230
FT      REPEAT 264 329
FT      ZN_FING 449 484
FT      ZN_FING 449 484
SQ      SEQUENCE 496 AA; 56072 MW; E250E3C77461A469 CRC64;

Query Match      27.6%; Score 904.5; DB 1; Length 496;
Best Local Similarity 33.2%; Pred. No. 1.7e-52;
Matches 206; Conservative 86; Mismatches 155; Indels 173; Gaps 15;

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QY      198 FLSPSELARAGFYIIGPGDRAVACAFACGKLSNWEKDKAMSEHRRHFNCPPL----- 250
DB      178 HSPRELASAGLYYIGIDQYOCFCGCGKLRKMWEPDRAMSEHRRHFPNCFVYLGKRVNV 237
QY      251 -----ENSLFRLRFSISNSMGTTHAARMTFMYWSSVYVQPEOLASGEFYV 298
DB      238 REESGVSDRNPNSTNSR-----NPAAEYDARRIYTFGTWLYS--VNKEQLARAGFYAL 291
QY      299 GRNDVYKPCFCGCGGLRCWESGDDPWVHAHAKWPFCEFLIRMGQFVDEIOGRYPHILEQ 358
DB      292 GEGDKYKCHCGGGLTDWKPSPEDPMPQAHKWPFGCKYLLDEKQGEYINNI-----HLTSS 346
QY      359 LSTSDTGEENADPEIHFPGSESSSEDAVMANTPVVKSALEMGNRDLVKQYVQSKTL 418
DB      347 LGEISVYRTAEKT-----PSVTKIDDTITFONPMVOEAIRMGFNFDIKTKMEKIQ 397
QY      419 TTGENKTYNDIVSALINMADEKREERKQAEENASDDLILRKRMALFQOLCVLPI 478
DB      398 TSGSNYLSLEVLIADLVSAOKNSODE-----SSQTSIQ----- 424
QY      479 LNLKANYINKOEHDIIKQTOIPLQARELIDTILVKGMAANIEKCKLEIDSTLYKN 538
DB      425 -----SSQTSIQ----- 431
QY      539 LVYDKMKYITPEDVSGLSLEBQLRLQERFCCKYCKMKEVSVIPGCHLYVQCECAPS 598
DB      432 -----KDISTEBQLRLQERFKLCKMDRNIIVFPGCHLYVQCKOCABA 476
QY      599 LKRCPIRCGIIRKGVTFPLS 618
DB      477 VDKCPMCCTVITFKQIFMS 496

RESULT 10
IAP2.DROME
ID      IAP2.DROME      STANDARD:      PRT:      498 AA.
AC      Q24307; Q24177; Q24115; Q24149; Q9V7G1;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Apoptosis 2 inhibitor (inhibitor of apoptosis 2) (DIAP2) (DIAP) (IAP
DE      homolog A) (IAP-1like protein) (DIAP).
GN      IAP2 OR IIP OR DIHA OR CG8293.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC      Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC      Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_Taxid=7227;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Tissue-Eye imaginal disk;
RC      MEDLINE-96149249; PubMed-8548811;
RA      Hay B.A., Massarman D.A., Rubin G.M.;
RT      "Drosophila homologs of baculovirus inhibitor of apoptosis proteins
RT      function to block cell death.";
RL      Cell 83:1253-1262(1995).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Tissue-Embryo;
RC      MEDLINE-96149249; PubMed-8552191;
RA      Liston P., Roy N., Tamal K., Iefevre C., Baird S., Chertton-Horvat G.,
RA      Farhan R., McLean M., Ikeda J., MacKenzie A., Korneluk R.G.;
RT      "Suppression of apoptosis in mammalian cells by NAIP and a related
RT      family of IAP genes.";
RL      Nature 379:349-353(1996).
RN      [3]
RP      SEQUENCE FROM N.A.
RA      STRAIN-Canton-S;
RC      MEDLINE-96256286; PubMed-8654366;
RA      Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,
RA      Gillilan M.C., Shields H., Hardwick J.M., Thompson C.B.;
RT      "A conserved family of cellular genes related to the baculovirus IAP

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RT gene and encoding apoptosis inhibitors.";  
 RL EMBL J. 15:2685-2694(1996).  
 RN [4]  
 RC SEQUENCE FROM N.A.  
 RA STRAIN=Canlon-S;  
 RL Ross J.L.;  
 RN Thesis (1991), Vanderbilt University / Nashville, U.S.A.  
 RP [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bekeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,  
 RA Abirli J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borzova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mikhlov G., Mitsuhashi N.V., Modarres C., Morris J., Mostreli A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,  
 RA Palazozo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Stronge R., Sun E.,  
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Weissman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RN Science 287:2185-2195(2000).  
 RL [6]  
 RP SEQUENCE OF 17-498 FROM N.A.  
 RC TISSUE=Larva;  
 RX MEDLINE=96209843; PubMed=863514;  
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
 RT "Cloning and expression of apoptosis inhibitory protein homologs that  
 RT function to inhibit apoptosis and/or bind tumor necrosis factor  
 RT receptor-associated factors.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RRR AND  
 CC HID-DEPENDENT CELL DEATH IN THE EYE.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS THROUGHOUT  
 CC DEVELOPMENT.  
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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CC -----  
 DR EMBL: L49441; AAC1610.1; -  
 DR EMBL: U45881; AAC46988.1; -  
 DR EMBL: U32373; AAC47155.1; -  
 DR EMBL: M96581; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: AE003809; AAF58095.1; -  
 DR EMBL: U38809; AAB08398.1; -  
 DR HSSP: Q13480; 10RR.  
 DR Flybase; FBgn015247; 1ap2.  
 DR InterPro; IPR001370; BIR.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR Pfam; PF00653; BIR; 3.  
 DR SMART; SM00238; BIR; 3.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE; PS00143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS00518; zf-RING\_1; FALSE\_NEG.  
 DR PROSITE; PS00089; zf-RING\_2; 1.  
 KW Apoptosis; Zinc-finger; Repeat.  
 FT REPEAT 9  
 FT REPEAT 113 179 BIR 1.  
 FT REPEAT 212 279 BIR 2.  
 FT ZN\_FING 451 486 RING-TYPE.  
 FT CONFLICT 5 5 G -> V (IN REF. 2).  
 FT CONFLICT 40 40 N -> K (IN REF. 2).  
 FT CONFLICT 64 65 ER -> AG (IN REF. 3).  
 FT CONFLICT 94 94 E -> K (IN REF. 1).  
 FT CONFLICT 282 282 A -> D (IN REF. 6).  
 FT CONFLICT 286 286 P -> S (IN REF. 3).  
 FT CONFLICT 302 302 P -> Q (IN REF. 2 AND 5).  
 FT CONFLICT 303 303 P -> T (IN REF. 6).  
 FT CONFLICT 327 327 A -> T (IN REF. 2).  
 FT CONFLICT 369 376 ALEVRPP -> DMRCASR (IN REF. 3).  
 SQ SEQUENCE 498 AA; 54506 MW; 66EC36DA6ED24AD6 CRC64;  
 Query Match 22.7%; Score 744.5; DB 1; Length 498;  
 Best local similarity 30.8%; Pred. No. 6,2e-42;  
 Matches 182; Conservative 85; Mismatches 206; Indels 117; Gaps 16;  
 QY 46 ELYRMSTYTFPAGVPSERSLARAGFYTYGVNDKYCFCCGLMDNKLGDSPICKHQ 105  
 DB 9 ESVRLTLPFEPMLNVAVSADYVAFNFPATGMNLEAHCYHRIDRWYGGQVVAERHR 68  
 QY 106 IVPSCFIGNIVASLSGSKNTSPMRNSFANSLPTLHSSLFSGSYSLSNPINRSRA 165  
 DB 69 SSFICSMV--LAPNRCGNVPR-----SOSDNGNS-- 97  
 QY 166 VEDISSRTNPYSAMSTEAREFLTYHMPPLTFLSPSELARAGFYTYGPDVACFACGG 225  
 DB 98 VYDSPESCSCP--DLLLEANRLVTFKDPNPIITFQALAKAGFYLYNRLDHYKVCWCG 154  
 QY 226 KLSNWEPKDAMSEHRHHPNCPFLE-----NSLETLEFSLNSMOTH---AA 271  
 DB 155 VIAKWKNNAEENHRFPPOCPOMPLIFATCKNLDELGIOTPLPLRKYACVDA 214  
 QY 272 RMTETWYSPSVYOP--EOLASAGFYVGRNDVYKFCDDGGLRGESDDPVEHAKMF 330  
 DB 215 RLRTFTDWPIS-NIOPASLAADAGLYYQKIGDOVRCFNGNIGLRSMQKDEDFEAKKS 273  
 QY 331 PRCEPLIRKGOGEFYDEIOGRYPHLEOLLSTSDTTEENADPPIIHFGSSSSDAVM 390  
 DB 274 PKQGFLLAKGPAYVEVLA-----TTAANASSPPAT--APAPTLGADVLM 317  
 QY 391 MNTPVYKSLMGFNMDYKQYVOSKILTGENYKIVNDIVSALNADEKKEEENKKA 450  
 DB 318 DEAP-AKEALALGIDGIVVNAIQRLLSSGCAFSTLDELIDFDGAGAALEVRPP 376  
 QY 451 EEMASDLESLIRNRALFQQLTQVPIIDNLLKANVINKQEHDIKQTKIPL--QARE 508  
 DB 377 EPSA-----FPIEPCQATTKASVPIPADS-----IPAKQAAE 412  
 QY 509 LIDTILVKNMAANIFKNCLEIKETIDSTLYKNLPVDKNMKYIPEDVSGLSLEQRLQEE 568

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Db      413 -----AVANISK-----ITDEIOKM;VATPNGN;SLEENRQLMDA 448
Oy      569 RCTCKMDEKSVVFIPCGHLVWCOEAPSLKPCITCG;INGVTRFELS 618
      1 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      449 RICKKCIDEEGVVFLPCGHATCNOCAPSVANCNCMRALITIGVFRTELS 498

RESULT 11
IAP3..NPVOP          STANDARD:      PRF:      268 AA.
AC      P41437:
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Apoptosis inhibitor 3 (IAP-3).
GN      IAP3 OR IAP.
OS      Orgyria pseudotsugata multicapsid polyhedrosis virus (OPMNPV).
OC      Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC      Nucleopolyhedrovirus.
OX      NCBI_TaxID=164623;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=94187094; PubMed=8139034;
RA      Birnbaum M.J., Clem R.J., Miller L.R.;
RT      "An apoptosis-inhibiting gene from a nuclear polyhedrosis virus
      encoding a polypeptide with Cys/His sequence motifs."
      J. Virol. 68:2521-2528(1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97271300; PubMed=9126251;
RA      Athens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
      Rohrmann G.F.;
RT      "The sequence of the Orgyria pseudotsugata multinuclcapsid nuclear
      polyhedrosis virus genome."
      Virology 229:381-399(1997).
CC      -1- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY
      PREVENTING VIRAL STIMULATION OF APOPTOSIS.
CC      -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC      -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: L22564; AAB02610.1; -.
DR      EMBL: U75930; AAC59034.1; -.
DR      HSSP: Q13490; 10BH.
DR      InterPro: IPR001370; BIR.
DR      InterPro: IPR001841; Znf_fing.
DR      Pfam: PF00097; zf-C3HC4; 1.
DR      Pfam: PF00653; BIR; 2.
DR      SMART: SMO0238; BIR; 2.
DR      SMART: SMO0184; RING; 1.
DR      PROSITE: PS01282; BIR_REPEAT_1; 2.
DR      PROSITE: PS0143; BIR_REPEAT_2; 2.
DR      PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR      PROSITE: PS50089; ZF_RING_2; 1.
KW      Apoptosis; zinc-finger; Repeat.
FT      REPEAT      18      BIR 1.
FT      REPEAT      84      BIR 1.
FT      REPEAT      111     BIR 1.
FT      ZN_FING      221     RING-TYPE.
FT      ZN_FING      256     RING-TYPE.
SQ      SEQUENCE      268 AA; 30076 MW; DF89175FDE85A708 CRC64;

Query Match      15.7%; Score 513; DB 1; length 268;
Best Local Similarity 24.1%; Pred. No. 5, 1e-27;
Matches 107; Conservative 51; Mismatches 86; Indels 200; Gaps 4;

181 MSTEARFLTYHMMELFLFSLSELARACFYIIGPDVYACFACGKLSNWEPKDDAMSEH 240

```

[illegible]

CC SIGNALS.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.  
CC -----  
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DR EMBL: AF135492; AAC56764.1; -  
DR EMBL: AF131205; AAC56760.1; -  
DR HSSP: U66326; AAC52974.1; -  
DR HSSP: Q13490; 10BH.  
DR MGD: MGI:1298220; Birtle.  
DR InterPro: IPR001370; BIR.  
DR Pfam: PF00653; BIR; 3.  
DR SMART: SMO0238; BIR; 3.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
DR PROSITE: PS01443; BIR\_REPEAT\_2; 3.  
DR PROSITE: PS50837; NACHT; 1.  
KW Apoptosis; Repeat; Multigene family.  
FT REPEAT 60 127 BIR 1.  
FT REPEAT 159 227 BIR 2.  
FT REPEAT 278 345 BIR 3.  
FT DOMAIN 464 759 NACHT.  
FT CONFLICT 92 92 K -> R (IN REF. 1).  
FT CONFLICT 144 144 S -> R (IN REF. 1).  
FT CONFLICT 242 242 S -> G (IN REF. 2).  
FT CONFLICT 472 472 T -> A (IN REF. 2).  
FT CONFLICT 516 516 A -> D (IN REF. 2).  
FT CONFLICT 521 521 A -> T (IN REF. 2).  
FT CONFLICT 533 533 V -> A (IN REF. 2).  
FT CONFLICT 538 538 S -> I (IN REF. 2).  
FT CONFLICT 1092 1092 E -> D (IN REF. 2).  
FT CONFLICT 1129 1129 H -> L (IN REF. 2).  
FT CONFLICT 1137 1137 R -> Q (IN REF. 2).  
FT CONFLICT 1242 1242 V -> I (IN REF. 2).  
FT CONFLICT 1276 1276 D -> N (IN REF. 2).  
SQ SEQUENCE 1403 AA; 159695 MW; B27F645043BCE; 42 CRC64;

Query Match 15.4%; Score 506; DB 1; Length 1403;  
Best Local Similarity 27.3%; Pred. No. 1,4e-25  
Matches 175; Conservative 73; Mismatches 216; Indels 176; Gaps 27;

OY 14 SYONKISIMEDSTILSDWTNSKOKMYDFSC-----LYRMSTYSTFPAGVPSERS 66  
DB 31 AFOVAKSOEE-----HKERMKKKGFNSQMSAKRLTFTYDFPSWTP---QE 80  
OY 67 IARAGFYTVGVNDKYKCCGGLMDNMLGSDPIOKHOLYFSCFIONLYVASLGSTSK 126  
DB 81 MAAGFYTVGVNKGVLQVCCSLIFGNSLRKPIERHKKLRCECFLO---GKDVGNIGK 137  
OY 127 NTSFARNSFAHSLSPTEHSSLFSGSYSLSPNPLNSRAVEDISSRTNPYSAMSTEEA 186  
DB 138 YDIRK-----SPEKM-----LRGKARY--HEEEA 161  
OY 187 RFLYTHAMPPLTF--LSPBELARAGFYVGGPDVACFACGKGLSWEBKRDAMSEHRRHF 244  
DB 162 RLESSEDMPPFAHAGTSPVLSSAGFVFGKRDYQCFSCGSGIAGNWBEGDDPWKEHAKWF 221  
OY 245 PNCPLEN--SLETFRFSISNLSMOTHA-----R 272  
DB 222 PKCEFLQKSSSEELAYOTIQSEGVHTGEHFVKSWMRRELIMWSAYCNDVSFANEELR 281  
OY 273 MTFWYSSVVPVOPDOLASAGFYVGRNDVKCCDCGGLKWCESGDDPWVHAHAKFPR 332  
DB 282 KDMFKDMQESVGEALVYAGFFYTGKKDIYRCSCGGLKNAEGDDPMEDHKKFPE 341  
OY 333 CEFILRMKGQ--EFVDEIGRPHLLQLLSDTTGEEN--ADEPLTH----- 377

DB 342 CVFLQTLKSSAEVITLOSQ-----ALPEATETTRSNHGDAAVHSTVVDLGSEAKW 396  
OY 378 FCGESESSEDA-----VMANTPVYKSAI-----EMGFNRDLVKQVQSKILLT 420  
DB 397 FQEAHSLDEQLNDYNTKATFRMNLPEVCCSLGTHLSCDVSIISKHISQVQ--EALFI 455  
OY 421 GENTYVLDIYSALLNADEKREERK---EKOAEASDLSLIRKNMALFOULTVLP 477  
DB 456 PEVEFNLMSVMC---VEGETGSGKTTFELKRIAFILMASGCCPLVFPQVFLYSLSTIP 511  
OY 478 ILDNLKLNVIKOEHDIIKQTOIPLQARELIDTILVGNMAAMIFKNCL-KEIDSTLY 536  
DB 512 --DGL-ANIIQAQ-----LHGAGGCTSEY---CLASS10QLOH 544  
OY 537 KNLFDVKNMKYIPTEDVSGI-SLEBQLRLQEE---RTC 571  
DB 545 QVLF-----LDYSGIASLPQALHTLTITKNYLSRFC 576

RESULT 13  
BIR\_MOUSE STANDARD; PRT; 1403 AA.  
ID BIR\_MOUSE  
AC Q9JIB6; P81704; O09122; O09121;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 1f (Neuronal apoptosis  
DE Inhibitory protein 6).  
GN BIRCLF OR NAIP6 OR NAIP-Rs4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20414747; PubMed=10958627;  
RA Endrizzi M.G., Hadnoto V., Growney J.D., Miller W., Dietrich W.F.;  
RT "Genomic sequence analysis of the mouse Naip gene array."  
RL Genome Res. 10:1093-1102(2000).  
RN [2]  
RP SEQUENCE OF 82-168 FROM N.A.  
RX STRAIN=129/SvJ;  
RA MEDLINE=97131520; PubMed=8975718;  
RA Scharf J.M., Damron D., Fritsella A., Bruno S., Beggs A.H.,  
RA Kunkel L.M., Dietrich W.F.;  
RT "The mouse region syntenic for human spinal muscular atrophy lies  
RT within the Igml critical interval and contains multiple copies of Naip  
RT exon 5."  
RL Genomics 38:405-417(1996).  
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
CC SIGNALS.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.  
CC -----  
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FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1403 AA; 159823 MW; 9D4912503356C4E9 CRC64;

Query Match 15.2%; Score 499.5; DE 1; Length 1403;
Best Local Similarity 27.4%; Pred. No. 3.7e-25;
Matches 169; Conservative 73; Mismatches 214; Indels 161; Gaps 25;

OY 33 NSNKKKKYDFSC-----LYRMSTYSTFPAGVPYSEBSLARAGFYTVGNDKVCFC 85
D 43 HKERMKKKKGFNSQMRSEAKRLKTFESYDTRFSWT- QEMAAAGYHGVKLGVCFC 99
OY 86 CGMLDMWKLGDSPLOKHOLYPCSFQNLVNASLSTSKNTSPMNSFAHSLSPLEH 145
D 100 CSILFGNSLRKLPTEHKKLRPECEFLQ--GNDVGNICKYDIRK----- 143
OY 146 SLSFGSYSLSPNPLNSRAVEDISSRTNPIYSAMTEEARLTYMMLTF--LSPSE 203
D 144 -----SPEKM-----LRGKARY--HEEERLESFEDWPFYAGHSIPRA 180
OY 204 LARAGFYIGPGRVACFACGKLSNMPKDDAMSEHRRHFPNCPLEN--SLETLRFST 261
D 181 LSAAGFYFTGKRDTVQCFSCGSLGNWBGDDPWKEHAKMPPKCEFLQSKKSSEIAGYI 240
OY 262 SNLSMOTHA-----RMRTMYTPSSVPVQPBOLA 291
D 241 QDEGEFVHTGEHFVKSVMRELPMVSAYCNDSVFTNEELRMFMFKDMPQESPVEALV 300
OY 292 SAGFYVGRNDVYKCCDGGDLRCWESGDDPWYEHAKMPPKCEFLIMKGO--EVDYDIOG 350
D 301 RAGFYTGKDIYKCFSCGGLKEMAGDDPMEDHIFPEECVFLQTLKSAEVIPTLQS 360
OY 351 RYPHLLQLLSTDTTGEENAD-----PRIHFGPE-----SSEDA----- 388
D 361 QY-----ALPEATETRESHNDAAVHSTVVDLGRSEAGMFOEARSLSQLRITYTKTS 415
OY 389 -VMANTPVVKSAL-----MGFNRLVYQVQSKI--LTTGENKYTVNDIVSALLNDE 440
D 416 FCHMNLPEVCSLGTDLHLCDSVSIISKHVSOPVQALTPPIVFSNLSVWCEGEGSG 475
OY 441 KREERKQAEEMASDLSLRKNRMALFOOLCVLPILNLKANYINKEHDIIOKT 500
D 476 KTTFLK-RIFLWASGCCPLIRPOLVFLYLSLSTIP--DQGLANITCQ----- 522
OY 501 QIPLOARELIDTILVKNAANIFKNCL-KEIDSTLYKNLFDVKNMKYIPTEDVSGI--SL 558
D 523 -----LLGAGGCISEV---CLSSSIQOLQHQVLF-----LDVSGIASLI 559
OY 559 EEOURLQEE-----RTG 571
D 560 PQALHTLITLITKNYLFRTG 576

RESULT 14
BIR_MOUSE
ID BIR_MOUSE STANDARD; PRT; 1402 AA.
AC 09J1B3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis
DE Inhibitory protein 7).
GN BIRC1G OR NAIIP).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=20414747; PubMed=10958627;
RA Endritz M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;

```

```

RT "Genomic sequence analysis of the mouse Nalp gene array.";
RL Genome Res. 10:11095-1102(2000).
CC - FUNCTION: PREVENTS MOTOR NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC - SIMILARITY: CONTAINS 3 BIR REPEATS.
CC - SIMILARITY: CONTAINS 1 NACHT DOMAIN.
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CC
DR EMBL; AF242433; AAF82749.1; -.
DR HSSP; O13490; IQBH.
DR MGD; MGI:1858256; Birc1g.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR_3.
DR SMART; SM00238; BIR_3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS50837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1402 AA; 159662 MW; C1DFPBA359893E0D CRC64;

Query Match 15.2%; Score 498.5; DE 1; Length 1402;
Best Local Similarity 26.9%; Pred. No. 4.3e-25;
Matches 167; Conservative 69; Mismatches 217; Indels 167; Gaps 23;

OY 33 NSNKKKKYDFSC-----LYRMSTYSTFPAGVPYSEBSLARAGFYTVGNDKVCFC 85
D 43 HKERMKKKKGFNSQMRSEAKRLKTFESYDTRFSWT- QEMAAAGYHGVKLGVCFC 99
OY 86 CGMLDMWKLGDSPLOKHOLYPCSFQNLVNASLSTSKNTSPMNSFAHSLSPLEH 145
D 100 CSILFGNSLRKLPTEHKKLRPECEFLQ--GNDVGNICKYDIRK----- 143
OY 146 SLSFGSYSLSPNPLNSRAVEDISSRTNPIYSAMTEEARLTYMMLTF--LSPSE 203
D 144 -----SPEKM-----LRGKARY--HEEERLESFEDWPFYAGHSIPRV 180
OY 204 LARAGFYIGPGRVACFACGKLSNMPKDDAMSEHRRHFPNCPLEN--SLETLRFST 261
D 181 LSAAGFYFTGKRDTVQCFSCGSLGNWBGDDPWKEHAKMPPKCEFLQSKKSSEIAGYI 240
OY 262 SNLSMOTHA-----RMRTMYTPSSVPVQPBOLA 291
D 241 QDEGEFVHTGEHFVKSVMRELPMVSAYCNDSVFANEELRMFMFKDMPQESPVEALV 300
OY 292 SAGFYVGRNDVYKCCDGGDLRCWESGDDPWYEHAKMPPKCEFLIMKGO--EVDYDIOG 350
D 301 RAGFYTGKDIYKCFSCGGLKEMAGDDPMEDHIFPEECVFLQTLKSAEVIPTLQS 360
OY 351 RYPHLLQLLSTDTTGEEN-ADPPIH-----FPGSESSDA----- 388
D 361 QY-----ALPEATETRESHNGDAVHSTVVDLGRSEAGMFOEARSLSQLRITYTKTS 415
OY 389 -VMANTPVVKSAL-----MGFNRLVYQVQSKI--LTTGENKYTVNDIVSALLNDE 440
D 416 FCHMNLPEVCSLGTDLHLCDSVSIISKHVSOPVQALTPPIVFSNLSVWCEGEGSG 474
OY 440 KREERKQAEEMASDLSLRKNRMALFOOLCVLPILNLKANYINKEHDIIOKT 497
D 475 GKTTFLK-RIFLWASGCCPLIRPOLVFLYLSLSTIPDQGLANITCQ----- 524
OY 498 QKQIPLQARELIDTILVKNAANIFKNCL-KEIDSTLYKNLFDVKNMKYIPTEDVSGI 556

```



GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:57:12 ; Search time 150.94 Seconds

(without alignments)  
843.627 Million cell updates/sec

Title: us-08-569-749-2

Perfect score: 3277

Sequence: 1 MHRTASQRLFPSPSYONIKS.....LRKPCICRGIIKGTVTFTLS 618

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL\_21:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_virus:\*  
17: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2630	80.3	589	11	09QZC6
2	2625	80.1	589	11	09QZC6
3	2339	71.4	610	13	057319
4	2185	66.7	602	11	09ESD2
5	1833	55.9	628	13	08UWD2
6	1318	40.2	374	11	0921NO
7	1138.5	34.7	324	13	09DND2
8	945.5	28.9	224	11	088642
9	898.5	27.4	501	11	09E005
10	898.5	27.4	501	11	09E005
11	896.5	27.4	496	11	09ESF0
12	894	27.3	493	13	08UYF8
13	801.5	24.5	197	13	091A69
14	796.5	22.3	195	13	091A70
15	737.5	22.5	498	5	096003
16	684.5	20.9	405	13	08UWH2

17	500.5	15.3	346	5	0968T8
18	494	15.1	597	11	09R015
19	490	15.0	438	5	09VUX5
20	486	14.8	281	12	09VNL8
21	481.5	14.7	379	5	09U492
22	479	14.6	403	5	08WRD9
23	476	14.5	264	12	09EN27
24	475.5	14.5	276	12	089744
25	470	14.3	261	12	090ES9
26	466.5	14.2	377	5	09N107
27	463.5	14.1	298	4	096CA5
28	462.5	14.1	280	4	09HAP7
29	460.5	14.1	236	4	096RW5
30	460.5	14.1	298	4	09H2A8
31	459.5	14.0	236	6	095M71
32	458.5	14.0	236	4	096P09
33	457.5	14.0	236	6	095M72
34	456.5	13.9	402	5	08T621
35	423.5	12.9	313	12	09J827
36	366.5	12.1	276	12	08OL95
37	368.5	11.2	268	12	091F18
38	363.5	11.1	268	12	09E232
39	240	7.3	292	12	092394
40	239.5	7.3	210	4	09B0V0
41	231.5	7.1	284	12	09TKL5
42	222	6.8	285	12	09PY09
43	220	6.7	301	12	09P254
44	217.5	6.6	243	12	091EW1
45	207.5	6.3	517	11	08R4U8

## ALIGNMENTS

RESULT 1

09QZC6 PRELIMINARY; PRT: 589 AA.

ID 09QZC6: 01-MAY-2000 (TRENBLREL.13, Created)

DT 01-MAY-2000 (TRENBLREL.13, Last sequence update)

DT 01-DEC-2001 (TRENBLREL.19, Last annotation update)

DE Inhibitor of apoptosis protein 2.

OS Rattus norvegicus (Rat).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_taxid=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;

RA Dong Z., Denton M., Gu S.M., Sakumar P., Venkatachalam M.A.;

RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2.,"

RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL; AF190020; AAF04585.1; -

DR HSSP; Q13490; IOBH.

DR InterPro; IPR001370; BIR.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR001841; Znf\_fing.

DR Pfam; PF00653; BIR; 3.

DR Pfam; PF00619; CARD; 1.

DR SMART; PF00097; zf-C3HC4; 1.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.

DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.

DR PROSITE; PS50209; CARD; 1.

KW Zinc-finger.

SO SEQUENCE 589 AA; 66777 MW; E6812PFEJEA34142 CMC64;

Query Match 80.3%; Score 2630; DB 11; Length 589;

Best Local Similarity 81.7%; Pred. No. 1.6e-177;

Matches 488; Conservative 53; Mismatches 48; Indels 4;

```

OY 22 MEDSTLSDMTNSKOKMKYDFSCELYRMSTYSTFPAGVPVSESLARAGFYTGVDNV 81
DB 1 MENSTVLSNMTENKEMKAYDSCELYRMSTYSAPPRGVPSERSLARAGFYTGVDNV 60
OY 82 KCFCCGLMDNKLKSDSPLOKHOLYPCSCFQNTLVSAVSGSTSKNTSPMRSPASHSLP 141
DB 61 KCFCCGLMDNKKOGDSPLEKHOYFPCSFVQTLISGGLSAAKNTSPAKRFAHSL-- 118
OY 142 TLEHSLFSGSYSLSPNPLNSRAVEDISSRTNPTSYAMSTEAREFLTHMPLFLSP 201
DB 119 PLEQ----GGHSLSPSNPLNSRAVEDF-SLRMNPCTSYAMSTEAREFLTHMPLFLSP 173
OY 202 SELARAGFYTGPDGRVACFACGKLSNMPKDDAMSEHRRHFPNCPLENSLETFLRSI 261
DB 174 AELARAGFYTGPDGRVACFACGKLSNMPKDDAMSEHRRHFPNCPLENSLETFLRSI 233
OY 262 SNLSMOTHAARMTFMWPSVYVQPEOLASAGFYVGNDDVKFCDDGGLRCWESGDD 321
DB 234 SNLSMOTHAARMTFMWPSVYVQPEOLASAGFYVGNDDVKFCDDGGLRCWESGDD 293
OY 322 PVEHAKMFPCEFLIRMGQFVEIQARYPHLLLEQLLSTSDTGEENADPPIHFGG 381
DB 294 PVEHAKMFPCEFLIRMGQFVEIQARYPHLLLEQLLSTSDTGEENADPPIHFGG 353
OY 382 ESSSEDVAMANTPVYKSALEMGFNLDYKQVOSKILTTGNYKTVNDIVSALLNAEDK 441
DB 354 E-NMEDAVAMANTPVYKSALEMGFNLDYKQVOSKILTTGNYKTVNDIVSALLNAEDK 412
OY 442 REEEKEROSEETASGDSLIRKRNALFOQLTCVPIIDNLKAVYNKOEHDIIKORTO 501
DB 413 REEEKEROSEETASGDSLIRKRNALFOQLTCVPIIDNLKAVYNKOEHDIIKORTO 472
OY 502 IPLQARELIDTLVKGNAANAFKNCLEIDSTLYKNLFVDKNMKTIPEDVSGSLSEQ 561
DB 473 IPLQARELIDTLVKGNAANAFKNCLEIDSTLYKNLFVDKNMKTIPEDVSGSLSEQ 532
OY 562 LRRLOBERTCKYCMKEVSVFIPCGHLVYVCECAPSLRKCPCICGIIKGYRTFLS 618
DB 533 LRRLOBERTCKYCMKEVSVFIPCGHLVYVCECAPSLRKCPCICGIIKGYRTFLS 589

```

RESULT 2

Q9ESER PRELIMINARY: PRT: 589 AA.

AC 09ESER: 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)

DE Inhibitor of apoptosis protein 2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI\_Taxid=10116;

SEQUENCE FROM N.A.

RA Hojick M., Lefebvre C.A., Hicks K., Korneluk R.G.: "Cloning and Characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes." Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR HSSP: Q13490.1GBH.

DR InterPro: IPR001370: BIR.

DR InterPro: IPR001315: CARD.

DR InterPro: IPR001841: Znf\_fing.

DR Pfam: PF00653: BIR; 3.

DR Pfam: PF00619: CARD; 1.

DR Pfam: PF00097: zf-C3HC4; 1.

DR SMART: SM00238: BIR; 3.

DR SMART: SM00114: CARD; 1.

DR SMART: SM00164: RING; 1.

DR PROSITE: PS01282: BIR\_REPEAT\_1; 2.

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DR PROSITE: PS0143: BIR_REPEAT_2; 3.
DR PROSITE: PS0209: CARD; 1.
KM Zinc-finger.
SQ SEQUENCE 589 AA: 66750 MW: 847089BD7CD285B CRC64.
Query Match 80.1%; Score 2625; DB 11; Length 589;
Best Local Similarity 81.6%; Pred. No.3-7e-177;
Matches 487; Conservative 54; Mismatches 48; Indels 8; Gaps 4;

```

RESULT 3

O57319 PRELIMINARY: PRT: 610 AA.

AC 057319: 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)

DE Inhibitor of apoptosis PROTEIN 1 (IAP) (Inhibitor of T cell apoptosis PROTEIN).

GN IAP1.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

NCBI\_Taxid=9031;

SEQUENCE FROM N.A.

RP STRAIN-WHITE LEHORN; TISSUE-EMBRYONIC FIBROBLAST;

RC MEDLINE-9803801; PubMed-9372964;

RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.: "Ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a mediator of the antiapoptotic activity of the v-rel oncoprotein." Mol. Cell. Biol. 17:7328-7341(1997).

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CC -1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
CC CELLS.
CC -1- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF
CC THE V-REL-TRANSFORMED CELLS.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE
CC SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS
CC IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
CC -1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
CC PROCESS.
CC -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
CC -1- SIMILARITY: MEMBER OF THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF
CC APOPTOSIS PROTEIN REPEAT).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL: AF008592; AAB8044.1; -.
DR HSSP: Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 1.
DR Pfam: PF00619; CARD; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR Apoptosis; Zinc-finger; Repeat.
KM REPEAT 30 97 BIR_REPEAT 1.
FT REPEAT 176 242 BIR_REPEAT 2.
FT REPEAT 262 329 BIR_REPEAT 3.
FT ZN_FING 563 597 C3HC4-TYPE.
SQ SEQUENCE 610 AA: 68924 MW: ADF47619650B4A6 CRC64:

Query Match 71.4%; Score 2339; DB 13; Length 610;
Best Local Similarity 71.4%; Pred. No. 6,1e-157;
Matches 437; Conservative 78; Mismatches 81; Indels 16; Gaps 7;

QY 20 STMEDSTILSDMTNSNQ--KKKYPSCCLYRMSTSTPSPAGVPVSRSLARAGFYTYGV 77
DB 2 NIMDSSPLLASVWKNQAHGCELYKIDLSCELYRMSTSTPSPAGVPVSRSLARAGFYTYGV 61
QY 78 NDKVCFCCGLMDNMKLGDSPIQKHQOLYPCSCFIONLVSA-SLG-SF-----SKN 127
DB 62 QDKVCFCCGLMDNMKLGDSPIQKHQOLYPCSCFIONLVSA-SLG-SF-----SKN 121
QY 128 TSPMRNSFAHSLPTLHSSLSFGSYSLSPNPLNSRAVEDISSRTNPNYSYAMSTEAR 187
DB 122 LSPSLRSM--TLSPSEQYGVSGSFSPSPDPVTRRAEDLSHLRSKLHNSMSTEAR 179
QY 188 FLTHHMPPLTLFSPSELARAGFYTYIGPDRAVACGCGKLSNWEPRDDAMSEHRRFPNC 247
DB 180 LTFTHHMPPLTLFSPSELARAGFYTYIGPDRAVACGCGKLSNWEPRDDAMSEHRRFPNC 239
QY 248 PRLNLSL-ETLRFISINLSMOTHAARMRTFMVPSVPVQPEQLASAGFYTYGRNDVVC 306
DB 240 PEVENLMRQSPFNVSNTVMQHEARVKTFFIMVPIPIVQPEQLADAGFYTYGRNDVVC 299
QY 307 FCCDGLRCWESGDDPVWEHAKWPPRCFELIRMGQEFVDEIQRYPHLEQLLSTDTT 366
DB 300 FCCDGLRCWESGDDPVWEHAKWPPRCFELIRMGQEFVDEIQRYPHLEQLLSTSDP 359
QY 367 GRENADPPIIHGPGSSSEDAVMMNTPVYKSALEGEFRDLYKQVOKIITGTGNYKT 426
DB 360 VDENDN-PLIHFPGSPEDAIIMMTVPVKALEGEFRRLIKQVOKIITGTGNYKT 418
QY 427 VNDIVSALLNADEKREERKEKQAEEMASDDSLIRKNMALFOOLTQVLPITDNLTKAN 486
DB 419 VNDIVSDDLTADDEKREERKEKQAEEMASDDSLIRKNMALFOOLTQVLPITDNLTKAN 478
QY 487 VYNKQEHDIKQKQIPIQARELIDTILVKGNAANIIFKNCKLEIDSTLYKNLFDYDKNK 546
DB 487 VYNKQEHDIKQKQIPIQARELIDTILVKGNAANIIFKNCKLEIDSTLYKNLFDYDKNK 546

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DB 479 VTTELEHNDIKQKQIPIQARELIDTILVKGNAANISFNCKLDCDDPVLYKOLFVEKSMK 538
QY 547 YPTPEDVSLGLEQRLRIQEERTCKVCMDEKSVVFIQGLHVCQECAPSLRKPCPR 606
DB 539 YPTPEDVSLGLEQRLRIQEERTCKVCMDEKSVIIFQGLHVCQECAPSLRKPCPR 598
QY 607 GIITGVPRFELS 618
DB 599 GTIKGVPRFELS 610

RESULT 4
Q9ESE9 PRELIMINARY; PRT; 602 AA.
ID Q9ESE9
AC Q9ESE9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Inhibitor of apoptosis protein 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxId=101116;
RN [1]
RP SEQUENCE FROM N. A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes.
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF183430; AAG22970.1; -.
DR HSSP: Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
KM Zinc-finger.
SQ SEQUENCE 602 AA: 67326 MW: CC91385E6A2DE5A CRC64:

Query Match 66.7%; Score 2185; DB 11; Length 602;
Best Local Similarity 67.4%; Pred. No. 4,5e-146;
Matches 411; Conservative 86; Mismatches 93; Indels 20; Gaps 7;

QY 20 STMEDSTILSDMTNS-NKQKMYDPSCELYRMSTSTPSPAGVPVSRSLARAGFYTYGV 78
DB 2 NNVQDSAFIAKLKMSADTFLKYPSCLEYRSLYSTPSPAGVPVSRSLARAGFYTYGV 61
QY 79 DAVKFCGCCGLMDNMKLGDSPIQKHQOLYPCSCFIONLVSA-----LGSTSKTS 129
DB 62 DAVKFCGCCGLMDNMKLGDSPIQKHQOLYPCSCFIONLVSA-----LGSTSKTS 119
QY 130 PMRNSFAHSLPTLHSSLSFGSYSLSPNPLNSRAVEDISSRTNPNYSYAMSTEAR 189
DB 120 TMSGPAAS-----ISTGVSGSYSPSDPVNFRANQDCPAFSIPVHFAMNTEKARLL 174
QY 190 TYHMPPLTLFSPSELARAGFYTYIGPDRAVACGCGKLSNWEPRDDAMSEHRRFPNC 249
DB 175 TYQTPPLSLSPAELAKAFIYTGPDRAVACGCGKLSNWEPRDDAMSEHRRFPNC 234
QY 250 LENSLE-TLRFISINLSMOTHAARMRTFMVPSVPVQPEQLASAGFYTYGRNDVVC 308
DB 233 LKDVQGFISQIYVSNLSMOTHAARMRTFMVPSVPVQPEQLASAGFYTYGRNDVVC 294
QY 309 CDGGLRCWESGDDPVWEHAKWPPRCFELIRMGQEFVDEIQRYPHLEQLLSTDTTGE 368
DB 309 CDGGLRCWESGDDPVWEHAKWPPRCFELIRMGQEFVDEIQRYPHLEQLLSTDTTGE 368

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Db 295 CDGGLRCWESGDDPWVHAHAKWFPCEYLIRIKQGEVGVQAGYPHILBOLLSTSDSPD 354
Qy 369 ENADPPIIHFGCESSESEDAVMMNTPVVSALEMGNRLVYKOTVOSKILLTGENKTYN 428
Db 355 EGEALIVLHSGE-NMEVAMNPNPVKRAALDMGFSRLVRQVQRIILATGENRTYS 413
Qy 429 DIVSALLNAEDEKREBEKEKQAEEMASDDLILIRKRNMLUFOOLTCVPLILDLNLKANYI 488
Db 414 DIVIGLLADEKREBEQOTQOEAEESDDLILIRKRNMLUFOOLTCVPLILDLNLKANYI 473
Qy 489 NKEHDIKOKTOIPLQARELIDTILVKGNAANIFKNCYKEIDSTLYNLFVDMKMYI 548
Db 474 TQOEYAVAKOKPH-TLOARTLIDITVLAKGNFATSPRNSI,QEIDPGLYDIFVQKIRSL 532
Qy 549 PREDVSGLSLEQRLQOEERTCKVCMQKEVSVFIPCGHLVYCCASLRKPCIRGI 608
Db 533 PDDIALMEBQRLQOEERTCKVCMQKEVSVFIPCGHLVYCCASLRKPCIRGI 592
Qy 609 IKGTVRTFLS 618
Db 593 IKGTVRTFLS 602

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RESULT 5
Q8UMD2 PRELIMINARY: PRT: 628 AA.
AC 08UMD2:
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Iapi.
GN Iapi.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT *Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.
RT Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF442500; AAL3679.1; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR Pfam; PF00653; BIR_1; znf_ring.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-CRHC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50089; zf_RING_2; 1.
SQ SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87C8A95 CRC64;

```

Query Match 55.9%; Score 1833; DB 13; Length 628;  
 Best Local Similarity 56.1%; Pred. No. 3.5e-121;  
 Matches 353; Conservative 101; Mismatches 141; Indels 34; Gaps 9;

```

Qy 21 IMEDSTILSD-WTNSNKKQMKYDFSCELYRMSTYTFPGVPSERSLARAGFYTGVD 79
Db 3 ILONSFAFLGLGRLCTSGPADLQYDNSELFRISTYAKFPTTAVENTESLARAGFYTGVD 62
Qy 80 KYKCFCCGLMDNWKLGDSPIQKHQILYPSCSFIQNL-VSASIGTSKNT-SPMNSFAH 137

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Db 63 RIQCFRCNVTADNMOSGDCPARRHKQLSPNCSFIQSLPTANILSSHAFSLRNVAVL 122
Qy 138 SLS-----PTEHSSLFSGSYSSLP-NPLNSRAVEDISSRT----NP 176
Db 123 QLSAPATAAPSTTAPSTSGQTEQOYGLNMGFTNLAPSSPISRGVEDSHQRPACHNP 182
Qy 177 YSTASTEARELTYMMWPLFLBSBELARAGFYIIGPDRAFCACGKLSNMWEKDA 236
Db 183 ---GMRREQERLDITQNMWFLATVTPAELKAGLYLGGDRVACFSCGGQLGSMWEGDA 239
Qy 237 MSHRRHFPNCFPLE-NSLETFRS-----ISNLSMOTHAARMRFEMVPPSPVQPEQ 289
Db 240 VSEHQRYHNCFFVKGDRADNITPLSGGSLSNVSNMQCCERLLTFVWMPRIYRPQ 299
Qy 290 LASAGFYVGRNDVYCFCCDGLRCWESGDDPWVHAHAKWFPCEYLIRKMQGEFVDEIQ 349
Db 300 LAKAGFYVGRNDVYCFCCDGLRCWESGDDPWVHAHAKWFPCEYLIRKMQGEFVHQIQ 359
Qy 350 GRYPHILBOLLSTDPITGEENADPPIIHFGPSESSEDAVMMNTPVVSALEMGNFRLV 409
Db 360 ARFPRLEQLTNGDSNSREFPVPHLGPGEDRSDDAVMMNPNPVKSALEMGEFRLV 419
Qy 410 KOTVOSKILLTGENYKTVNDIVSALLNAEDEKREBEKEKQAEEMASDDLILIRKRNMALE 469
Db 420 KOTVOSKILLTGENYKTVQELVSDLSADEKREBEKEKQAEEMASDDLILIRKRNMALE 479
Qy 470 QOITCVPLILDLNLKANYINKEHDIKOKTOIPLQARELIDTILVKGNAANIFKNCIK 529
Db 480 ORLKSQVOSIMDLHLEENYISQKEYSIRNCTSVKOOTGOLILVLSKGNAAEVEFMNIX 539
Qy 530 EIDSTLYKNLFYDKMKYIPREDVSGLSLEQRLQOEERTCKVCMQKEVSVFIPCGHL 589
Db 540 KNDVYLIRELMQTNENASPSODLSLPHEQRLQOEERTCKVCMQKEVSVFIPCGHL 599
Qy 590 VVQCECAPSLRKCPCICRGIIKGTVRTFLS 618
Db 600 VVQCECAPSLRKCPCICRGVAKGTVRTFLS 628

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RESULT 6
Q921NO PRELIMINARY: PRT: 374 AA.
AC Q921NO;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to baculoviral IAP repeat-containing 2.
GN BIRC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC011338; AAH1338.1; -.
DR MGD; MGI:1197007; BIRC2.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
SQ SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7E46F3 CRC64;

```

Query Match 40.2%; Score 1318; DB 11; Length 374;  
 Best Local Similarity 66.7%; Pred. No. 4.1e-85;  
 Matches 242; Conservative 49; Mismatches 54; Indels 18; Gaps 5;

```

Qy 21 IMEDSTILSDWTNSNKKQMKYDFSCELYRMSTYTFPGVPSERSLARAGFYTGVD 79
Db 1 MYODSAFLAKLMKMSADTFLKIDYDFSCELYRLSTYSAFPGVPSERSLARAGFYTGVD 60

```

QY 80 KVCFCGGLMDNMKLGDSPIOKHOLYPCSGFIONLVSA-----SLGSTRKNTSP 130  
 DB 61 KVCFCGGLMDNMKLGDSPIOKHOLYPCSGFIONLVSA-----SLGSTRKNTSP 120  
 QY 131 MRNSFAHSLPTLEHSLFSGSYSLSPNPLNSRAVED:SSSRTNPYSYAMSTEAREFLT 190  
 DB 121 L--SFAS-----ENTGYFSGSYSPSPDPVFNFRANDC:CALSLSPHPHMANTEKALTLT 173  
 QY 191 YHMPPLTFLSPSELARAGFYIIGDGVYACFACGKLSNNEPKDAMSEHRHPPNCPFL 250  
 DB 174 YETWPLSLFSLPAKLAKAGFYIIGDGVYACFACGKLSNNEPKDAMSEHRHPPNCPFL 233  
 QY 251 EN-SLETRFSISNLSQTHAARMTFMWSSVYVQPEOLASAGFYIYGANDVYKFCFC 309  
 DB 234 KDLOGASRTYVSNLSQTHAARMTFMWSSVYVQPEOLASAGFYIYGANDVYKFCFC 293  
 QY 310 DGLRCWESGDDPWEHAKMPPRCEYLLIRKQGEFYVDEIOGRYPHLEOLLSTSDTYGEE 369  
 DB 294 DGLRCWESGDDPWEHAKMPPRCEYLLIRKQGEFYVDEIOGRYPHLEOLLSTSDTYGEE 353  
 QY 370 NAD 372  
 DB 354 NAD 356

## RESULT 7

Q9DDN2 PRELIMINARY; PRT; 324 AA.  
 AC Q9DDN2;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)  
 DE Apoptosis inhibitor ch-1Apl (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pendleton C.N., Bargmann W.J., Varadarajan J., Bose H.R. Jr.,  
 RT "The apoptosis inhibitor ch-1Apl is a direct transcriptional target of  
 v-Rel and c-Rel."  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF011289; AAC42316.1; -  
 DR HSSP: Q13490; 10BH.  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR; 3.  
 DR SMART: SM00238; BIR; 3.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.  
 DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
 FT NON\_TER 324 324  
 SQ SEQUENCE 324 AA; 36567 MW; 5E2B89DEAE3733F3 CRC64;

Query Match 34.7%; Score 1138.5; DB 13; Length 324;  
 Best Local Similarity 63.4%; Pred. No. 1.6e-72;  
 Matches 206; Conservative 49; Mismatches 55; Indels 15; Gaps 6;

QY 20 SIMEDSTILSDWTNSNKO--KMKYDFECSELYRMSTYSTFPACVYVSRSLARAGFYITGV 77  
 DB 2 NIMDSPLASVYKQNHGCEKLDLSCELYRMSTYSTFPVNVYSRRLARAGFYITGV 61  
 QY 78 NDYKCCGCGGLMDNMKLGDSPIOKHOLYPCSGFIONLVSA--SLG--ST-----SKN 127  
 DB 62 QDKKCCSCGGLYLDNMPGDNAMKHKQVYVPCSFVONMLSLNMLGSTHSAFSPLYASN 121  
 QY 128 TSPARNFAHSLPTLEHSLFSGSYSLSPNPLNSRAVED:SSSRTNPYSYAMSTEAREFLT 187  
 DB 122 LSPSLRSM--TLSPSFQVGVTFSGSFSPDPVTTTAAEDLSLRKSLHPSSTEAR 179  
 QY 188 FLTYHMPPLTFLSPSELARAGFYIIGDGVYACFACGKLSNNEPKDAMSEHRHPPNCP 247  
 DB 180 LRTHHMPPLTFLSPSELARAGFYIIGDGVYACFACGKLSNNEPKDAMSEHRHPPNCP 239

QY 248 PLENSL-ETLRFSISNLSQTHAARMTFMWSSVYVQPEOLASAGFYIYGANDVYK 306  
 DB 240 PVEVNLMRDOPSEFVSNVYQTHAARMTFMWSSVYVQPEOLASAGFYIYGANDVYK 299  
 QY 307 FCCDGLRCWESGDDPWEHAKMPP 331  
 DB 300 FCCDGLRCWESGDDPWEHAKMPP 324

## RESULT 8

Q98642 PRELIMINARY; PRT; 224 AA.  
 AC Q98642;  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)  
 DE Inhibitor of apoptosis protein (Fragment).  
 GN RIAP1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-WISTAR; TISSUE-OVARY;  
 RA Bradley C.K., Laren R.R., Dharmarajan A.M.;  
 RT "Cloning and characterisation of an inhibitor of apoptosis protein  
 (IAP) in the rat corpus luteum."  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF081503; AAC32497.1; -  
 DR HSSP: Q13490; 10BH.  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR; 3.  
 DR SMART: SM00238; BIR; 2.  
 DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 224 AA; 25209 MW; 213A52534D5EB56A CRC64;

Query Match 28.9%; Score 945.5; DB 11; Length 224;  
 Best Local Similarity 74.9%; Pred. No. 4.2e-59;  
 Matches 173; Conservative 18; Mismatches 33; Indels 7; Gaps 3;

QY 93 WKLGDSPIOKHOLYPCSGFIONLVSA:SLGSTRKNTSPMNSFAHSLPTLEHSLFSGS 152  
 DB 1 WKGDSPTEKHROPYPCSFVOTLSCGLQSAKNTSPAKSRFAHSL--PLEQ---GCI 54  
 QY 153 YSSLSPLNLSRAVED:SSSRTNPYSYAMSTEAREFLT:YHMPPLTFLSPSELARAGFYI 212  
 DB 55 HSSLSPLNLSRAVED--SLNMPCSYAMSTEAREFLT:YHMPPLTFLSPSELARAGFYI 113  
 QY 213 GPGDGVYACFACGKLSNNEPKDAMSEHRHPPNCPLENSLLETRFSISNLSQTHAAR 272  
 DB 114 GPGDGVYACFACGKLSNNEPKDAMSEHRHPPNCPLENSLLETRFSISNLSQTHAAR 173  
 QY 273 MRFTHMPSSVYVQPEOLASAGFYIYGRNDVYKFCDDGLRCWESGDDPW 323  
 DB 174 MRFTHMPSSVYVQPEOLASAGFYIYGRNDVYKFCDDGLRCWESGDDPW 224

## RESULT 9

Q9E005 PRELIMINARY; PRT; 501 AA.  
 AC Q9E005;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)  
 DE Inhibitor of apoptosis protein 3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;

[1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-WISTAR; TISSUE-Ovary;  
 RC Lareu R.R., Bradley C.K., Lacher M., Fils R.R., Dharmarajan A.M.;  
 RT "Cloning, characterization and regulation of an inhibitor of apoptosis  
 protein in the rat corpus luteum."  
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AF304333; AAC41192.1;  
 DR HSSP: O13490; 10BH;  
 DR InterPro: IPR001370; BIR;  
 DR InterPro: IPR001841; Znf\_fing.  
 DR Pfam: PF00653; BIR; 3.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00238; BIR; 3.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 DR Zinc-finger.  
 SQ SEQUENCE 501 AA; 56548 MW; 0973FBF28E81C5A0 CRC64;

Query Match 27.4%; Score 898.5; DB 11; Length 501;  
 Best local similarity 33.4%; Pred. No. 2.7e-55;  
 Matches 204; Conservative 84; Mismatches 150; Indels 173; Gaps 15;

QY 33 NSNRKMKYDFSCELYRMSTYTFPAGVYSESLARAGFYTYGVNDKVCFCGGLMDN 92  
 DB 16 DTNDE---EEVEEFNRKLTFFANFPSSPVASATLARGFLYTGEGTVQCFSCHAADR 72  
 QY 93 WKLDSPLOKHKOLYPCSCFIONLVASLSGSTKNTSP-----MNSFAHS 138  
 DB 73 WQYDSSAVGRHRRISPCRFNGFYFEN-GAT-OSTSPGIONGOYKSENCVGNHFA-- 128  
 QY 139 LSPTEHSLSFGSYSLSPNPLNSRAVEDISSRTNYPYASYMTEAREFLTYHMP-LT 197  
 DB 129 ---LDRSETHAYL-----LRTGVNDISDT-IYPRNAPKSEERARKTFQWPDYA 177  
 QY 198 FLSPSELARAGFYTYIGPDRVACFCGGLSNWEPKDDAMSEHRRHPNCPFL----- 250  
 DB 178 HLSPEELASAGLYTYGIDVQCFCCGGLKNWEPKDDAMSEHRRHPNCFVLYGRNVY 237  
 QY 251 -----ENSLERFSISNLSMOTHAARMRTFMTYPSVPVQPEOLASAGFYTY 298  
 DB 238 RSESGVSSDRNFPNSTNSPR---NPMAEYDARIYFETGLYS--VNKEQLARAGFYAL 291  
 QY 299 GRNDVACFCGGLRCMESGDDPWVHAHAKWPRCEFLIRKGOEFVDEIGRYPHLEQ 358  
 DB 292 GEGDKVACFCGGLADMKPSEDPWQHAKWPRCKYLLDKGQETINNT-----HLTHS 346  
 QY 359 LLSISDTTGEENADPPIIHGPGSSSEDAVMANTPYVKSALENGFNRLVKQTVOSKIL 418  
 DB 347 LGESVVRTAERT-----PSYTKRKIDPTIFQNPVQOAIRGPNFKDIKTMEKIQ 397  
 QY 419 TTGENYTVNDIVSALLNADEKREERKQAEEMASDDLSLRKNMALFOQLTVLP 478  
 DB 398 TSGSNYLSLEVLIADLVSAQKNSQDE----- 424  
 QY 479 LDNLKANVINIKOEHDIKQTIQIOLARELIDTILVKGNAANIIFKNCKLEIDSTLYKN 538  
 DB 425 -----SSQTSIQ----- 431  
 QY 539 LFVDKNNKYIPTEDVSGLSLEBOLRLQOERTKVCMDKEVSVVFIPCGHLVYQCECAPS 598  
 DB 432 -----KDISTEBOLRLQOERTKICMDRNIAIVFVPCGHLVYQCECAEA 476  
 QY 599 LKPCICRGIT 609  
 DB 477 VDKPCICGTIV 487

RESULT 10  
 Q9EQ04 PRELIMINARY; PRT; 501 AA.  
 ID Q9EQ04

AC Q9EQ04:  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Inhibitor of apoptosis protein 3.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NX NCBI TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-WISTAR; TISSUE-Ovary;  
 RA Lareu R.R., Bradley C.K., Lacher M., Fils R.R., Dharmarajan A.M.;  
 RT "Cloning, characterization and regulation of an inhibitor of apoptosis  
 protein in the rat corpus luteum."  
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AF304334; AAC41193.1;  
 DR HSSP: O13490; 10BH;  
 DR InterPro: IPR001370; BIR;  
 DR InterPro: IPR001841; Znf\_fing.  
 DR Pfam: PF00653; BIR; 3.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00238; BIR; 3.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 DR Zinc-finger.  
 SQ SEQUENCE 501 AA; 56578 MW; 4863B69FE2E0C8CD CRC64;

Query Match 27.4%; Score 898.5; DB 11; Length 501;  
 Best local similarity 33.4%; Pred. No. 2.7e-55;  
 Matches 204; Conservative 84; Mismatches 150; Indels 173; Gaps 15;

QY 33 NSNRKMKYDFSCELYRMSTYTFPAGVYSESLARAGFYTYGVNDKVCFCGGLMDN 92  
 DB 16 DTNDE---EEVEEFNRKLTFFANFPSSPVASATLARGFLYTGEGTVQCFSCHAADR 72  
 QY 93 WKLDSPLOKHKOLYPCSCFIONLVASLSGSTKNTSP-----MNSFAHS 138  
 DB 73 WQYDSSAVGRHRRISPCRFNGFYFEN-GAT-OSTSPGIONGOYKSENCVGNHFA-- 128  
 QY 139 LSPTEHSLSFGSYSLSPNPLNSRAVEDISSRTNYPYASYMTEAREFLTYHMP-LT 197  
 DB 129 ---LDRSETHAYL-----LRTGVNDISDT-IYPRNAPKSEERARKTFQWPDYA 177  
 QY 198 FLSPSELARAGFYTYIGPDRVACFCGGLSNWEPKDDAMSEHRRHPNCPFL----- 250  
 DB 178 HLSPEELASAGLYTYGIDVQCFCCGGLKNWEPKDDAMSEHRRHPNCFVLYGRNVY 237  
 QY 251 -----ENSLERFSISNLSMOTHAARMRTFMTYPSVPVQPEOLASAGFYTY 298  
 DB 238 RSESGVSSDRNFPNSTNSPR---NPMAEYDARIYFETGLYS--VNKEQLARAGFYAL 291  
 QY 299 GRNDVACFCGGLRCMESGDDPWVHAHAKWPRCEFLIRKGOEFVDEIGRYPHLEQ 358  
 DB 292 GEGDKVACFCGGLADMKPSEDPWQHAKWPRCKYLLDKGQETINNT-----HLTHS 346  
 QY 359 LLSISDTTGEENADPPIIHGPGSSSEDAVMANTPYVKSALENGFNRLVKQTVOSKIL 418  
 DB 347 LGESVVRTAERT-----PSYTKRKIDPTIFQNPVQOAIRGPNFKDIKTMEKIQ 397  
 QY 419 TTGENYTVNDIVSALLNADEKREERKQAEEMASDDLSLRKNMALFOQLTVLP 478  
 DB 398 TSGSNYLSLEVLIADLVSAQKNSQDE----- 424  
 QY 479 LDNLKANVINIKOEHDIKQTIQIOLARELIDTILVKGNAANIIFKNCKLEIDSTLYKN 538  
 DB 425 -----SSQTSIQ----- 431  
 QY 539 LFVDKNNKYIPTEDVSGLSLEBOLRLQOERTKVCMDKEVSVVFIPCGHLVYQCECAPS 598  
 DB 432 -----KDISTEBOLRLQOERTKICMDRNIAIVFVPCGHLVYQCECAEA 476



QY 599 LRKPCIRGII 609  
Db 477 VDKCPMCTVI 487

## RESULT 11

Q9ESFO

PRELIMINARY; PRT; 496 AA.

AC Q9ESFO;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Inhibitor of apoptosis protein 3.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.

OX NCBI\_TaxId=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA HOLICK M., LeFebvre C.A., Hicks K., Korneluk R.G.;

RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes."

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL: AF183429; AAC22969.1; -

DR HSSP: Q13490; IQB.

DR InterPro: IPR001370; BIR.

DR Pfam: PF00653; BIR; 3.

DR SMART: SM00238; BIR; 3.

DR SMART: SM00184; RING; 1.

DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.

DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.

KW Zinc-finger.

SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AEC5B738 CRC64;

Query Match 27.4%; Score 896.5; DB 11; Length 496;

Best Local Similarity 33.1%; Pred. No. 3, 6e-55;

Matches 205; Conservative 86; Mismatches 155; Indels 173; Gaps 15;

QY 33 NSKKKKKKYDFSCELRMSTYTFPPAGVPYSEKSLARAGYYGVNDKVKPCCGGLMDN 92  
Db 16 DTKKDE---EFVEENRKLKTFANFPSSPVASSTLARAGFLYTGEGDYVOCFSCHAAYDR 72

QY 93 WKLGDSPIOKHQLYPCSCFIQNLVSAISLSTSKNTSP-----NRNFAHS 138  
Db 73 WQYGDASVGRHRIISPNCRIINGFEEN-GAT-QSTSPGICNGQYKSENCVGRNHPA-- 128

QY 139 LSTLEHSLFSGSYSLSPNPLNSRAVEDISSRTNPYSYAMSTEFARFLTYHAMF-LT 197  
Db 129 ---LDRPSTHADYL-----LRTGOVVDISDT-IYPRNPACSEARPKITQNPVDYA 177

QY 198 FLSPSELARAGFYIYIGPDVACFACGKSLNWEPRKDDAMSEHRHPNCPFL----- 250  
Db 178 HLSPRELHSLAGLYTIGDIDVOYFCGCGKLKNEPCDRANSRHRHPNCFEVLGRNVY 237

QY 251 -----ENSLTELFSSISLNSMOTHAARMRTFMYTPSSVPVOPOLASAGFYVY 298  
Db 238 RSESGVSSDRNFPNSNTPR-----NPAMAEYDARIYTFGTWLYS--VNRQGLARAGFYAL 291

QY 299 GRNDVYKFCGCGGLKRCWESGDDPWYBHAQWPRCEFLIMKQOEYVDEIQGRYPHLLEO 358  
Db 292 GEDBKACFCGCGGLTDWKSEDPWEDHAKWPGCKYLLDEKGOEYINNI-----HLTHS 346

QY 359 LLESTSDTGEENADPPIIHGPGESSEDAVMNTPPVKSGALMGFNRLDVKOTVOSKIL 418  
Db 347 LGSVYVTKAKT-----PSYTKKIDDTITQNPVQDAIIMGFENKIDKTMEEKIQ 397

QY 419 TTGENTKYVNDIVSALLNADEKREBEKEQAQEMASDDLIRKRNMAFLQOOLTCVLP 478  
Db 398 TSGSNLTSLLEVLIADIVLSAQKNSODE----- 424

QY 479 LDNLKANVINKOEHDIIKQTOIPLQARELIDTILVKGNAANIRKNCLEIDSTLYKN 538  
Db 425 -----SSQTSIQ----- 431

## RESULT 12

Q8UVF8

PRELIMINARY; PRT; 493 AA.

AC Q8UVF8;

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Inhibitor of apoptosis protein 3.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OX NCBI\_TaxId=9031;

RN [1]

RP SEQUENCE FROM N.A.

RA Bridgman J.T., Johnson A.L.;

RT Identification of chicken inhibitor of apoptosis protein XIAP

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF451854; AAL47170.1; -

DR InterPro: IPR001370; BIR.

DR Pfam: PF00653; BIR; 3.

DR SMART: SM00238; BIR; 3.

DR SMART: SM00184; RING; 1.

DR PROSITE: PS01282; BIR\_REPEAT\_1; UNKNOWN\_2.

DR PROSITE: PS50089; ZF\_RING\_2; 1.

KW SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;

Query Match 27.3%; Score 894; DB 13; Length 493;

Best Local Similarity 34.5%; Pred. No. 5, 4e-55;

Matches 210; Conservative 77; Mismatches 150; Indels 172; Gaps 18;

QY 30 DWTNSKKKKYDFSCELRMSTYTFPPAGVPYSEKSLARAGYYGVNDKVKPCCGGLM 89  
Db 22 EWTQ-----EHYRTGTFVEFPHPDCPPASALARAGFYVGEGRKVCFCSCHTY 69

QY 90 LDWKKLGDSPIOKHQLYPCSCFIQNLVSAISLSTSKNTSPMNSPAH-----SLS 140  
Db 70 VEGMEPQSDSIDRKNLSPCRFTG--SAFL--BNNHPLVQSHQHRNENSSWLALP 124

QY 141 PTLHSLFSGSYSLSPNPLNSRAVEDISSRTNPYSYAMSTEFARFLTYHAMF-PLTEFL 199  
Db 125 SAEEDLSVDEADVL-----LRTROVVDMSDT-LYKKNPAMCEEARLKSFNHWPEYGL 177

QY 200 SPSELARAGFYIYIGPDVACFACGKSLNWEPRKDDAMSEHRHPNCPFL-----ENS 253  
Db 178 TPKEHLSAGLYTIGDIDVOYFCGCGKLKNEPCDRANSRHRHPNCFEVLGRNVY 237

QY 254 LELTARSTIS-----NLSMOTHAARMRTFMYTPSSVPVOPOLASAGFYVGRND 302  
Db 238 TDSICAEIGRSCNNQHRNPNSMAEYERRIQFLAH--IYVKNKHLAAGYTSIGNED 295

QY 303 DYKFCGCGGLKRCWESGDDPWYBHAQWPRCEFLIMKQOEYVDEIQGRYPHLLEO 362  
Db 296 HVCFCGCGGLQEWKNEBPDWDHAKWPGCKFLRDEKGLFEITNV-----HLRD--GC 347

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QY 363 SDTGEADNPRIIFHGSGSSSDAVMNTPVYKSALEMGFNDRDYKQVOSKIITGE 422
D 348 RDSI-TEAEVTL-----PRDDLQN-OLVONALHMGFSUSEIRISMEKRLHSGE 397
QY 423 NYKVNDIVSALNAEDEKREKEKQAEWASDLSTRNRNALFOQLCVPIIDLNT 482
D 398 SYTSVEDVADLISAKENIKNGEPPKES----- 425
QY 483 LKANVINKQEHDIKQITQIPLQARELIDTILVGNMAANIFKNCLEIDSTLYKNLEFVD 542
D 426 -----PLE----- 428
QY 543 KMKYIPTEDVSGLSLEQLRLQERTCKYCKMDKEVSVFPGHLYVCOCAPSLJKC 602
D 429 -----QDLSIEKRLROBEKCKCKCMKADISVILPGCHLVACECAAVAKK 477
QY 603 PI-CRGIIR 610
D 478 PLCCITNIK 486

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## RESULT 13

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QY 091A69 PRELIMINARY; PRT; 197 AA.
AC 091A69;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BREED FAYOUMI; TISSUE=SPLEEN;
RX MEDLINE=21158006; PubMed=11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
RT specific genes."
RL Poul. Sci. 80:284-288(2001).
DR EMBL; AF221083; AAF35320.1;
DR HSSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00338; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT NON_TER 197
SO SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

```

Query Match 24.5%; Score 801.5; DB 13; Length 197;  
 Best Local Similarity 68.4%; Pred. No. 5.2e-49;  
 Matches 134; Conservative 33; Mismatches 28; Indels 1; Gaps 1;

```

QY 155 SLSPNPINRAVEDISSRTNPTYSAMSTEARFLTYHMPILTFSPSELARAGTYTGP 214
D 2 SFDDPVTTRAEDLSHRSLKLNHPMSSTEARLRTFHAWPLMPLSPLELAKAGLYTGT 61
QY 215 GDRVACFCAGGKLSNWEKDDAMSEHRRHPNCPLENSL-ETLRFISINLSMOTHAARM 273
D 62 ADKVAACFTCGQLSNWEKDDAMSEHRRHPNCPLENSL-ETLRFISINLSMOTHAARM 121
QY 274 RTFMWPSVVPVQPEOLASAGFYVGRNDVYKFCGCGGLFCWESGDDPWVEHAKWPPRC 333
D 122 KTFIMWPRIPVQPEOLADAGFYVGRNDVYKFCGCGGLFCWESGDDPWVEHAKWPPRC 181
QY 334 EFLIRMKGOEFVDEIQ 349
D 182 EYLLRVKGGEFVSQVQ 197

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## RESULT 14

```

QY 091A70 PRELIMINARY; PRT; 195 AA.
AC 091A70;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BREED LEGHORN; TISSUE=SPLEEN;
RX MEDLINE=21158006; PubMed=11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
RT specific genes."
RL Poul. Sci. 80:284-288(2001).
DR EMBL; AF221082; AAF35319.1;
DR HSSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00338; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT NON_TER 195
SO SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

```

Query Match 24.3%; Score 796.5; DB 13; Length 195;  
 Best Local Similarity 68.2%; Pred. No. 1.2e-48;  
 Matches 133; Conservative 33; Mismatches 28; Indels 1; Gaps 1;

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QY 155 SLSPNPINRAVEDISSRTNPTYSAMSTEARFLTYHMPILTFSPSELARAGTYTGP 214
D 1 SFDDPVTTRAEDLSHRSLKLNHPMSSTEARLRTFHAWPLMPLSPLELAKAGLYTGT 60
QY 215 GDRVACFCAGGKLSNWEKDDAMSEHRRHPNCPLENSL-ETLRFISINLSMOTHAARM 273
D 61 ADKVAACFTCGQLSNWEKDDAMSEHRRHPNCPLENSL-ETLRFISINLSMOTHAARM 120
QY 274 RTFMWPSVVPVQPEOLASAGFYVGRNDVYKFCGCGGLFCWESGDDPWVEHAKWPPRC 333
D 121 KTFIMWPRIPVQPEOLADAGFYVGRNDVYKFCGCGGLFCWESGDDPWVEHAKWPPRC 180
QY 334 EFLIRMKGOEFVDEI 348
D 181 EYLLRVKGGEFVSQVQ 195

```

Query Match 24.3%; Score 796.5; DB 13; Length 195;  
 Best Local Similarity 68.2%; Pred. No. 1.2e-48;  
 Matches 133; Conservative 33; Mismatches 28; Indels 1; Gaps 1;

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QY 096003 PRELIMINARY; PRT; 498 AA.
AC 096003;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE I03477P.
GN IAP2 OR CG8293.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

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RA Champe M Chavez C., Dorsett V., Farfan D., Fritse E., George R.,  
RA Gonzalez M., Guerin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nunoo J., Paclcel J., Patagas V., Park S., Ploumangvong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,  
RL Submitted (AUG-2001) to the EMBL/Genbank/DBE databases.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC EMBL: AY051844; AAK93268.1; --  
DR FlyBase: FBgn0015247; Iap2.  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR001841; znf\_ring.  
DR Pfam: PF00653; BIR: 3  
DR Pfam: PF00097; zf-C3HC4\_1.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; UNKNOWN\_3.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
DR Zinc-finger.  
SQ SEQUENCE 498 AA: 54537 MW: 00D0303DB2526FFA22 CRC64;

GenCore version 5.1.4-p5.4578  
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OK protein - protein search, using sw model

Run on: May 5, 2003, 15:59:02 ; Search time 3.73848 Seconds

(Without alignments)  
432.866 Million cell updates/sec

Title: US-08-569-749-5

Perfect score: 307

Sequence: 1 CELYRMSTYSTFPAGVPVSE.....KVKCCGGLMDNKLGDSP 55

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCrus.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/Backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	307	100.0	55 4 US-08-569-749-5	Sequence 5, Appli
2	307	100.0	55 5 PCT-US96-12860-5	Sequence 5, Appli
3	307	100.0	618 2 US-08-511-485-8	Sequence 8, Appli
4	307	100.0	618 3 US-09-212-971-8	Sequence 8, Appli
5	307	100.0	618 4 US-08-800-929A-8	Sequence 8, Appli
6	307	100.0	618 4 US-08-569-749-2	Sequence 2, Appli
7	307	100.0	618 4 US-09-617-053A-8	Sequence 2, Appli
8	307	100.0	618 4 US-09-069-023-29	Sequence 29, Appli
9	307	100.0	618 5 PCT-US96-12860-2	Sequence 2, Appli
10	301	98.0	55 4 US-08-569-749-6	Sequence 2, Appli
11	301	98.0	55 5 PCT-US96-12860-6	Sequence 6, Appli
12	301	98.0	604 2 US-08-511-485-6	Sequence 6, Appli
13	301	98.0	604 3 US-09-212-971-6	Sequence 6, Appli
14	301	98.0	604 4 US-08-800-929A-6	Sequence 6, Appli
15	301	98.0	604 4 US-08-569-749-4	Sequence 4, Appli
16	301	98.0	604 4 US-09-617-053A-6	Sequence 4, Appli
17	301	98.0	604 5 PCT-US96-12860-4	Sequence 6, Appli
18	298	97.1	68 2 US-08-511-485-19	Sequence 19, Appli
19	292	95.1	68 2 US-08-511-485-18	Sequence 18, Appli
20	291	94.8	612 3 US-09-212-971-14	Sequence 14, Appli
21	291	94.8	612 4 US-08-800-929A-14	Sequence 14, Appli
22	291	94.8	612 4 US-08-569-749-14	Sequence 14, Appli
23	291	94.8	612 4 US-09-617-053A-14	Sequence 14, Appli
24	291	94.8	612 5 PCT-US96-12860-14	Sequence 14, Appli
25	284	92.5	600 4 US-09-212-971-12	Sequence 12, Appli
26	284	92.5	600 4 US-08-800-929A-12	Sequence 12, Appli
27	284	92.5	600 4 US-09-617-053A-12	Sequence 12, Appli

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31	159	51.8	497 4 US-08-800-929A-4	Sequence 4, Appli
32	159	51.8	497 4 US-09-617-053A-4	Sequence 4, Appli
33	153	49.8	68 2 US-08-511-485-16	Sequence 16, Appli
34	153	49.8	496 3 US-08-511-485-10	Sequence 10, Appli
35	153	49.8	496 3 US-09-212-971-10	Sequence 10, Appli
36	153	49.8	496 4 US-08-800-929A-10	Sequence 10, Appli
37	153	49.8	496 4 US-09-617-053A-10	Sequence 10, Appli
38	150	48.9	438 5 PCT-US95-05922A-2	Sequence 2, Appli
39	138	45.0	68 2 US-08-511-485-27	Sequence 27, Appli
40	133	43.3	68 2 US-08-511-485-26	Sequence 26, Appli
41	132	43.0	68 2 US-08-511-485-28	Sequence 28, Appli
42	132	43.0	268 4 US-08-836-134-22	Sequence 22, Appli
43	132	43.0	268 4 US-09-493-784-22	Sequence 22, Appli
44	130	42.3	68 2 US-08-511-485-21	Sequence 21, Appli
45	128	41.7	68 2 US-08-511-485-20	Sequence 20, Appli

## ALIGNMENTS

RESULT 1  
US-08-569-749-5  
Sequence 5, Application US/08569749  
Patent No. 6187557

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Goeddel, David V

TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,749

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brezner, David J.

REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)781-1989

TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 55 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-569-749-5

Query Match 100.0%; Score 307; DB 4; Length 55;

Best Local Similarity 100.0%; Pred. No. 4.9e-37;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDNKKVCFCCGGLMDNKLGDSP 55

Db 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDNKKVCFCCGGLMDNKLGDSP 55

RESULT 2  
PCT-US96-12860-5  
Sequence 5: Application PC/TUS9612860  
GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOMBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 55 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-5

Query Match 100.0%; Score 307; DB 5; Length 55;  
Best Local Similarity 100.0%; Pred. No. 4.9e-37;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTPAGVPSERSLARAGFYTGNDKVKFCGGLMDNKKLGDSP 55  
DB 1 CELYRMSTSTPAGVPSERSLARAGFYTGNDKVKFCGGLMDNKKLGDSP 55

RESULT 3  
US-08-511-485-8  
Sequence 8: Application US/08511485  
Patent No. 5919912  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07940/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-511-485-8

Query Match 100.0%; Score 307; DB 2; Length 618;  
Best Local Similarity 100.0%; Pred. No. 9.1e-36;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTPAGVPSERSLARAGFYTGNDKVKFCGGLMDNKKLGDSP 55  
DB 45 CELYRMSTSTPAGVPSERSLARAGFYTGNDKVKFCGGLMDNKKLGDSP 99

RESULT 4  
US-09-212-971-8  
Sequence 8: Application US/09212971B  
Patent No. 6107041  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212,971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017,354  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-212-971-8

Query Match 100.0%; Score 307; DB 3; Length 618;  
Best Local Similarity 100.0%; Pred. No. 9.1e-36;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTPAGVPSERSLARAGFYTGNDKVKFCGGLMDNKKLGDSP 55  
DB 45 CELYRMSTSTPAGVPSERSLARAGFYTGNDKVKFCGGLMDNKKLGDSP 99

RESULT 5  
US-08-800-929A-8

Sequence 8, Application US/08800929A  
Patent No. 633437  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF  
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996  
APPLICATION NUMBER: 60/017,354  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bieker-Brady, Kristina  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-800-929A-8

Query Match  
Best Local Similarity 100.0%; Score 307; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 9.1e-36;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTPPAGVPVSESLARAGFYTGVDNKVKCFCCGLMDNKKLGDSP 55  
DB 45 CELYRMSTSTPPAGVPVSESLARAGFYTGVDNKVKCFCCGLMDNKKLGDSP 99

RESULT 6  
US-08-569-749-2  
Sequence 2, Application US/08569749  
Patent No. 6187557  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Goeddel, David V  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco

STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-2

Query Match  
Best Local Similarity 100.0%; Score 307; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 9.1e-36;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTPPAGVPVSESLARAGFYTGVDNKVKCFCCGLMDNKKLGDSP 55  
DB 45 CELYRMSTSTPPAGVPVSESLARAGFYTGVDNKVKCFCCGLMDNKKLGDSP 99

RESULT 7  
US-09-617-053A-8  
Sequence 8, Application US/09617053A  
Patent No. 6300492  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
NUMBER OF SEQUENCES: 17  
CURRENT FILING DATE: 2000-07-14  
PRIOR FILING DATE: 1997-02-13  
CURRENT APPLICATION NUMBER: US 08/800,929  
PRIOR APPLICATION NUMBER: US 08/800,929  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 8  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-617-053A-8

Query Match  
Best Local Similarity 100.0%; Score 307; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 9.1e-36;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTPPAGVPVSESLARAGFYTGVDNKVKCFCCGLMDNKKLGDSP 55  
DB 45 CELYRMSTSTPPAGVPVSESLARAGFYTGVDNKVKCFCCGLMDNKKLGDSP 99

RESULT 8  
US-09-069-023-29  
Sequence 29, Application US/09069023A  
Patent No. 6348573  
GENERAL INFORMATION:  
APPLICANT: Nunez, Gabriel  
APPLICANT: Inohara, Naohiro  
APPLICANT: Koseki, Takeyoshi  
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
FILE REFERENCE: UM-0333  
CURRENT APPLICATION NUMBER: US/09/069,023A  
CURRENT FILING DATE: 1998-04-27  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 29  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-069-023-29

Query Match 100.0%; Score 307; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 9, 1e-36;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNWKLGDS 55  
Db 45 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNWKLGDS 99

RESULT 9  
PCT-US96-12860-2  
Sequence 2, Application PC/TUS9612860  
GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-2  
Query Match 100.0%; Score 307; DB 5; Length 618;

Best Local Similarity 100.0%; Pred. No. 9, 1e-36;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNWKLGDS 55  
Db 45 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNWKLGDS 99

RESULT 10  
US-08-569-749-6  
Sequence 6, Application US/08569749  
Patent No. 6187557  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Goeddel, David V  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)398-3249  
TELEFAX: (415)781-1989  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 55 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-6

Query Match 98.0%; Score 301; DB 4; Length 55;

Best Local Similarity 98.2%; Pred. No. 3, 6e-36;  
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNWKLGDS 55  
Db 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNWKLGDS 55

RESULT 11  
PCT-US96-12860-6  
Sequence 6, Application PC/TUS9612860  
GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 55 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-6

Query Match 98.0%; Score 301; DB 5; Length 55;  
Best Local Similarity 98.2%; Pred. No. 3.6e-16;  
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVKCCGGLMDNWKLGDSF 55  
Db 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVKCCGGLMDNWKRGDSP 55

RESULT 12  
US-08-511-485-6  
Sequence 6, Application US/08511485  
Patent No. 5919912  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
City: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:

LENGTH: 604 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-511-485-6

Query Match 98.0%; Score 301; DB 2; Length 604;  
Best Local Similarity 98.2%; Pred. No. 6.4e-35;  
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVKCCGGLMDNWKLGDSF 55  
Db 28 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVKCCGGLMDNWKRGDSP 82

RESULT 13  
US-09-212-971-6  
Sequence 6, Application US/09212971B  
Patent No. 6107041

GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212,971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017,354  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 604  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-212-971-6

Query Match 98.0%; Score 301; DB 3; Length 604;  
Best Local Similarity 98.2%; Pred. No. 6.4e-35;  
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVKCCGGLMDNWKLGDSF 55  
Db 28 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVKCCGGLMDNWKRGDSP 82

RESULT 14  
US-08-800-929A-6  
Sequence 6, Application US/08800929A  
Patent No. 6133437  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF  
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elding LLP



STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA: US/08/800,929A  
APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996  
APPLICATION NUMBER: 60/017,354  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bieker-Brady, Kristina  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 604 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-800-929A-6

Query Match 98.0%; Score 301; DB 4; Length 604;  
Best Local Similarity 98.2%; Pred. No. 6.4e-35;  
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPYSESLARAGFYTGVDKVKFCGGLMDWKRKGDSP 55  
DB 28 CELYRMSTYSTFPAGVPYSESLARAGFYTGVDKVKFCGGLMDWKRKGDSP 82

RESULT 15  
US-08-569-749-4  
Sequence 4, Application US/08569749  
Patent No. 6187557  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Goeddel, David V  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brenner, David J.  
REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 604 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-4

Query Match 98.0%; Score 301; DB 4; Length 604;  
Best Local Similarity 98.2%; Pred. No. 6.4e-35;  
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPYSESLARAGFYTGVDKVKFCGGLMDWKRKGDSP 55  
DB 28 CELYRMSTYSTFPAGVPYSESLARAGFYTGVDKVKFCGGLMDWKRKGDSP 82

Search completed: May 5, 2003, 16:09:09  
Job time : 4.73848 secs

GenCore version 5.1.4\_P5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 15:59:02 ; Search time 3.12673 Seconds

(without alignments)  
432.866 Million cell updates/sec

Title: US-08-569-749-7

Perfect score: 269

Sequence: 1 LARAGFYIIGDRVACFACGKLSNWEKDDAMSEHRRHPPNCPF 46

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2.6/ptodata/1/1aa/5A.COMB.fep:\*  
2: /cgn2.6/ptodata/1/1aa/5B.COMB.fep:\*  
3: /cgn2.6/ptodata/1/1aa/6A.COMB.fep:\*  
4: /cgn2.6/ptodata/1/1aa/6B.COMB.fep:\*  
5: /cgn2.6/ptodata/1/1aa/PCITUS.COMB.fep:\*  
6: /cgn2.6/ptodata/1/1aa/Backfiles1.fep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	269	100.0	46	4	US-08-569-749-7
2	269	100.0	46	5	PCT-US96-12860-7
3	269	100.0	67	2	US-08-511-485-23
4	269	100.0	438	5	PCT-US95-05922A-2
5	269	100.0	618	2	US-08-511-485-8
6	269	100.0	618	4	US-09-212-971-8
7	269	100.0	618	4	US-08-800-929A-8
8	269	100.0	618	4	US-08-569-749-2
9	269	100.0	618	4	US-09-617-053A-8
10	269	100.0	618	4	US-09-069-023-29
11	269	100.0	618	5	PCT-US96-12860-2
12	269	100.0	612	3	US-09-212-971-14
13	269	98.1	612	4	US-08-800-929A-14
14	269	98.1	612	4	US-08-569-749-14
15	269	98.1	612	4	US-09-617-053A-14
16	269	98.1	612	4	PCT-US96-12860-14
17	269	98.1	612	5	US-08-511-485-22
18	269	98.1	612	2	US-08-511-485-6
19	269	98.1	612	4	US-09-212-971-6
20	269	98.1	612	4	US-08-800-929A-6
21	269	98.1	612	4	US-09-617-053A-6
22	269	98.1	612	4	US-08-569-749-8
23	269	98.1	612	4	PCT-US96-12860-8
24	269	98.1	612	4	US-08-569-749-4
25	269	98.1	612	4	PCT-US96-12860-4
26	269	98.1	612	4	US-09-212-971-12
27	269	98.1	612	4	US-08-800-929A-12

28	241	89.6	600	4	US-09-617-053A-12	Sequence 12, Appl
29	192	71.4	68	2	US-08-511-485-21	Sequence 21, Appl
30	192	71.4	497	2	US-08-511-485-21	Sequence 4, Appl
31	192	71.4	497	3	US-09-212-971-4	Sequence 4, Appl
32	192	71.4	497	3	US-08-800-929A-4	Sequence 4, Appl
33	192	71.4	497	4	US-09-617-053A-4	Sequence 4, Appl
34	187	69.5	68	2	US-08-511-485-20	Sequence 20, Appl
35	187	69.5	496	3	US-08-511-485-10	Sequence 10, Appl
36	187	69.5	496	3	US-09-212-971-10	Sequence 10, Appl
37	187	69.5	496	4	US-08-800-929A-10	Sequence 10, Appl
38	187	69.5	496	4	US-09-617-053A-10	Sequence 10, Appl
39	155	57.6	236	4	US-09-121-979-4	Sequence 4, Appl
40	155	57.6	236	4	US-09-332-319-4	Sequence 4, Appl
41	155	57.6	236	4	US-09-239-867-2	Sequence 25, Appl
42	151	56.1	66	2	US-08-511-485-25	Sequence 25, Appl
43	151	56.1	236	4	US-09-239-867-4	Sequence 24, Appl
44	150	55.8	66	2	US-08-511-485-24	Sequence 24, Appl
45	149	55.4	1151	3	US-08-836-134-23	Sequence 23, Appl

#### ALIGNMENTS

RESULT 1  
US-08-569-749-7  
; Sequence 7, Application US/08569749  
; Patent No. 6187557  
; GENERAL INFORMATION:  
; APPLICANT: Rothe, Mike  
; APPLICANT: Goedel, David V  
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/569,749  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brezner, David J.  
; REGISTRATION NUMBER: 24,774  
; REFERENCE/DOCKET NUMBER: A-62464/DJB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)781-1989  
; TELEFAX: (415)398-3249  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 46 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-569-749-7

Query Match 100.0%; Score 269; DB 4; Length 46;  
Best local similarity 100.0%; Pred. No. 4.3e-28;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGDRVACFACGKLSNWEKDDAMSEHRRHPPNCPF 46  
DB 1 LARAGFYIIGDRVACFACGKLSNWEKDDAMSEHRRHPPNCPF 46

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RESULT 2
PCT-US96-12860-7
; Sequence 7, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBRACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-12860-7

Query Match          100.0%; Score 269; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 4,3e-28;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
Db 1 LARAGFYIIGPGRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46

RESULT 3
US-08-511-485-23
; Sequence 23, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; NUMBER OF SEQUENCES: 38
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

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SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-511-485-23

Query Match          100.0%; Score 269; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 6,4e-28;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
Db 21 LARAGFYIIGPGRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 66

RESULT 4
PCT-US95-05922A-2
; Sequence 2, Application PC/TUS9505922A
; GENERAL INFORMATION:
; APPLICANT: HE, ET AL.
; TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05922A
; FILING DATE: 11 MAY 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-292
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; PCT-US95-05922A-2
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Query Match 100.0%; Score 269; DB 5; Length 438;  
Best Local Similarity 100.0%; Pred. No. 4,7e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNMEPKDDAMSEHRRHFPNCPF 46  
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DB 24 LARAGFYIIGPDRVACFACGKLSNMEPKDDAMSEHRRHFPNCPF 69

RESULT 5  
US-08-511-485-8  
Sequence 8, Application US/08511485  
Patent No. 5919912

GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION/DOCKET NUMBER: 30,162  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ. ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein

US-08-511-485-8

Query Match 100.0%; Score 269; DB 2; Length 618;  
Best Local Similarity 100.0%; Pred. No. 6,8e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNMEPKDDAMSEHRRHFPNCPF 46  
|||||  
DB 204 LARAGFYIIGPDRVACFACGKLSNMEPKDDAMSEHRRHFPNCPF 249

RESULT 6  
US-09-212-971-8  
Sequence 8, Application US/092129718  
Patent No. 6107041

GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212,971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017,354  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 8  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-212-971-8

Query Match 100.0%; Score 269; DB 3; Length 618;  
Best Local Similarity 100.0%; Pred. No. 6,8e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNMEPKDDAMSEHRRHFPNCPF 46  
|||||  
DB 204 LARAGFYIIGPDRVACFACGKLSNMEPKDDAMSEHRRHFPNCPF 249

RESULT 7  
US-08-800-929A-8  
Sequence 8, Application US/08800929A  
Patent No. 6133437

GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
TITLE OF INVENTION: DETECTION AND MODULATION OF  
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT  
TITLE OF INVENTION: DISEASE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Ebling LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996  
APPLICATION NUMBER: 60/017,354  
FILING DATE: 26-APR-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Bleker-Brady, Kristina  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045

TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 618 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-800-929A-8

Query Match 100.0%; Score 269; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 6.8e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGRVACFACGKLSNWEPRDAMSEHRRHPNCPF 46  
DB 204 LARAGFYIIGPGRVACFACGKLSNWEPRDAMSEHRRHPNCPF 249

## RESULT 8

US-08-569-749-2  
; Sequence 2, Application US/08569749  
; Patent No. 618/537

GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Goeddel, David V  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: A-62464/DJB  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-2

Query Match 100.0%; Score 269; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 6.8e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGRVACFACGKLSNWEPRDAMSEHRRHPNCPF 46  
DB 204 LARAGFYIIGPGRVACFACGKLSNWEPRDAMSEHRRHPNCPF 249

RESULT 9  
US-09-617-053A-8  
; Sequence 8, Application US/09617053A  
; Patent No. 6300492

GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Teang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 07891/009003  
CURRENT APPLICATION NUMBER: US/09/617,053A  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-617-053A-8

Query Match 100.0%; Score 269; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 6.8e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGRVACFACGKLSNWEPRDAMSEHRRHPNCPF 46  
DB 204 LARAGFYIIGPGRVACFACGKLSNWEPRDAMSEHRRHPNCPF 249

RESULT 10  
US-09-069-023-29  
; Sequence 29, Application US/09069023A  
; Patent No. 6348573  
GENERAL INFORMATION:  
APPLICANT: Nunez, Gabriel  
APPLICANT: Inohara, Naohiro  
APPLICANT: Koseki, Takeyoshi  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
FILE REFERENCE: UM-03333  
CURRENT APPLICATION NUMBER: US/09/069,023A  
CURRENT FILING DATE: 1998-04-27  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-069-023-29

Query Match 100.0%; Score 269; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 6.8e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGRVACFACGKLSNWEPRDAMSEHRRHPNCPF 46  
DB 204 LARAGFYIIGPGRVACFACGKLSNWEPRDAMSEHRRHPNCPF 249

RESULT 11  
PCT-US96-12860-2  
; Sequence 2, Application PC/TUS9612860  
; GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco

STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-2

Query Match 100.0%; Score 269; DB 5; Length 618;  
Best Local Similarity 100.0%; Pred. No. 6.8e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGRVACFACGKLSNWEPRKDDAMSEHRRHPNCPF 46  
DB 204 LARAGFYIIGPGRVACFACGKLSNWEPRKDDAMSEHRRHPNCPF 249

RESULT 12  
US-09-212-971-14  
Sequence 14, Application US/09212971B  
Patent No. 6107041  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212,971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017,354  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 612  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-212-971-14

Query Match 98.1%; Score 264; DB 3; Length 612;  
Best Local Similarity 97.8%; Pred. No. 3e-26;

Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGRVACFACGKLSNWEPRKDDAMSEHRRHPNCPF 46  
DB 197 LARAGFYIIGPGRVACFACGKLSNWEPRKDDAMSEHRRHPNCPF 242

RESULT 13  
US-08-800-929A-14  
Sequence 14, Application US/08800929A  
Patent No. 6133437  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF  
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT  
TITLE OF INVENTION: DISEASE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Filding LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996  
APPLICATION NUMBER: 60/017,354  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bleker-Brady, Kristina  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TITLE:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 612 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-800-929A-14

Query Match 98.1%; Score 264; DB 4; Length 612;  
Best Local Similarity 97.8%; Pred. No. 3e-26;  
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGRVACFACGKLSNWEPRKDDAMSEHRRHPNCPF 46  
DB 197 LARAGFYIIGPGRVACFACGKLSNWEPRKDDAMSEHRRHPNCPF 242

RESULT 14  
US-08-569-749-14  
Sequence 14, Application US/08569749  
Patent No. 6187557

GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Goeddel, David V  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 612 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-14

Query Match 98.1%; Score 264; DB 4; Length 612;  
Best Local Similarity 97.8%; Pred. No. 3e-26;  
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGGKLSNWEPRKDDAMSEHRRHFPNCPF 46  
|||||  
DB 197 LARAGFYIIGPDRVACFACGGKLSNWEPRKDDAMSEHRRHFPNCPF 242

RESULT 15  
US-09-617-053A-14  
Sequence 14, Application US/09617053A  
Patent No. 6300492  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF VAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
FILE REFERENCE: 07891/009003  
CURRENT APPLICATION NUMBER: US/09/617,053A  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 612  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-617-053A-14

Query Match 98.1%; Score 264; DB 4; Length 612;  
Best Local Similarity 97.8%; Pred. No. 3e-26;  
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGGKLSNWEPRKDDAMSEHRRHFPNCPF 46  
|||||  
DB 197 LARAGFYIIGPDRVACFACGGKLSNWEPRKDDAMSEHRRHFPNCPF 242

Search completed: May 5, 2003, 16:09:10  
Job time : 3.12673 secs

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 15:50:57 ; Search time 9.06221 Seconds

(without alignments)  
676.383 Million cell updates/sec

Title: US-08-569-749-7

Perfect score: 269  
Sequence: 1 LARGFYRIGEDVACFAC.....WEPKDDAMSEHRHFPNCPF 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: A.Geneseq\_101002:\*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*
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- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	269	100.0	46	18 AAW13549	Human c-IAP1 repa
2	269	100.0	438	17 AAW04583	Human inhibitor of
3	269	100.0	618	18 AAW19746	Human inhibitor of
4	269	100.0	618	18 AAW19583	Human apoptosis in
5	269	100.0	618	18 AAW13545	Human c-IAP1. Hom
6	269	100.0	618	19 AAW69296	Human H1AP-2 prote
7	269	100.0	618	20 AAW33998	Human cellular inh
8	269	100.0	618	23 ABG65665	Human inhibitor of
9	264	98.1	612	18 AAW13555	Murine c-IAP. Mus
10	264	98.1	612	19 AAW69299	Murine H1AP-2 prot

11	257	95.5	306	22 AAW02925	Angiotensin conver
12	255	94.8	591	18 AAW19586	Mouse apoptosis in
13	255	94.8	591	23 ABG65668	Mouse inhibitor of
14	251	93.3	604	18 AAW19582	Human apoptosis in
15	251	93.3	604	19 AAW69295	Human H1AP-1 prote
16	251	93.3	604	23 ABG65664	Human inhibitor of
17	248	92.2	46	18 AAW13550	Human c-IAP2 repa
18	248	92.2	604	18 AAW19747	Human inhibitor of
19	248	92.2	604	18 AAW13546	Human c-IAP2. Hom
20	248	92.2	604	20 AAW52703	Human cellular inh
21	248	92.2	604	23 AAW33997	Human cysteine pro
22	248	92.2	1140	23 AAW97837	Human APT2-WT chl
23	248	92.2	1141	22 AAB50694	Human APT2-WT chl
24	241	89.6	600	18 AAW69298	Murine H1AP-1 prot
25	241	89.6	602	19 AAW19585	Mouse apoptosis in
26	241	89.6	602	23 ABG65667	Mouse inhibitor of
27	192	71.4	497	18 AAW19581	Human apoptosis in
28	192	71.4	497	19 AAW69294	Human X1AP protein
29	192	71.4	497	21 AAW99885	Human X1AP-linked inh
30	192	71.4	497	21 AAW98451	Human X1AP protein
31	192	71.4	497	23 ABG65663	Human inhibitor of
32	188	69.9	464	23 AAW5747	Human inhibitor of
33	187	69.5	496	18 AAW19745	Mouse inhibitor of
34	187	69.5	496	18 AAW19584	Mouse apoptosis in
35	187	69.5	496	19 AAW69297	Murine X1AP protel
36	187	69.5	496	23 ABG65666	Mouse inhibitor of
37	155	57.6	236	21 AAW81440	Human H1AP (an inh
38	155	57.6	236	22 AAE00365	Human IAP-like pro
39	155	57.6	236	22 AAE00366	Chimpanzee IAP-1lk
40	155	57.6	236	23 AAW75066	Human testes spect
41	154	57.2	236	22 AAE00367	Human testes spect
42	151	56.1	278	23 AAO20511	Corilla IAP-like p
43	149	55.4	1232	17 AAW96217	Protein of APP rel
44	149	55.4	1295	17 AAW14080	Neuronal apoptosis
45	149	55.4	1295	20 AAW09540	Gonadotropic hormo

#### ALIGNMENTS

RESULT 1	AAW13549	AAW13549 standard; Protein; 46 AA.
ID	AAW13549;	
AC	AAW13549;	
DT	22-JUL-1997	(first entry)
XX		
DE	Human c-IAP1 repeat 2.	
XX		
KW	IAP; inhibitor; apoptosis; RING finger domain; restlinosis;	
KW	myocardial infarction; nephritis; HIV.	
XX		
OS	Homo sapiens.	
XX		
PN	W09706182-A1.	
XX		
PD	20-FEB-1997.	
XX		
PF	06-AUG-1996;	96WO-US12860.
XX		
PR	08-DEC-1995;	95US-0569749.
XX		
PR	08-AUG-1995;	95US-0512946.
XX		
PA	(TULIA-)TULIARIK INC.	
XX		
PI	Goeddel DV, Rothe M;	
XX		
DR	WPI; 1997-154209/14.	
XX		
PT	Nucleic acids encoding cellular inhibitor of apoptosis proteins	
PT	useful for apoptosis regulation in cells to reduce or increase	
PT	apoptosis and for pharmacological screening	



XX Claim 3; Page 24; 35pp; English.  
 PS  
 CC The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -  
 CC AAT1590/T1591) comprise a series of defined structural domain  
 CC repeats and/or a RING finger domain; in particular, at least two of  
 CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat  
 CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)  
 CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus  
 CC sequences derived from these human genes.  
 CC The nucleic acid is used for recombinant prodn. of human cellular  
 CC inhibitor of apoptosis protein which modulates apoptosis  
 CC regulation. The nucleic acids are useful in therapies where  
 CC increased cell-specific apoptosis is desired, e.g. in restinosis,  
 CC inflammatory disease states, myocardial infarction, glomerular  
 CC nephritis, transplant rejection and infectious diseases, e.g. HIV.  
 CC They can also be used in conditions requiring a reduction in  
 CC apoptosis.  
 CC  
 CC Sequence 46 AA;  
 SQ  
 Query Match 100.0%; Score 269; DB 18; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 1e-26;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 LARAGFYIGPDGVACFACGKLSNWEKDDAMSEHRHFPNCP 46  
 DB 1 LARAGFYIGPDGVACFACGKLSNWEKDDAMSEHRHFPNCP 46  
 RESULT 2  
 AAW04583  
 ID AAW04583 standard; Protein; 438 AA.  
 AC AAW04583;  
 XX  
 DT 07-FEB-1997 (first entry)  
 DE Human inhibitor of apoptosis gene 1.  
 DE  
 XX Inhibitor of apoptosis 1; hIAP-1; degenerative disease;  
 KM Rheumatoid arthritis; septic shock; antiviral; trauma; stroke;  
 KW cell death; oncogenesis; cancer; diagnosis; therapy.  
 OS  
 XX Homo sapiens.  
 OS  
 PN WO9635703-A1.  
 XX  
 PD 14-NOV-1996.  
 XX  
 PF 11-MAY-1995; 95WO-US05922.  
 XX  
 PR 11-MAY-1995; 95WO-US05922.  
 XX  
 PA (HDMA-) HDMA GENOME SCI INC.  
 XX  
 PI He WM, Hudson PL, Rosen CA;  
 XX  
 DR WPI: 1996-518608/51.  
 DR N-PSDB: AAT43709.  
 XX  
 PT Polynucleotide encoding human inhibitor of apoptosis gene 1 - useful  
 PT for treating degenerative diseases, as antiviral defence mechanism  
 PT and preventing cell death during trauma and strokes  
 XX  
 PS Claim 1; Page 40-41; 53pp; English.  
 CC Human inhibitor of apoptosis 1 (hIAP-1) (AAW04583) is a protein  
 CC useful for treating degenerative diseases, Rheumatoid arthritis,  
 CC septic shock, as an antiviral defence mechanism, and for  
 CC preventing cell death during strokes or trauma. Its amino acid  
 CC sequence was deduced from a cDNA clone (AAT43709) that can be obtd.  
 CC from human Jurkat cell lines or human osteoclastoma stromal cell

CC lines. Recombinant hIAP-1 can be produced in prokaryotic or  
 CC eukaryotic host cells, or expressed in vivo. It can also be used  
 CC to screen for modulators of hIAP-1 activity.  
 CC  
 CC Sequence 438 AA;  
 SQ  
 Query Match 100.0%; Score 269; DB 17; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-25;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 LARAGFYIGPDGVACFACGKLSNWEKDDAMSEHRHFPNCP 46  
 DB 24 LARAGFYIGPDGVACFACGKLSNWEKDDAMSEHRHFPNCP 69  
 RESULT 3  
 AAW19746  
 ID AAW19746 standard; Protein; 618 AA.  
 AC AAW19746;  
 XX  
 DT 16-SEP-1997 (first entry)  
 DE Human inhibitor of apoptosis protein homologue M1HB.  
 DE  
 XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; M1HB;  
 KM degenerative disease; infectious disease; autoimmune disease;  
 KW cancer; therapy; diagnosis.  
 OS  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT Region 46..113  
 FT Region 184..250  
 FT Region 269..337  
 FT Region 569..606  
 FT Region /label= RING\_finger  
 FT  
 PN WO9723501-A1.  
 XX  
 PD 03-JUL-1997.  
 XX  
 PF 20-DEC-1996; 96WO-AU00827.  
 XX  
 PR 22-DEC-1995; 95AU-0007275.  
 XX  
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 XX  
 PI Vaux DL;  
 XX  
 DR WPI: 1997-350966/32.  
 DR N-PSDB: AAT72711.  
 XX  
 PT Isolated protein homologues of viral inhibitors of apoptosis - used  
 PT to modulate apoptosis for treatment of degenerative, infectious or  
 PT autoimmune diseases and cancer  
 XX  
 PS Claim 8; Page 51-54; 136pp; English.  
 CC Mammalian IAP homologue B (M1HB) (AAW19746) is a human homologue of  
 CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid  
 CC sequence was deduced from a cDNA clone (see also AAT72711) isolated  
 CC from a human foetal liver cDNA library using primers based on  
 CC human EST sequences that resembled the BIR repeats of Oryza  
 CC pseudotsugata polyhedrosis virus IAP. IAP homologues (see also  
 CC AAW19745 and AAW19747-52) and their derivatives and chemical analogues  
 CC can be used in methods for modulating apoptosis in animal cells,  
 CC specifically for treatment, by inhibition, of degenerative and  
 CC infectious disease or, by promotion, of cancer and autoimmune  
 CC disease.

XX Sequence 618 AA;  
 SO Query Match 100.0%; Score 269; DB 18; Length 618;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYITGPDRAVACFACGKLSNWEPKDDAMSEHRRHPNCPF 46  
 |||  
 DB 204 LARAGFYITGPDRAVACFACGKLSNWEPKDDAMSEHRRHPNCPF 249

RESULT 4  
 AAM19583  
 ID AAM19583 standard; Protein: 618 AA.  
 AC AAM19583;  
 XX 02-SEP-1997 (first entry)  
 DT XX  
 DE Human apoptosis inhibitor HIAP-2.  
 XX  
 KW Apoptosis inhibitor; HIAP-2; HIV; AIDS; neurodegeneration;  
 KM myelodysplastic syndrome; ischemia; myocardial infarction; stroke;  
 KM reperfusion injury; toxin-induced liver disease; gene therapy;  
 KM diagnosis.  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Domain 46..113  
 FT Domain /label- BIR-1  
 FT Domain 184..250  
 FT Domain /label- BIR-2  
 FT Domain 269..336  
 FT Domain /label- BIR-3  
 FT Domain 560..605  
 FT Domain /label- Ring\_zinc\_finger

XX W09706255-A2.  
 XX  
 XX 20-FEB-1997.  
 XX  
 XX 05-AUG-1996; 96WO-IB01022.  
 XX  
 XX 22-DEC-1995; 95US-0576956.  
 XX 04-AUG-1995; 95US-0511485.  
 XX  
 XX (UYOT-) UNIV OTTAWA.  
 XX  
 PI Baird S, Korneluk RG, Liston P, Mackenzie AE;  
 DR WPI: 1997-154262/14.  
 DR N-PSDB; AAT70838.  
 XX  
 PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used  
 PT to inhibit apoptosis in e.g. HIV or AIDS patients; and for detection  
 PT of susceptibility to apoptotic disease  
 PT  
 PS Claim 27; Page 75-77; 219pp; English.  
 XX  
 CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and  
 CC M-HIAP-2 (AAM19581-86) are a new class of mammalian proteins that  
 CC are inhibitors of apoptosis (IAP) and which are characterized by  
 CC the presence of a ring zinc finger domain (see also AAM19587) and at  
 CC least one BIR (baculovirus IAP repeat) domain (see also AAM19588).  
 CC The HIAP amino acid sequences were deduced from cDNA clones (AAT70837  
 CC and AAT70838) from a human liver library. IAP polypeptides can be  
 CC expressed in host cells (in vitro or in vivo) and used in methods  
 CC for treating diseases and disorders involving apoptosis, esp. in a  
 CC human diagnosed as HIV-positive or as having AIDS, a  
 CC neurodegenerative disease, a myelodysplastic syndrome or an  
 CC ischaemic injury, selected from myocardial infarction, stroke,

CC reperfusion injury, or a toxin-induced liver disease.  
 XX  
 SO Sequence 618 AA;  
 OY Query Match 100.0%; Score 269; DB 18; Length 618;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYITGPDRAVACFACGKLSNWEPKDDAMSEHRRHPNCPF 46  
 |||  
 DB 204 LARAGFYITGPDRAVACFACGKLSNWEPKDDAMSEHRRHPNCPF 249

RESULT 5  
 AAM13545  
 ID AAM13545 standard; Protein: 618 AA.  
 AC AAM13545;  
 XX 22-JUL-1997 (first entry)  
 DT XX  
 DE Human c-IAP1.  
 XX  
 KW IAP; inhibitor; apoptosis; RING finger domain; restinosis;  
 KM myocardial infarction; nephritis; HIV.  
 OS Homo sapiens.  
 XX  
 FN W09706182-A1.  
 XX  
 PD 20-FEB-1997.  
 XX  
 XX 06-AUG-1996; 96WO-US12860.  
 XX  
 XX 08-DEC-1995; 95US-0569749.  
 XX 08-AUG-1995; 95US-0512946.  
 XX  
 XX (TULDA-) TULARIK INC.  
 XX  
 PI Goeddel DV, Rothe M;  
 DR WPI: 1997-154209/14.  
 DR N-PSDB; AAT61590.  
 XX  
 PT Nucleic acids encoding cellular inhibitor of apoptosis proteins -  
 PT useful for apoptosis regulation in cells to reduce or increase  
 PT apoptosis and for pharmacological screening  
 PT  
 PS Disclosure; Page 18-20; 35pp; English.  
 XX  
 CC The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -  
 CC AAT61590/761591) comprise a series of defined structural domain  
 CC repeats and/or a RING finger domain; in particular, at least two of  
 CC a first domain repeat (AAM13547 or AAM13548), a second domain repeat  
 CC (AAM13549 or AAM13550), and a third domain repeat (AAM13551 or AAM13552)  
 CC and/or a RING finger domain (AAM13553 or AAM13554), or a consensus  
 CC sequences derived from these human genes.  
 CC The nucleic acid is used for recombinant prodn. of human cellular  
 CC inhibitor of apoptosis protein which modulates apoptosis  
 CC regulation. The nucleic acids are useful in therapies where  
 CC increased cell-specific apoptosis is desired, e.g. in restinosis,  
 CC inflammatory disease states, myocardial infarction, glomerular  
 CC nephritis, transplant rejection and infectious diseases, e.g. HIV.  
 CC They can also be used in conditions requiring a reduction in  
 CC apoptosis.  
 XX  
 SO Sequence 618 AA;  
 OY Query Match 100.0%; Score 269; DB 18; Length 618;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYITGPDRAVACFACGKLSNWEPKDDAMSEHRRHPNCPF 46

DB 204 LARAGFYIIGPDRVACFCAGGKLSNWEKDDAMSEHRRHFPNCPP 249

RESULT 6  
AAW69296  
ID AAW69296 standard; Protein; 618 AA.

AC AAW69296;

DT 13-NOV-1998 (first entry)

DE Human HIAP-2 protein.

KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
KW proliferative disease; IAP; therapy; cancer; human; HIAP-2 protein.

OS Homo sapiens.

PN MO9835693-A2.

PD 20-AUG-1998.

PF 13-FEB-1998; 98WO-IB00781.

PR 13-FEB-1997; 97US-0800929.

PA (UYOT-) UNIV OTTAWA.

PI Baird S, Korneluk R, Liston P, Mackenzie AI, Pratt C;  
PI Tsang B;

DR MPI: 1998-467164/40.

DR N-PSDB; AAV55040.

PT Inducing apoptosis in proliferative mammalian cells with inhibitor  
PT of IAP or NAIP polypeptide - also methods for prognosis based on  
PT presence of IAP and NAIP, specifically applied to cancers involving  
PT p53 mutations

PS Disclosure: Fig 3; 147pp; English.

CC This sequence is the human HIAP-2 protein, which is a inhibitor of  
CC apoptosis protein (IAP), and can be used in the method of the invention.  
CC The method is for enhancing apoptosis in cells from a mammal with  
CC proliferative disease by treatment with a compound that inhibits  
CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
CC compounds are used to treat proliferative diseases, specially cancers of  
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,  
CC rectum, cervix or endometrium, particularly to increase their sensitivity  
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
CC detected in many cancers and are associated with poor prognosis,  
CC resistance to chemotherapeutic agents and mutations in p53 (it is  
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
CC genes). Transgenic animals are used for testing the effects of antisense  
CC oligonucleotides and for screening for the inhibitors.

SO Sequence 618 AA:

Query Match 100.0%; Score 269; DB 19; Length 618;  
Best Local Similarity 100.0%; Pred. No. 1.6e-25;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFCAGGKLSNWEKDDAMSEHRRHFPNCPP 46  
|||||  
DB 204 LARAGFYIIGPDRVACFCAGGKLSNWEKDDAMSEHRRHFPNCPP 249

RESULT 7  
AAV33998  
ID AAV33998 standard; Protein; 618 AA.

AC AAV33998;

DT 26-NOV-1999 (first entry)

DE Human cellular inhibitor of apoptosis-1 sequence.

KW Cellular inhibitor of Apoptosis-1; antisense; diagnostic; therapeutic;  
KW c-IAP-1; prophylaxis; infection; inflammation; tumor formation.

OS Homo sapiens.

PN US5958772-A.

PD 28-SEP-1999.

PF 03-DEC-1998; 98US-0205204.

PR 03-DEC-1998; 98US-0205204.

PA (ISTS-) ISTS PHARM INC.

PI Bennett CF, Cowser LM, Ackermann EJ;

DR MPI: 1999-561047/47.

DR N-PSDB; AA222143.

PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-1  
PT useful for e.g. diagnostics, therapeutics, and as research reagents -  
PT Example 13; Columns 41-46; 32pp; English.

CC The invention provides antisense compounds of 8-30 nucleotides that  
CC inhibit the expression of human Cellular Inhibitor of Apoptosis-1  
CC (c-IAP-1). The antisense compounds may be used for diagnostics,  
CC therapeutics (for modulating the expression of c-IAP-1), prophylaxis  
CC (e.g. to prevent or delay infection, inflammation, or tumor formation),  
CC as research reagents (e.g. to distinguish between members of a biological  
CC pathway) and in kits. The present sequence represents the human cellular  
CC inhibitor of apoptosis-1.

PS Sequence 618 AA:

Query Match 100.0%; Score 269; DB 20; Length 618;  
Best Local Similarity 100.0%; Pred. No. 1.6e-25;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFCAGGKLSNWEKDDAMSEHRRHFPNCPP 46  
|||||  
DB 204 LARAGFYIIGPDRVACFCAGGKLSNWEKDDAMSEHRRHFPNCPP 249

RESULT 8  
ABG65665  
ID ABG65665 standard; Protein; 618 AA.

AC ABG65665;

DT 26-AUG-2002 (first entry)

DE Human inhibitor of apoptosis, HIAP2.

KW Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
KW pancreatic cancer; embryonic development; viral pathogenesis;  
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
KW lupus erythematosus; herpes virus infection; pox virus infection;  
KW adenovirus infection; proliferative disease.

OS Homo sapiens.

PN WO200226968-A2.

PD 04-APR-2002.

```
XX 27-SEP-2001; 2001WO-CA01379.
PE
XX
XX 28-SEP-2000; 2000US-0672717.
PR
XX
XX (UYOT-) UNIV OTTAWA.
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Korneiluk RG, Lacasse E, Baird S, Holcik M, Young S;
PI WPI: 2002-479562/51.
XX N-PSDB; AAK33871.
DR
XX
PT Novel antisense inhibitor of apoptosis nucleic acid useful for
PT enhancing apoptosis in a cell, for treating cancer and other
PT proliferative diseases
XX
XX Disclosure; Fig 3; 135pp; English.
XX
XX The invention relates to an inhibitor of apoptosis (IAP) antisense
XX nucleic acid (1) that inhibits IAP biological activity, regardless of
XX length of the antisense nucleic acid, the IAP proteins may be mouse
XX or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
XX composition comprising a mammalian IAP antisense molecule and a method of
XX enhancing apoptosis in a cell, comprising administering a negative
XX regulator of the IAP anti-apoptotic pathway to the cell. The IAP
XX antisense inhibitor is useful for enhancing apoptosis in a cell in a
XX mammal diagnosed with a proliferative disease. The method is useful for
XX treating a patient diagnosed with a proliferative disease like cancer.
XX The IAP antisense molecule is useful to treat, ameliorate, improve,
XX sustain or prevent proliferative diseases (e.g. ovarian cancer,
XX adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
XX conditions where apoptosis is involved or implicated (e.g. embryonic
XX development, viral pathogenesis, autoimmune disorders, neurodegenerative
XX diseases, multiple sclerosis, lupus erythematosus and infection by herpes
XX virus, pox virus and adenovirus). The present sequence is a human IAP
XX protein sequence.
SQ
XX
XX Sequence 618 AA;
Query Match 100.0%; Score 269; DB 23; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LARAGFYIIGDVRVACFACGKLSNNEPKDAMSEHRRHPPNCPF 46
DB 204 LARAGFYIIGDVRVACFACGKLSNNEPKDAMSEHRRHPPNCPF 249
RESULT 9
AAW13555
ID AAW13555 standard; Protein: 612 AA.
XX
XX AAW13555;
AC
XX
XX 22-JUL-1997 (first entry)
DT
XX
XX Murine c-IAP.
DE
XX
XX IAP; inhibitor; apoptosis; RING finger domain; restinosis;
KW myocardial infarction; nephritis; HIV.
XX
XX Mus musculus.
OS
XX
XX WO9706182-A1.
XX
XX 20-FEB-1997.
PD
XX
XX 06-AUG-1996; 96WO-US12860.
PE
XX
XX 08-DEC-1995; 95US-0569749.
PR
XX
XX 08-AUG-1995; 95US-0512946.
PT
XX
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```
PA (TULA-) TULARIK INC.
XX
XX Goeddel DV, Rothe M;
PI
XX
XX WPI: 1997-154209/14.
DR
XX
XX N-PSDB; AAT61592.
DR
XX
XX Nucleic acids encoding cellular inhibitor of apoptosis proteins -
PT useful for apoptosis regulation in cells to reduce or increase
PT apoptosis and for pharmacological screening
XX
XX
XX Disclosure; Page 28-29; 35pp; English.
XX
XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
XX AAT61590/761591) comprise a series of defined structural domain
XX repeats and/or a RING finger domain; in particular, at least two of
XX a first domain repeat (AAW13547 or AAW13548), a second domain repeat
XX (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
XX and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
XX sequences derived from these human genes.
XX The nucleic acid is used for recombinant prodn. of human cellular
XX inhibitor of apoptosis protein which modulates apoptosis
XX regulation. The nucleic acids are useful in therapies where
XX increased cell-specific apoptosis is desired, e.g. in restinosis,
XX inflammatory disease states; myocardial infarction, glomerular
XX nephritis, transplant rejection and infectious diseases; e.g. HIV.
XX They can also be used in conditions requiring a reduction in
XX apoptosis.
SQ
XX
XX Sequence 612 AA;
Query Match 98.1%; Score 264; DB 18; Length 612;
Best Local Similarity 97.8%; Pred. No. 6.6e-25;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LARAGFYIIGDVRVACFACGKLSNNEPKDAMSEHRRHPPNCPF 46
DB 197 LARAGFYIIGDVRVACFACGKLSNNEPKDAMSEHRRHPPNCPF 242
RESULT 10
AAW69299
ID AAW69299 standard; Protein: 612 AA.
XX
XX AAW69299;
AC
XX
XX 13-NOV-1998 (first entry)
DT
XX
XX Murine HIAP-2 protein.
DE
XX
XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; mouse; HIAP-2 protein.
XX
XX Mus sp.
OS
XX
XX WO9835693-A2.
XX
XX 20-AUG-1998.
PD
XX
XX 13-FEB-1998; 98WO-IB00781.
PE
XX
XX 13-FEB-1997; 97US-0800929.
PR
XX
XX (UYOT-) UNIV OTTAWA.
XX
XX Baird S, Korneiluk R, Liston P, Mackenzie AE, Pratt C;
PI Tsang B;
XX
XX WPI: 1998-467164/40.
DR
XX
XX N-PSDB; AAV55043.
PT
XX
XX Inducing apoptosis in proliferative mammalian cells with inhibitor
XX of IAP or NAIP polypeptide - also methods for prognosis based on
```

PT presence of IAP and NAIP, specifically applied to cancers involving  
PT p53 mutations  
XX  
XX  
PS Disclosure: Fig 6: 147pp; English.  
XX  
CC This sequence is the murine H1AP-2 protein, which is a inhibitor of  
CC apoptosis protein (IAP), and can be used in the method of the invention.  
CC The method is for enhancing apoptosis in cells from a mammal with  
CC proliferative disease by treatment with a compound that inhibits  
CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
CC compounds are used to treat proliferative diseases, specially cancers of  
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,  
CC rectum, cervix or endometrium, particularly to increase their sensitivity  
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
CC detected in many cancers and are associated with poor prognosis,  
CC resistance to chemotherapeutic agents and mutations in p53 (it is  
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
CC genes). Transgenic animals are used for testing the effects of antisense  
CC oligonucleotides and for screening for the inhibitors.  
XX  
SQ Sequence 612 AA;  
XX  
Query Match 98.1%; Score 264; DB 19; Length 612;  
Best Local Similarity 97.8%; Pred. No. 6.6e-23;  
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LARAGFYITGPDVAVACFACGKLSNWEPRKDDAMSEHRHFPNCP 46  
|||||  
DB 197 LARAGFYITGPDVAVACFACGKLSNWEPRKDDAMSEHRHFPNCP 242  
\*  
RESULT 11  
AAU02925  
ID AAU02925 standard; Protein: 306 AA.  
XX  
AC AAU02925;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Angiotensin converting enzyme (ACEV) splice variant protein #25.  
XX  
XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;  
XX granulocyte colony stimulating factor receptor; glucagon; hypertrophy;  
XX platelet-derived endothelial cell growth factor; cardiovascular disease;  
XX cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;  
XX vasodilator intestinal polypeptide receptor 2; arteriosclerosis; cancer;  
XX myocardial infarction; coronary arterial thrombosis; renal disease;  
XX diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;  
XX multiple sclerosis; immune complex nephritis; deep vein thrombosis;  
XX nonarcolidotic pulmonary granulomatous disease; endothelial abnormality;  
XX vascular disorder; asbestosis.  
OS Homo sapiens.  
XX  
XX WO200136632-A2.  
XX  
PD 25-MAY-2001.  
XX  
PF 17-NOV-2000; 2000MO-IL00766.  
XX  
XX 17-NOV-1999; 99IL-0132978.  
XX PR 10-DEC-1999; 99IL-0133455.  
XX  
XX (COMP-) COMPUGEN LTD.  
XX  
XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;  
XX  
XX WPI; 2001-336004/35.  
XX DR N-PSDB; AAS06025.  
XX  
XX Novel alternative splicing variants e.g. variant of angiotensin  
PT converting enzyme (ACEV), useful in identifying candidate compounds

PT capable of binding to the variant and to detect anti-variant antibodies  
PT  
XX  
XX Claim 4; Fig 25; 519pp; English.  
XX  
XX  
PS The sequence represents an angiotensin converting enzyme splice variant  
CC (ACEV) polypeptide. The polypeptides of the invention include variants of  
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,  
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase  
CC inhibitor 1C, cellular tumour antigen p53, and vasodilator intestinal  
CC polypeptide receptor 2. The polypeptides and their associated nucleic  
CC acids are useful for identification of variant sequences and detection of  
CC candidate compounds capable of binding to the molecules. The sequences of  
CC the invention can be used in the treatment and diagnosis of various  
CC disorders including cardiovascular diseases such as arteriosclerosis,  
CC myocardial infarction and coronary arterial thrombosis, renal diseases  
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,  
CC immune disorders such as immune complex nephritis, multiple sclerosis,  
CC cancer, sarcoidosis, nonarcolidotic pulmonary granulomatous diseases such  
CC as asbestosis and vascular pathologies involving an endothelial  
XX abnormality such as deep vein thrombosis.  
XX  
SQ Sequence 306 AA;  
XX  
Query Match 95.5%; Score 257; DB 22; Length 306;  
Best Local Similarity 95.7%; Pred. No. 2.4e-24;  
Matches 44; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 LARAGFYITGPDVAVACFACGKLSNWEPRKDDAMSEHRHFPNCP 46  
|||||  
DB 204 LARAGFYITGPDVAVACFACGKLSNWEPRKDDAMSEHRHFPNCP 245  
\*  
RESULT 12  
AAW19586  
ID AAW19586 standard; Protein: 591 AA.  
XX  
XX AAW19586;  
XX  
DT 02-SEP-1997 (first entry)  
XX  
DE Mouse apoptosis inhibitor M-HIAP-2.  
XX  
XX Apoptosis inhibitor; M-HIAP-2; HIV; AIDS; neurodegeneration;  
XX myelodysplastic syndrome; ischemia; myocardial infarction; stroke;  
XX reperfusion injury; toxin-induced liver disease; gene therapy;  
XX diagnosis.  
OS Mus sp.  
XX  
XX  
XX Key Location/Qualifiers  
XX Domain 25..92  
XX /label= BIR-1  
XX FT 156..222  
XX /label= BIR-2  
XX FT 241..308  
XX /label= BIR-3  
XX FT 541..578  
XX /label= Ring\_zinc\_finger  
XX  
XX WO9706255-A2.  
XX  
XX 20-FEB-1997.  
XX  
XX  
XX 05-AUG-1996; 96WO-1B01022.  
XX  
XX 22-DEC-1995; 95US-0576956.  
XX PR 04-AUG-1995; 95US-0511485.  
XX  
XX (UYOT-) UNIV OTTAWA.  
XX  
XX Baird S, Korneluk RG, Liston P, Mackenzie AE;  
XX

DR	WPI; 1997-154262/14.
DR	N-PSDB; AAT70841.
PT	Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT	to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
PT	of susceptibility to apoptotic disease
PS	Claim 30; Page 100-102; 219pp; English.
XX	
CC	Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC	M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC	are inhibitors of apoptosis (IAP) and which are characterised by
CC	the presence of a ring zinc finger domain (see also AAW19587) and at
CC	least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC	The M-HIAP amino acid sequences were deduced from isolated m-hiap
CC	cDNA clones (AAT70840-41). IAP polypeptides can be expressed in host
CC	cells (in vitro or in vivo) and used in methods for treating
CC	diseases and disorders involving apoptosis, esp. in a human
CC	diagnosed as HIV-positive or as having AIDS, a neurodegenerative
CC	disease, a myelodysplastic syndrome or an ischemic injury, selected
CC	from myocardial infarction, stroke, reperfusion injury, or a toxin-
CC	induced liver disease.
SQ	
SQ	Sequence    591 AA;
Query_Match	94.8%; Score 255; DB 18; Length 591;
Best Local Similarity	95.7%; Pred. NO. 8.7e-24;
Matches    44; Conservative    1; Mismatches    1; Indels         0; Gaps         0;	
OY	
OY	1 LARAEFYIIGPDDRYACFACGCKLSNWEKXDAMEHRRHFPCPF 46
OY	:
Db	176 LARAEFYIIGPDDRYACFACGCKLSNWEKXDAMEHRRHFPCPF 221
RESULT 13	
ID	ABG65668 standard; Protein; 591 AA.
ABG65668	
AC	ABG65668;
XX	
DT	26-AUG-2002 (first entry)
DE	
DE	Mouse Inhibitor of apoptosis, HIAP2.
XX	
KM	Mouse; antisense; Inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KM	Cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KM	Pancreatic cancer; embryonic development; viral pathogenesis;
KM	Autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KM	Lupus erythematosus; herpes virus infection; pox virus infection;
KM	adenovirus infection; proliferative disease.
XX	
OS	Mus sp.
PN	
PN	WO200226968-A2.
PD	
PD	04-APR-2002.
XX	
XX	27-SEP-2001; 2001WO-CA01379.
XX	
PR	28-SEP-2000; 2000US-0672717.
PA	(UYOT-) UNIV OTTAWA.
PA	(ABGE-) ABGERA THERAPEUTICS INC.
XX	
PL	Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX	
DR	WPI; 2002-479562/51.
DR	N-PSDB; ABK93874.
XX	
PT	Novel antisense inhibitor of apoptosis nucleic acid useful for
PT	enhancing apoptosis in a cell, for treating cancer and other
PT	proliferative diseases
XX	

PS	Disclosure; Fig 6; 135pp; English.
xx	
CC	The invention relates to an inhibitor of apoptosis (IAP) antisense
CC	nucleic acid (1) that inhibits IAP biological activity, regardless of
CC	length of the antisense nucleic acid, the IAP proteins may be mouse
CC	or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC	composition comprising a mammalian IAP antisense molecule and a method of
CC	enhancing apoptosis in a cell, comprising administering a negative
CC	regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC	antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC	mammal diagnosed with a proliferative disease. The method is useful for
CC	treating a patient diagnosed with a proliferative disease like cancer.
CC	The IAP antisense molecule is useful to treat, ameliorate, improve,
CC	sustain or prevent proliferative diseases (e.g., ovarian cancer,
CC	adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC	conditions where apoptosis is involved or implicated (e.g., embryonic
CC	development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC	diseases, multiple sclerosis), lupus erythematosus and infection by herpes
CC	virus, pox virus and adenovirus). The present sequence is a mouse IAP
CC	protein sequence.
CC	
CC	
SO	Sequence 591 AA;
Oy	
Dd	Query Match 94.8%; Score 255; DB 23; Length 591; Best Local Similarity 95.7%; Pred. No. 8.7e-24; Matches 44; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
	1 LARAGFYITIGPDRVACFACGCGKLSNWEPRKDAMSEHRRHPNCPF 46       176 LARAGFYITIGPDRVACFACGCGKLSNWEPRKDAMSEHRRHPNCPF 221
RESULT 14	
ID	AAW19582 standard; Protein: 604 AA.
AC	AAW19582;
XX	
DT	02-SEP-1997 (first entry)
XX	
DE	Human apoptosis inhibitor HIAP-1.
KW	Apoptosis inhibitor; HIAP-1; HIV; AIDS; neurodegeneration;
KW	myelodysplastic syndrome; ischemia; myocardial infarction; stroke;
KW	reperfusion injury; toxin-induced liver disease; gene therapy;
KW	diagnosis.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Domain 29..96
FT	/label= BIR-1 169..235
FT	Domain /label= BIR-2 255..322
FT	Domain /label= BIR-3 546..591
FT	Domain /label= Ring_zinc_finger
XX	
FN	WO9706255-A2.
XX	
PD	20-FEB-1997.
XX	
PF	05-AUG-1996; 96WO-IB01022.
PR	22-DEC-1995; 95US-0576956.
PR	04-AUG-1995; 95US-0511485.
PA	(UYOT-) UNIV OTTAWA.
P1	Baird S, Korneluk RG, Liston P, Mackenzie AE;
OR	WPI; 1997-154262/14.

DR N-PSDB; AAT70837.  
 XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used  
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection  
 PT of susceptibility to apoptotic disease  
 XX  
 PS Claim 27; Page 72-74; 219pp; English.  
 XX  
 CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and  
 CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that  
 CC are inhibitors of apoptosis (IAP) and which are characterised by  
 CC the presence of a ring zinc finger domain (see also AAW19587) and at  
 CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).  
 CC The HIAP amino acid sequences were deduced from cDNA clones (AAT70837  
 CC and AAT70838) from a human liver library. IAP polypeptides can be  
 CC expressed in host cells (in vitro or in vivo) and used in methods  
 CC for treating diseases and disorders involving apoptosis, esp. in a  
 CC human diagnosed as HIV-positive or as having AIDS, a  
 CC neurodegenerative disease, a myelodysplastic syndrome or an  
 CC ischaemic injury, selected from myocardial infarction, stroke,  
 CC reperfusion injury, or a toxin-induced liver disease.  
 CC  
 SQ Sequence 604 AA;

Query Match 93.3%; Score 251; DB 18; Length 604;  
 Best Local Similarity 93.5%; Pred. No. 2.9e-23;  
 Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPGRVACFACGKLSNMEPKDDAMSEHRRHFPNCPF 46  
 |||  
 DB 189 LARAGFYIIGPGRVACFACGKLSNMEPKDDAMSEHRRHFPNCPF 234

RESULT 15  
 AAW69295  
 ID AAW69295 standard; Protein; 604 AA.  
 XX  
 AC AAW69295;  
 XX  
 DT 13-NOV-1998 (first entry)  
 XX  
 DE Human HIAP-1 protein.  
 XX  
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
 XX proliferative disease; IAP; therapy; cancer; human; HIAP-1 protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9835693-A2.  
 XX  
 PD 20-AUG-1998.  
 XX  
 PF 13-FEB-1998; 98WO-IB00781.  
 XX  
 PR 13-FEB-1997; 97US-0800929.  
 XX  
 PA (UYOT-) UNIV OTTAWA.  
 XX  
 PI Balrd S, Korneluk R, Liston P, Mackenzie AE, Pratt C;  
 PI Tsang B;  
 XX  
 DR WPI: 1998-467164/40.  
 DR N-PSDB; AAV55039.  
 XX  
 PT Inducing apoptosis in proliferative mammalian cells with inhibitor  
 PT of IAP or NAIP polypeptide - also methods for prognosis based on  
 PT presence of IAP and NAIP, specifically applied to cancers involving  
 PT p53 mutations  
 XX  
 PS Disclosure; Fig 2; 147pp; English.  
 XX  
 CC This sequence is the human HIAP-1 protein, which is a inhibitor of  
 CC apoptosis protein (IAP), and can be used in the method of the invention.

CC The method is for enhancing apoptosis in cells from a mammal with  
 CC proliferative disease by treatment with a compound that inhibits  
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
 CC compounds are used to treat proliferative diseases, specially cancers of  
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
 CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,  
 CC rectum, cervix or endometrium, particularly to increase their sensitivity  
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
 CC detected in many cancers and are associated with poor prognosis,  
 CC resistance to chemotherapeutic agents and mutations in p53 (it is  
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
 CC genes). Transgenic animals are used for testing the effects of antisense  
 CC oligonucleotides and for screening for the inhibitors.  
 CC  
 SQ Sequence 604 AA;

Query Match 93.3%; Score 251; DB 19; Length 604;  
 Best Local Similarity 93.5%; Pred. No. 2.9e-23;  
 Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPGRVACFACGKLSNMEPKDDAMSEHRRHFPNCPF 46  
 |||  
 DB 189 LARAGFYIIGPGRVACFACGKLSNMEPKDDAMSEHRRHFPNCPF 234

Search completed: May 5, 2003, 16:02:00  
 Job time : 10.0622 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:02:07 ; Search time 5.67051 Seconds

(without alignments)  
699.970 Million cell updates/sec

Title: US-08-569-749-7

Perfect score: 269

Sequence: 1 LARAGFYTGPGDRVACFAC.....WPKDDAMSEHRRHFPNCPF 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	269	100.0	67	9	US-09-201-936-23
2	269	100.0	438	1	US-08-464-588-2
3	269	100.0	618	9	US-09-201-936-8
4	269	100.0	618	10	US-09-974-592-8
5	264	98.1	612	10	US-09-974-592-14
6	257	95.5	306	10	US-09-778-927A-62
7	255	94.8	591	9	US-09-201-936-42
8	251	93.3	67	9	US-09-201-936-22
9	251	93.3	604	9	US-09-201-936-6
10	251	93.3	604	10	US-09-974-592-6
11	241	89.6	600	10	US-09-974-592-12
12	241	89.6	602	9	US-09-201-936-40
13	192	71.4	68	9	US-09-201-936-21
14	192	71.4	110	9	US-09-965-967-21
15	192	71.4	497	9	US-09-201-936-4
16	192	71.4	497	10	US-09-974-592-4
17	187	69.5	68	9	US-09-201-936-20
18	187	69.5	496	9	US-09-201-936-10
19	187	69.5	496	10	US-09-974-592-10

## ALIGNMENTS

20	151	56.1	66	9	US-09-201-936-25	Sequence 25, Appl
21	151	56.1	107	9	US-09-965-967-20	Sequence 20, Appl
22	151	56.1	278	9	US-09-964-899-39	Sequence 39, Appl
23	150	55.8	66	9	US-08-201-936-24	Sequence 24, Appl
24	149	55.4	1403	8	US-08-913-322-22	Sequence 22, Appl
25	149	55.4	1403	8	US-08-913-322-24	Sequence 24, Appl
26	140	52.0	67	9	US-09-201-936-15	Sequence 15, Appl
27	140	52.0	498	9	US-09-201-936-13	Sequence 13, Appl
28	139	51.7	68	9	US-09-201-936-19	Sequence 19, Appl
29	138	51.3	68	9	US-09-201-936-18	Sequence 18, Appl
30	138	51.3	68	9	US-09-201-936-27	Sequence 27, Appl
31	135	50.2	68	9	US-09-201-936-16	Sequence 16, Appl
32	132	49.1	68	9	US-09-201-936-26	Sequence 26, Appl
33	132	49.1	68	9	US-09-201-936-28	Sequence 28, Appl
34	132	49.1	68	9	US-10-041-859-18	Sequence 18, Appl
35	132	49.1	172	9	US-10-041-859-8	Sequence 8, Appl
36	132	49.1	172	9	US-10-041-859-12	Sequence 12, Appl
37	132	49.1	345	9	US-10-041-859-2	Sequence 2, Appl
38	131	48.7	68	9	US-09-201-936-17	Sequence 17, Appl
39	131	48.7	110	9	US-09-965-967-22	Sequence 22, Appl
40	129	48.0	67	9	US-09-201-936-11	Sequence 11, Appl
41	129	48.0	68	9	US-10-041-859-19	Sequence 19, Appl
42	129	48.0	109	9	US-09-965-967-30	Sequence 30, Appl
43	129	48.0	172	9	US-10-041-859-13	Sequence 13, Appl
44	128	47.6	109	9	US-09-965-967-19	Sequence 19, Appl
45	126	46.8	172	9	US-10-041-859-10	Sequence 10, Appl

RESULT 1  
US-09-201-936-23  
; Sequence 23, Application US/09201936  
; Publication No. US20020187946A1  
GENERAL INFORMATION:  
APPLICANT: Kornelux, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
EARLIER FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 23  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-201-936-23

Query Match 100.0%; Score 269; DB 9; Length 67;  
Best Local Similarity 100.0%; Pred. No. 4.7e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 1 LARAGFYTGPGDRVACFACGKLSNMWPKDDAMSEHRRHFPNCPF 46  
|||||  
Db 21 LARAGFYTGPGDRVACFACGKLSNMWPKDDAMSEHRRHFPNCPF 66  
|||||

RESULT 2  
US-08-464-588-2  
; Sequence 2, Application US/08464588



Publication No. US20030073159A1  
GENERAL INFORMATION:  
APPLICANT: HE, ET AL.  
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,588  
FILING DATE: June 5, 1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05922  
FILING DATE: 11 MAY 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 438 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-464-588-2

Query Match 100.0%; Score 269; DB 1; Length 438;  
Best Local Similarity 100.0%; Pred. No. 3.5e-26;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYTGPDVRVACFACGGKLSNWEPRDDAMSEHRRHFPNCPF 46  
DB 24 LARAGFYTGPDVRVACFACGGKLSNWEPRDDAMSEHRRHFPNCPF 69

RESULT 3:  
US-09-201-936-8  
Sequence 8, Application US/09201936  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
APPLICANT: Liston, Peter  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
CURRENT FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/TB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 8  
LENGTH: 618  
TYPE: PRP  
ORGANISM: Homo sapiens  
US-09-201-936-8

Query Match 100.0%; Score 269; DB 9; Length 618;  
Best Local Similarity 100.0%; Pred. No. 5.1e-26;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYTGPDVRVACFACGGKLSNWEPRDDAMSEHRRHFPNCPF 46  
DB 204 LARAGFYTGPDVRVACFACGGKLSNWEPRDDAMSEHRRHFPNCPF 249

RESULT 4:  
US-09-974-592-8  
Sequence 8, Application US/09974592  
Patent No. US20020120121A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
FILE REFERENCE: 07891/009004  
CURRENT APPLICATION NUMBER: US/09/974,592  
CURRENT FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: US 09/617,053  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 618  
TYPE: PRP  
ORGANISM: Homo sapiens  
US-09-974-592-8

Query Match 100.0%; Score 269; DB 10; Length 618;  
Best Local Similarity 100.0%; Pred. No. 5.1e-26;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYTGPDVRVACFACGGKLSNWEPRDDAMSEHRRHFPNCPF 46  
DB 204 LARAGFYTGPDVRVACFACGGKLSNWEPRDDAMSEHRRHFPNCPF 249

RESULT 5:  
US-09-974-592-14  
Sequence 14, Application US/09974592  
Patent No. US20020120121A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
FILE REFERENCE: 07891/009004  
CURRENT APPLICATION NUMBER: US/09/974,592  
CURRENT FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: US 09/617,053  
PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 612  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-974-592-14

Query Match 98.1%; Score 264; DB 10; Length 612;  
Best Local Similarity 97.8%; Pred. No. 2,2e+35;  
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGYYTIGPDRAVACFACGKLSNWEKDDAMSEHRRHFPNCP 46  
|||||  
DB 197 LARAGYYTIGPDRAVACFACGKLSNWEKDDAMSEHRRHFPNCP 242

RESULT 6  
US-09-778-927A-62

Sequence 62, Application US/09778927A  
Patent No. US2002068342A1  
GENERAL INFORMATION:  
APPLICANT: KHOSRAVI, Rami et al.  
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL  
VARIANTS OF ALTERNATIVE SPLICING  
FILE REFERENCE: 2786-0160P  
CURRENT APPLICATION NUMBER: US/09/778,927A  
CURRENT FILING DATE: 2001-02-08  
PRIOR APPLICATION NUMBER: IL 134453  
PRIOR FILING DATE: 2000-02-09  
PRIOR APPLICATION NUMBER: IL1335341  
PRIOR FILING DATE: 2000-03-29  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 62  
LENGTH: 306  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: (1)..(306)  
OTHER INFORMATION: Xaa - any amino acid, unknown, or other  
US-09-778-927A-62

Query Match 95.5%; Score 257; DB 10; Length 306;  
Best Local Similarity 95.7%; Pred. No. 7,9e+25;  
Matches 44; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LARAGYYTIGPDRAVACFACGKLSNWEKDDAMSEHRRHFPNCP 46  
|||||  
DB 204 LARAGYYTIGPDRAVACFACGKLSNWEKDDAMSEHRRHFPNCP 249

RESULT 7  
US-09-201-936-42

Sequence 42, Application US/09201936  
Publication No. US20020187946A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
PROBES, AND DETECTION METHODS  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
CURRENT FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05

EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 42  
LENGTH: 591  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-201-936-42

Query Match 94.8%; Score 255; DB 9; Length 591;  
Best Local Similarity 93.7%; Pred. No. 2,9e+24;  
Matches 44; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LARAGYYTIGPDRAVACFACGKLSNWEKDDAMSEHRRHFPNCP 46  
|||||  
DB 176 LARAGYYTIGPDRAVACFACGKLSNWEKDDAMSEHRRHFPNCP 221

RESULT 8  
US-09-201-936-22

Sequence 22, Application US/09201936  
Publication No. US20020187946A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
PROBES, AND DETECTION METHODS  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
CURRENT FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 22  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-201-936-22

Query Match 93.3%; Score 251; DB 9; Length 67;  
Best Local Similarity 93.5%; Pred. No. 8,9e+25;  
Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LARAGYYTIGPDRAVACFACGKLSNWEKDDAMSEHRRHFPNCP 46  
|||||  
DB 21 LARAGYYTIGPDRAVACFACGKLSNWEKDDAMSEHRRHFPNCP 66

RESULT 9  
US-09-201-936-6

Sequence 6, Application US/09201936  
Publication No. US20020187946A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
PROBES, AND DETECTION METHODS  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936

```
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-201-936-6
```

```
Query Match          93.3%; Score 251; DB 3; Length 604;
Best Local Similarity 93.5%; Pred. No. 9.5e-24;
Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 LARAGFYIIGPDRVACFCAGKLSNWEPRKDMSEHRRHFPNCPF 46
Db 189 LARAGFYIIGPDRVACFCAGKLSNWEPRKDMSEHRRHFPNCPF 234
```

```
RESULT 10
US-09-974-592-6
; Sequence 6, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-974-592-6
```

```
Query Match          93.3%; Score 251; DB 10; Length 604;
Best Local Similarity 93.5%; Pred. No. 9.5e-24;
Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 LARAGFYIIGPDRVACFCAGKLSNWEPRKDMSEHRRHFPNCPF 46
Db 189 LARAGFYIIGPDRVACFCAGKLSNWEPRKDMSEHRRHFPNCPF 234
```

```
RESULT 11
US-09-974-592-12
; Sequence 12, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
```

```
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-974-592-12
```

```
Query Match          89.6%; Score 241; DB 10; Length 600;
Best Local Similarity 89.1%; Pred. No. 1.7e-22;
Matches 41; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 LARAGFYIIGPDRVACFCAGKLSNWEPRKDMSEHRRHFPNCPF 46
Db 187 LARAGFYIIGPDRVACFCAGKLSNWEPRKDMSEHRRHFPNCPF 232
```

```
RESULT 12
US-09-201-936-40
; Sequence 40, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-201-936-40
```

```
Query Match          89.6%; Score 241; DB 9; Length 602;
Best Local Similarity 89.1%; Pred. No. 1.8e-22;
Matches 41; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 LARAGFYIIGPDRVACFCAGKLSNWEPRKDMSEHRRHFPNCPF 46
Db 189 LARAGFYIIGPDRVACFCAGKLSNWEPRKDMSEHRRHFPNCPF 234
```

```
RESULT 13
US-09-201-936-21
; Sequence 21, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
```



GenCore version 5.1.4-p5-4578  
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# OM protein - protein search, using sw model

Run on: May 5, 2003, 15:58:42 ; Search time 5.03456 Seconds  
(without alignments)  
878.365 Million cell updates/sec

Title: US-08-569-749-7

Perfect score: 269  
Sequence: 1 LARAGFYIIGPDGVACFAC.....WIPKDDAMSEHRRHFPNCPF 46

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*

1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	269	100.0	618 2	S68450 apoptos is inhibito
2	256	95.2	358 2	JCS964 apoptos is inhibito
3	251	93.3	604 2	S68449 apoptos is inhibito
4	192	71.4	497 2	S69544 apoptos is inhibito
5	149	55.4	1232 2	A55478 neuronal apoptos is
6	140	52.0	496 2	S68452 apoptos is inhibito
7	140	52.0	497 2	S69545 apoptos is inhibito
8	138	51.3	1447 2	T42628 neuronal apoptos is
9	133.5	49.6	4845 2	T31067 BIR repeat contain
10	132	49.1	268 2	T10304 inhibitor of apopt
11	132	49.1	268 2	A53989 apoptos is inhibito
12	137	47.2	298 2	JC7568 kidney inhibitor o
13	134	46.1	275 2	A45679 inhibitor-of-apopt
14	117	43.5	208 2	T03183 probable apoptos is
15	111	41.3	150 2	T28409 ORF MSV248 probabl
16	107	39.8	155 2	T30489 apoptos is inhibito
17	104	38.7	997 2	T43523 apoptos is inhibito
18	98	36.4	292 2	T41772 cut17 protein - fi
19	96	35.7	286 2	D36828 IAP1 orf27 - Bomby
20	93	34.6	275 2	T10310 orf13 protein - Au
21	80	29.7	249 2	H72858 apoptos is-inhibiti
22	80	29.7	249 2	T41814 IAP2 orf71 - Bomby
23	72	26.8	155 2	T37471 apoptos is inhibito
24	66.5	24.7	329 2	T28403 ORF MSV242 probabl
25	63.5	23.6	278 2	S25690 hup1 protein - Rho
26	63	23.4	234 2	T30427 probable apoptos is
27	63	23.4	308 2	T37474 apoptos is inhibito
28	58.5	21.7	284 1	A41382 UTP-glucose-1-phos
29	57	21.2	122 2	S09314 phospholipase A2 (

30	57	21.2	138 2	F48188 phospholipase A2 (
31	56.5	21.0	181 2	E36794 hypothetical prote
32	56	20.8	2111 2	T15390 hypothetical prote
33	55.5	20.6	340 2	AD0701 tetrahydronate redu
34	55	20.4	357 2	T50696 DNA primase small
35	55	20.4	409 2	S72438 phosphatidylserine
36	55	20.4	838 2	A48440 rtm-infected eryt
37	54.5	20.3	424 2	E30857 hypothetical prote
38	54.5	20.3	424 2	T10400 alkaline exonuclea
39	54.5	20.3	517 1	D37831 phenol 2-monooxyge
40	54	20.1	355 2	G64549 conserved hypotet
41	54	20.1	355 2	G71958 hypothetical prote
42	54	20.1	954 2	S57108 hypothetical prote
43	54	20.1	1004 2	JH0470 Na+/K+-exchanging
44	53.5	19.9	297 2	T39905 protein transport
45	53.5	19.9	525 1	S39834 myb-related protel

## ALIGNMENTS

RESULT 1  
S68450  
apoptos is inhibitor h1ap-2 - human  
C/Species: Homo sapiens (man)  
C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 21-Jul-2000  
C/Accession: S68450  
R/Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha  
Nature 379, 349-353, 1996  
A/Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of  
A/Reference number: A58182; MIMD:96149249; PMID:8552191  
A/Accession: S68450  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-618 <LIS>  
A/Cross-references: EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g1184318  
C/Function:  
A/Description: apoptotic suppressor  
C/Superfamily: RING finger homology  
C/Keywords: apoptosis; zinc finger  
F:567-611/Domain: RING finger homology <RNG>

Query Match 100.0%; Score 269; DB 2; Length 618;  
Best Local Similarity 100.0%; Pred. No. 1.8e-25;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDGVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46  
DB 204 LARAGFYIIGPDGVACFACGKLSNWEKDDAMSEHRRHFPNCPF 249

RESULT 2  
JCS964  
apoptos is inhibitor - pig  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 02-Sep-2000  
C/Accession: JCS964  
R/Stenlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.  
Biochem. Biophys. Res. Commun. 243, 827-832, 1998  
A/Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (Iap)  
A/Reference number: JCS964; MIMD:98162622; PMID:9501011  
A/Accession: JCS964  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-358 <STE>  
A/Cross-references: GB:U79142; NID:92957174; PIDN:AAC39171.1; PID:92957175  
C/Superfamily: RING finger homology  
F:307-351/Domain: RING finger homology <RRN>

Query Match 95.2%; Score 256; DB 2; Length 358;  
Best Local Similarity 93.5%; Pred. No. 4.4e-24;  
Matches 43; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNMEPKDAMSEHRRHPNCF 46  
 Db 24 LAKAGFYIIGPDRVACFACGKLSNMEPKDAMSEHRRHPNCF 69

## RESULT 3

568449  
 Apoptosis inhibitor hlap-1 - human  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 21-Jul-2000  
 C:Accession: S68449  
 R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996  
 A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP  
 A:Reference number: A58182; MUID:96149249; PMID:8552191  
 A:Accession: S68449  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-604 <LIS>  
 A:Cross-references: EMBL:U45878; NID:g1184315; PIDN:AAC50371.1; PID:g1184316  
 C:Function:  
 A:Description: apoptotic suppressor  
 C:Superfamily: RING finger homology  
 C:Keywords: apoptosis; zinc finger  
 F:533-597/Domain: RING finger homology <RNG>

Query Match 93.3%; Score 251; DB 2; Length 604;  
 Best Local Similarity 93.5%; Pred. No. 3e-23; Indels 0; Gaps 0;  
 Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNMEPKDAMSEHRRHPNCF 46  
 Db 189 LARAGFYIIGPDRVACFACGKLSNMEPKDAMSEHRRHPNCF 234

## RESULT 4

569544  
 Apoptosis inhibitor IAP homolog - human  
 C:Species: Homo sapiens (man)  
 C>Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Nov-2000  
 C:Accession: S69544; S68451  
 R:Duckett, C.S.; Nave, V.E.; Gedrich, R.W.; Clem, F.J.; van Dongen, J.L.; Gillfillan, M.C. EMBO J. 15, 2685-2694, 1996  
 A:Title: A conserved family of cellular genes related to the baculovirus iap gene and et  
 A:Reference number: S69544; MUID:96256286; PMID:8654366  
 A:Accession: S69544  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-497 <DUC>

A:Cross-references: EMBL:U32974; NID:g1016687; PIDN:AAC50518.1; PID:g1016688  
 R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996  
 A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP  
 A:Reference number: A58182; MUID:96149249; PMID:8552191  
 A:Accession: S68451  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>

A:Cross-references: EMBL:U45880; NID:g1184319; PIDN:AAC50373.1; PID:g1184320  
 C:Genetics:  
 A:Gene: i1p  
 C:Function:  
 A:Description: apoptotic suppressor  
 C:Superfamily: apoptotic inhibitor IAP homolog; RING finger homology  
 C:Keywords: apoptosis; zinc finger  
 F:446-490/Domain: RING finger homology <RRN>

Query Match 71.4%; Score 192; DB 2; Length 497;  
 Best Local Similarity 73.9%; Pred. No. 5e-16;  
 Matches 34; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNMEPKDAMSEHRRHPNCF 46  
 Db 11 LARAGFYIIGPDRVACFACGKLSNMEPKDAMSEHRRHPNCF 46

Db 184 LASAGLYTIGDVOECGCGKLSNMEPKDAMSEHRRHPNCF 229

## RESULT 5

A55478  
 neuronal apoptosis inhibitory protein - human  
 N:Alternate names: NAIP  
 C:Species: Homo sapiens (man)  
 C>Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 02-Feb-2001  
 C:Accession: A55478  
 R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shuttler, G.; Yareghli, Z.; Farahani, R.; Baird, T.O.; de Jong, P.J.; Suth, L.; Ikeda, J.E.; Korneluk, R.G.; Mackenzie, A. Cell 80, 167-178, 1995  
 A:Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in 1  
 A:Reference number: A55478; MUID:95112344; PMID:7813013  
 A:Accession: A55478  
 A:Molecule type: mRNA  
 A:Residues: 1-1232 <ROY>  
 A:Cross-references: GB:U19251  
 C:Genetics:  
 A:Gene: GDB:SMA6; SMA  
 A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300  
 A:Map position: 5q12.2-5q13  
 C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane p  
 F:94-110/Domain: transmembrane #status predicted <TM1>  
 F:470-477/Region: nucleotide-binding motif A (P-loop)  
 F:479-496/Domain: transmembrane #status predicted <TM2>  
 F:476/Binding site: ATP (Lys) #status predicted  
 F:618,632,823,923,1035/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 55.4%; Score 149; DB 2; Length 1232;  
 Best Local Similarity 54.3%; Pred. No. 2.4e-10;  
 Matches 25; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNMEPKDAMSEHRRHPNCF 46  
 Db 299 LAKAGFYIIGPDRVACFACGKLSNMEPKDAMSEHRRHPNCF 344

## RESULT 6

568452  
 Apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster  
 C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 17-Nov-2000  
 C:Accession: S68452; S78528  
 R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996  
 A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of  
 A:Reference number: A58182; MUID:96149249; PMID:8552191  
 A:Accession: S68452  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-496 <LIS>

A:Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314  
 R:Baird, S.D.  
 submitted to the EMBL data library, January 1996  
 A:Reference number: S78528  
 A:Accession: S78528

A:Molecule type: mRNA  
 A:Residues: 1-36, 'AT', 37, 'K', 39, 'L', 41-44, 'H', 46-58, 'O', 60-412, 'A', 414-427, 'A', 429-49  
 A:Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314  
 C:Genetics:  
 A:Cross-references: FlyBase:FBgn0015247

A:Function:  
 A:Description: apoptotic suppressor  
 C:Superfamily: apoptotic inhibitor IAP homolog; RING finger homology  
 C:Keywords: apoptosis; zinc finger  
 F:445-489/Domain: RING finger homology <RNG>

Query Match 52.0%; Score 140; DB 2; Length 496;  
 Best Local Similarity 51.1%; Pred. No. 1.4e-09;  
 Matches 23; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

OY 1 LARAGFYITGPDRAVACFACGKLSNMEPKDAMSEHRRHNPNC 45  
|||:||||:| | | | | :| | :| | | | | | | |  
Db 131 LAKAGFYITLRLDHVKCYWCMGCVIAKMEKNDNAFEHKKRFFPQCP 175

## RESULT 7

S69545  
apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: S69545  
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gillfillan, M.C.  
EMBO J. 15, 2685-2694, 1996  
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and en  
A:Reference number: S69544; MUID:96256286; PMID:8634366  
A:Accession: S69545  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-497 <DUC>  
A:Cross-references: EMBL:U32373; NID:91019116; PIDD:MAC47155.1; PID:91019117  
C:Genetics:  
A:Gene: IIP  
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology  
F:446-490/Domain: RING finger homology <RRN>

Query Match 52.0%; Score 140; DB 2; Length 497;  
Best Local Similarity 51.1%; Pred. No. 1.4e-05;  
Matches 23; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

OY 1 LARAGFYITGPDRAVACFACGKLSNMEPKDAMSEHRRHNPNC 45  
|||:||||:| | | | | :| | :| | | | | | | |  
Db 133 LAKAGFYITLRLDHVKCYWCMGCVIAKMEKNDNAFEHKKRFFPQCP 177

## RESULT 8

T42628  
neuronal apoptosis inhibitory protein 2 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000  
C:Accession: T42628  
R:Yaraghi, Z.; Diez, E.; Gros, P.; Mackenzie, A.  
Mamm. Genome 10, 761-763, 1999  
A:Title: cDNA cloning and the 5' genomic organization of Nalp2, a candidate gene for mur  
A:Reference number: 222179; MUID:99315342; PMID:10384056  
A:Accession: T42628  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1447 <YAR>  
A:Cross-references: EMBL:AF102871; NID:g3860228; PID:g3860229; PIDD:AACT3002.1  
C:Genetics:  
A:Gene: Nalp2

Query Match 51.3%; Score 138; DB 2; Length 1447;  
Best Local Similarity 52.2%; Pred. No. 6.5e-09;  
Matches 24; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

OY 1 LARAGFYITGPDRAVACFACGKLSNMEPKDAMSEHRRHNPNC 46  
|||:||||:| | | | | :| | :| | | | | | | |  
Db 181 LSAAGFVFTGKRDTVQCSCGCLGNWEGDDPMKEHAKWPFKCEP 226

## RESULT 9

T31067  
BIR repeat containing ubiquitin-conjugating enzyme BRUCE - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
C:Accession: T31067  
R:Hauser, H.P.; Bardroff, M.; Pyrowolakis, G.; Jentsch, S.  
J. Cell Biol. 141, 1415-1422, 1998  
A:Title: A giant ubiquitin-conjugating enzyme related to IAP apoptosis inhibitors.  
A:Reference number: 220963; MUID:98292517; PMID:9628897  
A:Accession: T31067  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-4845 <HAB>  
A:Cross-references: EMBL:Y17267; NID:g3319989; PIDD:CAA76720.1; PID:g3319990  
A:Note: localized to the Golgi compartment and the vesicular system  
C:Keywords: membrane-associated protein

Query Match 49.6%; Score 133.5; DB 2; Length 4845;  
Best Local Similarity 51.0%; Pred. No. 7.3e-08;  
Matches 25; Conservative 4; Mismatches 17; Indels 3; Gaps 1;

OY 1 LARAGFYITGPDRAVACFACGKLSNMEPKDAMSEHRRHNPNC 46  
|||:||||:| | | | | :| | :| | | | | | | |  
Db 264 MAQAGFYITQPASSGDDRAVACFACGKLSNMEPKDAMSEHRRHNPNC 332

## RESULT 10

T10304  
inhibitor of apoptosis protein 3 - Orygia pseudotsugata nuclear polyhedrosis virus  
C:Species: Orygia pseudotsugata nuclear polyhedrosis virus, OpMPV  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 15-Sep-2000  
C:Accession: T10304  
R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.  
Virology 229, 381-399, 1997  
A:Title: The sequence of the Orygia pseudotsugata multinucleocapsid nuclear polyhedro  
A:Reference number: 217011; MUID:97271300; PMID:9126251  
A:Accession: T10304  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-268 <AHR>  
A:Cross-references: EMBL:U75930; NID:g2934903; PIDD:AA59034.1; PID:g1911281  
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology  
F:217-261/Domain: RING finger homology <RRN>

Query Match 49.1%; Score 132; DB 2; Length 268;  
Best Local Similarity 45.7%; Pred. No. 7.6e-09;  
Matches 21; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 1 LARAGFYITGPDRAVACFACGKLSNMEPKDAMSEHRRHNPNC 46  
|||:||||:| | | | | :| | :| | | | | | | |  
Db 132 LAAGFYTGGDKTRCFCGGLKDWEPDAPWQOAHWYDRCEY 177

## RESULT 11

A53989  
apoptosis-inhibiting protein - Orygia pseudotsugata multicapsid nuclear polyhedrosis  
C:Species: Orygia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMPV  
C:Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 15-Sep-2000  
C:Accession: A53989  
R:Bitrbum, M.J.; Clem, R.J.; Miller, L.K.  
J. Virol. 68, 2521-2528, 1994  
A:Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a po  
A:Accession: A53989  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-268 <BIR>  
A:Cross-references: GB:L22564; NID:g456111; PIDD:AB02610.1; PID:g456114  
A:Note: authors translated the codon TGG for residue 28 as TTT, GAC for residue 50 as  
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology  
F:217-261/Domain: RING finger homology <RRN>

Query Match 49.1%; Score 132; DB 2; Length 268;  
Best Local Similarity 45.7%; Pred. No. 7.6e-09;  
Matches 21; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 1 LARAGFYITGPDRAVACFACGKLSNMEPKDAMSEHRRHNPNC 46  
|||:||||:| | | | | :| | :| | | | | | | |  
Db 132 LAAGFYTGGDKTRCFCGGLKDWEPDAPWQOAHWYDRCEY 177

## RESULT 12

JC7568  
kidney inhibitor of apoptosis protein - human

C:Species: Homo sapiens (man)  
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001  
C:Accession: J07568  
R:Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.  
Biochem. Biophys. Res. Commun. 279, 820-831, 2000  
A:Title: KIAA, a novel member of the inhibitor of apoptosis protein family.  
A:Reference number: J07568; MUID: 21092523; PMID:11162435  
A:Contents: Fetal kidney  
A:Accession: J07568  
A:Molecule type: mRNA  
A:Residues: 1-238 <LIN>  
C:Comment: This protein, a new member of the inhibitor of apoptosis protein family, plays  
C:Genetics:  
A:Gene: Kiap  
A:Map position: 20q13.3  
C:Keywords: apoptosis

Query Match 47.2%; Score 127; DB 2; Length 298;  
Best Local Similarity 47.8%; Pred. No. 3.5e-08;  
Matches 22; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46  
DB 108 LAAAGFHTGHODKVCFCYGLQSMKRGGDWPTEHAKRFPSCOF 153

RESULT 13  
A45679  
Inhibitor of apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV  
C:Species: Cydia pomonella granulosis virus CpGV  
C:Date: 21-Sep-1993 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000  
C:Accession: A45679  
R: Crook, N.E.; Clem, R.J.; Miller, L.K.  
J. Virol. 67, 2168-2174, 1993  
A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.  
A:Reference number: A45679; MUID:93188168; PMID:8445726  
A:Accession: A45679  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-275 <CRO>  
A:Cross-references: GB:L05494; NID:9289583; PIDN:AAA3835.1; PID:9289584  
A:Note: sequence extracted from NCBI backbone (NCBI:N:127014, NCBI:P:127015)  
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 46.1%; Score 124; DB 2; Length 275;  
Best Local Similarity 45.7%; Pred. No. 7.6e-08;  
Matches 21; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46  
DB 129 MADAGFYITGYDNTKCFYCGDGLKDMPEDPVMEQHVRWFDRCAV 174

RESULT 14  
T03183  
probable apoptosis inhibitor - Chilo iridescent virus  
C:Species: Chilo iridescent virus  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 02-Sep-2000  
C:Accession: T03183  
R: Bahr, U.; Tildona, C.A.; Darai, G.  
Virus Genes 15, 235-245, 1997  
A:Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101  
A:Reference number: 214834; MUID:98141693; PMID:9482589  
A:Accession: T03183  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-208 <BAH>  
A:Cross-references: EMBL:AF003534; NID:92738385; PIDN:AAB94481.1; PID:92738454  
C:Superfamily: RING finger homology  
F:159-202/Domain: RING finger homology <RRN>

Query Match 43.5%; Score 117; DB 2; Length 208;

Best Local Similarity 44.0%; Pred. No. 4.3e-07;  
Matches 22; Conservative 7; Mismatches 17; Indels 4; Gaps 1;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46  
DB 58 LSRAGFYITNIGDVOVCFYCDLKRKMKRSDNPFEEHKKHTOLKINCLF 107

RESULT 15  
T28409  
ORF MSV248 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes ent  
C:Species: Melanoplus sanguinipes entomopoxvirus  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T28409  
R: Alfonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.  
J. Virol. 73, 533-552, 1999  
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.  
A:Reference number: T28409; MUID:99102612; PMID:9847359  
A:Accession: T28409  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-150 <AF0>  
A:Cross-references: EMBL:AF063866; NID:94049647; PIDN:AAC97724.1; PID:94049764  
C:Genetics:  
A:Note: MSV248

Query Match 41.3%; Score 111; DB 2; Length 150;  
Best Local Similarity 43.5%; Pred. No. 1.8e-06;  
Matches 20; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46  
DB 37 LCPAGFYITNIGDITVCFNCGLKIKRMWLYNDPWIEHSMKSPNCNY 82

Search completed: May 5, 2003, 16:08:09  
Job time : 7.03456 secs



GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:51:32 ; Search time 1.90783 Seconds

(without alignments)  
1000.040 Million cell updates/sec

Title: US-08-569-749-7

Perfect score: 269  
Sequence: 1 IARAGTYRIGPDRAVACFAC.....WPKDDAMSEHRRHPCPF 46

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	269	100.0	BIR3_HUMAN	Q13490 homo sapien
2	264	98.1	BIR3_MOUSE	Q62210 mus musculu
3	256	95.2	PIAP_PIG	Q62640 sus scrofa
4	248	92.2	BIR2_HUMAN	Q13489 homo sapien
5	241	89.6	BIR2_MOUSE	Q08863 mus musculu
6	192	71.4	BIR4_HUMAN	P98170 homo sapien
7	191	71.0	BIR1_CHICK	Q90660 gallus gall
8	187	69.5	BIR4_MOUSE	Q60989 mus musculu
9	185	68.8	BIR4_RAT	Q91016 mus musculu
10	155	57.6	BIR8_HUMAN	Q96009 homo sapien
11	155	57.6	BIR8_PANTR	Q95M72 pan troglod
12	154	57.2	BIR8_GORGO	Q95M71 gorilla gor
13	149	55.4	BIR1_HUMAN	Q13075 homo sapien
14	141	52.4	BIR1_MOUSE	Q91133 mus musculu
15	141	52.4	BIR1_MOUSE	Q99W55 mus musculu
16	141	52.4	BIR1_MOUSE	Q91016 mus musculu
17	141	52.4	BIR1_MOUSE	Q91016 mus musculu
18	140	52.0	IAF2_DROME	Q24307 drosophila
19	138	51.3	BIR6_MOUSE	Q99U43 mus musculu
20	133.5	49.6	BIR6_HUMAN	Q99U43 mus musculu
21	132	49.1	IAF3_NPVOP	P41437 oryza pseu
22	129	48.0	IAF1_DROME	Q24306 drosophila
23	127	47.2	BIR7_HUMAN	Q96C45 homo sapien
24	124	46.1	IAF_GVCP	P41436 cydia pomon
25	117	43.5	ZFP_IRV6	P47732 chilo lride
26	108.5	40.3	BIR5_MOUSE	Q70201 mus musculu
27	108.5	40.3	BIR5_RAT	Q91H77 rattus norv
28	104	38.7	BIR1_SCHPO	Q14064 schizosacch
29	102.5	38.1	BIR5_HUMAN	Q15392 homo sapien
30	96	35.7	IAF1_NPVAC	P41435 autographa
31	93	34.6	IAF1_NPVOP	P41454 autographa
32	80	29.7	IAF1_NPVAC	P41454 autographa
33	78.5	29.2	IAF1_ASFB7	Q65138 african swi

34	73.5	27.3	224	1	IAF1_ASFMI	C11452 african swi
35	72.5	27.0	224	1	IAF1_ASFCH	Q11451 african swi
36	72.5	27.0	224	1	IAF1_ASFCH	Q12407 african swi
37	72.5	27.0	238	1	IAF1_ASFMI	Q11453 african swi
38	63.5	23.6	278	1	HUPJ_RHOCA	Q03009 rhodobacter
39	58.5	21.7	284	1	CELA_ACEXY	P27897 acetoabacter
40	58.5	21.7	404	1	FPRA_METTM	Q50497 methanobact
41	57	21.2	122	1	PA21_BOTAS	P20474 botitrops as
42	56.5	21.0	181	1	VG79_HSV11	Q00148 ictaluriid h
43	56	20.8	211	1	YP84_CAEEL	Q11107 caenorhabdi
44	55	20.4	370	1	DPSD_CRIGR	P27465 cricetus
45	54.5	20.3	424	1	EXON_NPVOP	P24081 oryza pseu

## ALIGNMENTS

RESULT 1  
BIR3\_HUMAN STANDARD; PRT; 618 AA.

AC Q13490; Q16516;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 3 (inhibitor of apoptosis protein 2) (HAP2) (HAP-2) (C-IAP1) (TNFR2-TNFR signaling complex protein 2) (IAP homolog B).  
GN BIRC3 OR API2 OR IAP2 OR MIBB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-96128127; Pubmed-8548810;  
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;  
RT "The TNFR2-TNFR signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";  
RL Cell 83:1243-1252(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-96149249; Pubmed-8552191;  
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertnon-Horvat G., Farfante R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";  
RL Nature 379:349-353(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX TISSUE-Fetal liver;  
RA uen A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX TISSUE-Uterus;  
RA Strausberg R.;  
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP STRUCTURE BY NMR OF 266-363.  
RX MEDLINE-99332054; Pubmed-10404221;  
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;  
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP) repeat".  
RL Nat. Struct. Biol. 6:648-651(1999).  
CC - FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

```
CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
CC -1- Inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- DATABASE: NAME-Atlas Genet. CytoGenet. Oncol. Haematol.;
CC WWW="http://www.infobloggen.fr/services/chromosome/genes/BIRC3ID239.html".
CC -----
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CC -----
DR EMBL: LA9431; AAC4942.1; -
DR EMBL: U45879; AAC50372.1; -
DR EMBL: U37547; AAC50508.1; -
DR EMBL: BC016174; AAH16174.1; -
DR PDB: 1OBN; 20-OCT-99.
DR Genew: HGNC:590; BIRC2.
DR MIM: 601721; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS00209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
DR Apoptosis; Znf_finger; Repeat; 3D-structure.
DR KW REPEAT 46 113 BIR 1.
DR REPEAT 184 250 BIR 2.
DR REPEAT 269 336 BIR 3.
DR DOMAIN 453 543 CARD.
DR ZN_RING 571 606 CARD.
DR ZN_RING 157 157 RING-TYPE.
DR CONFLICT 157 157 S -> P (IN REF. 2).
DR CONFLICT 308 308 C -> G (IN REF. 2).
DR CONFLICT 414 414 Q -> L (IN REF. 2).
DR CONFLICT 514 514 L -> W (IN REF. 2).
DR CONFLICT 514 514 L -> W (IN REF. 2).
DR SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

Query Match 100.0%; Score 269; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 2,5e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARGFYIIGDGVACFACGCKLSNRPDDANSEHRRHPCPF 46
DB 204 LARGFYIIGDGVACFACGCKLSNRPDDANSEHRRHPCPF 249

RESULT 2
BIR3_MOUSE
ID BIR3_MOUSE STANDARD; PRT; 612 AA.
AC Q62210; Q08864;
DC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
protein 2) (MIP2) (MIP-2).
```

```
GN BIRC3 OR API2 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8546810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins."
RT Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: LA9433; AAC42078.1; -
DR EMBL: U88909; AAC53532.1; -
DR HSSP: Q13490; IOBH.
DR MGD: MGI:1197009; Birc3.
DR InterPro: IPR001370; BIRC3.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS00209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
DR Apoptosis; Znf_finger; Repeat.
DR KW REPEAT 46 113 BIR 1.
DR REPEAT 177 243 BIR 2.
DR REPEAT 262 329 BIR 3.
DR DOMAIN 447 537 CARD.
DR ZN_RING 565 600 CARD.
DR ZN_RING 380 380 RING-TYPE.
DR CONFLICT 380 380 E -> K (IN REF. 2).
DR SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match 98.1%; Score 264; DB 1; Length 612;
Best Local Similarity 97.8%; Pred. No. 1.1e-26;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 1 LARAGFYIIGPDRVACFACGKLSNWKPKDMSERRRRPNCPE 46
    |||||||||||||||||||||||||||||||||||||||
Db 197 LARAGFYIIGPDRVACFACGKLSNWKPKDMSERRRRPNCPE 242

RESULT 3
PIAP_PIG STANDARD; PRT; 358 AA.
ID PIAP_PIG
AC 062640;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative inhibitor of apoptosis.
GN PIAP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=98162622; PubMed=9501011;
RA Stehlik C., de Martin R., Binder B.R., Lippe J.;
RT "Cytokine induced expression of porcine inhibitor of apoptosis
RT protein (Iap) family member is regulated by NF-kappa B.";
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC 1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC 1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC 1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC 1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U79142; AAC39171.1; -.
DR HSSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_Ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR APOPTOSIS: Zinc-finger: Repeat.
KM REPEAT 4 70 BIR 1.
FT REPEAT 90 157 BIR 2.
FT DOMAIN 193 283 CARD.
FT ZN_RING 311 346 RING-TYPE.
SQ SEQUENCE 358 AA; 40977 MW; EB2268FA9A6190A4 CRC64;

Query Match 95.28; Score 256; DB 1; Length 358;
Best Local Similarity 93.58; Freq. No. 6.9e-26;
Matches 43; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY 1 LARAGFYIIGPDRVACFACGKLSNWKPKDMSERRRRPNCPE 46
    |||||||||||||||||||||||||||||||||||||||
Db 24 LARAGFYIIGPDRVACFACGKLSNWKPKDMSERRRRPNCPE 69

RESULT 4
BIR2_HUMAN

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ID BIR2_HUMAN STANDARD; PRT; 604 AA.
AC Q13489; Q16628; Q9UP46; Q9HC27;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1 (inhibitor of apoptosis
DE protein 1) (IAP1) (H1AP1) (C-IAP2) (TNFR2-TRAF signaling complex
DE protein 1) (IAP homolog C).
GN BIRC2 OR Ap1 OR IAP1 OR MHC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins."
RL Cell 83:1243-1252(1995).
RN 2
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertov-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes."
RL Nature 379:349-353(1996).
RN 3
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN 4
RP SEQUENCE FROM N.A.
RX MEDLINE=99252096; PubMed=10233894;
RA Horvath A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
RA ten Cate J.W., Pannekoek H.;
RT "Vascular endothelial genes that are responsive to tumor necrosis
RT factor-alpha in vitro are expressed in atherosclerotic lesions,
RT including inhibitor of apoptosis protein-1, stannin, and two novel
RT genes."
RL Blood 93:3418-3431(1999).
RN 5
RP SEQUENCE OF 362-441 FROM N.A.
RX MEDLINE=20519161; PubMed=11066071;
RA Baens M., Steyts A., Dierlam J., De Wolf-Peeters C., Marynen P.;
RT "Structure of the M17 gene and molecular characterization of the
RT genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone
RT B-cell lymphomas of MALT type."
RL Genes Chromosomes Cancer 29:281-291(2000).
RN 6
RP FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
RN WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
RN FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
RN NECROSIS FACTOR RECEPTOR 2 (TNFR2).
RN 7
RP SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
RN inhibit apoptotic suppressor activity.
RN 8
RP SUBCELLULAR LOCATION: Cytoplasmic (Potential).
RN 9
RP TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN
RN THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,
RN INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
RN 10
RP DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
RN recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid
RN tissue). This translocation is found in approximately 50% of
RN cytogenetically abnormal low-grade MALT lymphoma and involves
RN MALT1 and BIRC2.
RN 11
RP 1- SIMILARITY: BELONGS TO THE IAP FAMILY.
RN 12
RP 1- SIMILARITY: CONTAINS 3 BIR REPEATS.

```

CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -----  
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 CC or send an email to [license@sdb.ch](mailto:license@sdb.ch)).  
 CC -----  
 DR EMBL: L49432; AAC41943.1; -  
 DR EMBL: U45878; AAC50371.1; -  
 DR EMBL: U37546; AAC50507.1; -  
 DR EMBL: AF178945; AAC09369.1; -  
 DR HSSP: Q13490; 10BH.  
 DR GENE: HGNC:591; BIRC3.  
 DR MIM: 601712; -  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR001841; Znf\_ring.  
 DR Pfam: PF00097; Zf-C3HC4; 1.  
 DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00653; BIR; 3.  
 DR SMART: SM00238; BIR; 3.  
 DR SMART: SM00114; CARD; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE: PS50209; CARD; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 DR KX Apoptosis; Zinc-finger; Repeat; Chromosomal translocation.  
 FT REPEAT 29 96 BIR 1.  
 FT REPEAT 169 235 BIR 2.  
 FT REPEAT 255 322 BIR 3.  
 FT DOMAIN 439 529 CARD.  
 FT ZN\_FING 557 592 RING-TYPE.  
 FT SITE 442 443 BREAKPOINT FOR TRANSLOCATION TO FORM  
 FT BIRC2-MULTI.  
 FT CONFLICT 18 18 BIRC2-MULTI.  
 FT CONFLICT 119 119 N -> Y (IN REF. 4).  
 FT CONFLICT 153 153 D -> E (IN REF. 2).  
 FT CONFLICT 163 163 H -> P (IN REF. 2).  
 FT CONFLICT 165 165 A -> P (IN REF. 2).  
 FT CONFLICT 191 191 K -> R (IN REF. 2).  
 FT CONFLICT 364 364 F -> L (IN REF. 2).  
 FT CONFLICT 552 552 Q -> P (IN REF. 2).  
 FT SEQUENCE 604 AA; 68371 MW; 8581A00BA9AA4A7 CRC64;  
 SQ  
 Query Match 92.2%; Score 248; DB 1; Length 604;  
 Best Local Similarity 91.3%; Pred. No. 1.3e-24;  
 Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LARAGFYITGPDRAVACGKLSNWEKDDAMSEHRRHFPNCP 46  
 DB 189 LAKAGFYITGPDRAVACGKLSNWEKDDAMSEHRRHFPNCP 234  
 RESULT 5  
 ID BIR2\_MOUSE STANDARD; PRT; 600 AA.  
 AC 008863;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis  
 DE protein 1) (MIAP1) (MIAP-1).  
 GN BIRC2 OR API1 OR IAP1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE= Skeletal muscle;  
 RX MEDLINE=98110590; PubMed=9441758;  
 RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Koronluk R.G.;  
 RT "Genomic characterization of the mouse inhibitor of apoptosis protein  
 RT 1 and 2 genes".  
 RL Genomics 46:495-503(1997).  
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
 CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
 CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
 CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).  
 CC -1- SUBUNIT: Interacts with SMAC and with PR555; these interactions  
 CC inhibit apoptotic suppressor activity (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -----  
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 CC -----  
 DR EMBL: U88908; AAC53531.1; -  
 DR HSSP: Q13490; 10BH.  
 DR MGI: MGI:1197007; Birc2.  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR001841; Znf\_ring.  
 DR Pfam: PF00097; Zf-C3HC4; 1.  
 DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00653; BIR; 3.  
 DR SMART: SM00238; BIR; 3.  
 DR SMART: SM00114; CARD; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE: PS50209; CARD; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 DR KX Apoptosis; Zinc-finger; Repeat.  
 FT REPEAT 27 94 BIR 1.  
 FT REPEAT 167 233 BIR 2.  
 FT REPEAT 253 320 BIR 3.  
 FT DOMAIN 436 525 CARD.  
 FT ZN\_FING 553 588 RING-TYPE.  
 FT SEQUENCE 600 AA; 67198 MW; AD/F73E649317D1 CRC64;  
 SQ  
 Query Match 89.6%; Score 241; DB 1; Length 600;  
 Best Local Similarity 89.1%; Pred. No. 1e-23;  
 Matches 41; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LARAGFYITGPDRAVACGKLSNWEKDDAMSEHRRHFPNCP 46  
 DB 187 LAKAGFYITGPDRAVACGKLSNWEKDDAMSEHRRHFPNCP 232  
 RESULT 6  
 ID BIR4\_HUMAN STANDARD; PRT; 497 AA.  
 AC P98170; Q9N014;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis  
 DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)  
 DE (IAP-like protein) (HILP).

GN BIRC4 OR PI3 OR IAP3 OR XIAP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal brain;  
RX MEDLINE=96149249; PubMed=8552191;  
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertont-Horvat G.,  
RT Farahani R., Mclean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RT "Suppression of apoptosis in mammalian cells by NIP and a related  
RL family of IAP genes";  
RN Nature 379:349-353(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal heart;  
RX MEDLINE=96256286; PubMed=8654366;  
RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,  
RT Glifflin M.C., Shleis H., Hardwick J.M., Thompson C.B.;  
RT "A conserved family of cellular genes related to the baculovirus IAP  
RN gene and encoding apoptosis inhibitors";  
RN EMBO J. 15:2685-2694(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC Grafton D.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RN FUNCTION.  
RX MEDLINE=97373959; PubMed=9230442;  
RA Dervaux O.L., Takahashi R., Salvesen G.S., Reed J.C.;  
RT "X-linked IAP is a direct inhibitor of cell-death proteases.";  
RN Nature 386:300-304(1997).  
RN [5]  
RP MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.  
RX MEDLINE=21634829; PubMed=11604410;  
RA Verhaegen A.M., Silke J., Ekert P.G., Pakusch M., Kaufmann H.,  
RA Connolly L.M., Day C.L., Tikoo A., Burke R., Wöbel C., Moritz R.J.,  
RT "HtrA2 promotes cell death through its serine protease activity and  
RL its ability to antagonize inhibitor of apoptosis proteins";  
RN J. Biol. Chem. 277:445-454(2002).  
RN [6]  
RP STRUCTURE: BY NMR OF 241-356 IN COMPLEX WITH SMAC.  
RX MEDLINE=21020961; PubMed=11140637;  
RA Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T.,  
RA Herrmann J., Wu J.C., Fesik S.W.;  
RT "Structural basis for binding of Smac/DIABLO to the XIAP BIR3  
RN domain";  
RL Nature 406:1004-1008(2000).  
RL [7]  
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3  
CC and -7, while the third BIR is involved in caspase-9 inhibition.  
CC The interactions with SMAC and PRSS5 are mediated by the second  
CC and third BIR domains.  
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC  
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OR EMBL; U45880; AAC50373.1; -

[illegible]





```

RT  "Molecular cloning of ILP-2, a novel member of the inhibitor of
RL  apoptosis protein family."
CC  Mol. Cell. Biol. 21:4292-4301(2001).
CC  -1- FUNCTION: Protects against apoptosis mediated by BAX (By
CC  similarity).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC  -1- SUBUNIT: Binds to caspase-9 (By similarity).
CC  -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC  -1- SIMILARITY: CONTAINS 1 BIR REPEAT.
CC  -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AY030052; AAK49776.1; -.
DR  InterPro; IPR001370; BIR.
DR  InterPro; IPR001841; Znf_rlng.
DR  Pfam; PF00653; BIR.1.
DR  Pfam; PF00097; zf-C3HC4; 1.
DR  PROSITE; PS01282; BIR_REPEAT_1; 1.
DR  PROSITE; PS0143; BIR_REPEAT_2; 1.
DR  PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR  PROSITE; PS00089; ZF_RING_2; 1.
DR  Apoptosis; Zinc-finger.
DR  REPEAT 7 70 BIR.
DR  ZN_FING 189 224 RING-TYPE.
SQ  SEQUENCE 236 AA; 27136 MW; 64CCA3A251420EDE CRC64;

Query Match 57.6%; Score 155; DB 1; Length 236;
Best Local Similarity 54.3%; Pred. No. 5.7e-13;
Matches 25; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGRVACFACGKLSWNEPRDMSHRHFPNCPF 46
DB 23 LARAGFYAIGQEDKIQCFHGGGLANWKREDEQHAHWKPGCKY 68

RESULT 12
BIR8_GORGO STANDARD; PRT; 236 AA.
AC 095M71;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral iAP repeat-containing protein 8 (inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2).
GN BIR8 OR ILP2.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21286921; PubMed-11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
RA Fratini A., Tian L., Frank S., Youle R.D., Nelson D.L.,
RA Notarangelo L.D., Vezoni P., Fearhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family."
RT Mol. Cell. Biol. 21:4292-4301(2001).
RL Cell. Biol. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SUBUNIT: Binds to caspase-9 (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BIR REPEAT.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----

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CC -----
DR  EMBL; AY030053; AAK49777.1; -.
DR  InterPro; IPR001370; BIR.
DR  InterPro; IPR001841; Znf_rlng.
DR  Pfam; PF00653; BIR.1.
DR  Pfam; PF00097; zf-C3HC4; 1.
DR  PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.
DR  PROSITE; PS0143; BIR_REPEAT_2; 1.
DR  PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR  PROSITE; PS00089; ZF_RING_2; 1.
DR  Apoptosis; Zinc-finger.
DR  REPEAT 7 70 BIR.
DR  ZN_FING 189 224 RING-TYPE.
SQ  SEQUENCE 236 AA; 27120 MW; C3A70E39E442E4C CRC64;

Query Match 57.2%; Score 154; DB 1; Length 236;
Best Local Similarity 52.2%; Pred. No. 7.7e-13;
Matches 24; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGRVACFACGKLSWNEPRDMSHRHFPNCPF 46
DB 23 LARAGFYAIGQEDKIQCFHGGGLANWKREDEQHAHWKPGCKY 68

RESULT 13
BIR1_HUMAN STANDARD; PRT; 1403 AA.
AC Q13075; Q13730; Q99796; O75857;
DT 01-NOV-1997 (Rel. 35, Created).
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral iAP repeat-containing protein 1 (Neuronal apoptosis
DE inhibitory protein).
GN BIR1 OR NAIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-Petal Brain;
RX MEDLINE-95112344; PubMed-7813013;
RA Roy N., Mahadevan M.S., McLean M., Shuttler G., Yaraqhi Z.,
RA Farahini R., Baird S., Besner-Johnston A., Lefebvre C., Kang X.,
RA Salih M., Aubry H., Tamal K., Guan X., Ioannou P., Crawford T.O.,
RA de Jong P.J., Surh L., Ikeda J., Korneluk R.G., Mackenzie A.;
RT "The gene for neuronal apoptosis inhibitory protein is partially
RT deleted in individuals with spinal muscular atrophy."
RT Cell 80:167-178(1995).
RL Cell 80:167-178(1995).
RN [2]
RP SEQUENCE FROM N.A., AND REVISIONS.
RX TISSUE-Brain;
RX MEDLINE-95112345; PubMed-9503025;
RA Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farahani R.,
RA Xuan J.-Y., Kang X., Lefebvre C., Ikeda J.-E., Korneluk R.G.,
RA Mackenzie A.E.;
RT "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular
RT atrophy candidate genes SMN and NAIP."
RT Genomics 48:121-127(1998).
RL Genomics 48:121-127(1998).
RN [3]
RP SEQUENCE OF 386-623 FROM N.A.
RX der Steege G., Draaijers F.G., Grootsholten P.M., Ozinga J.,
RX Anzerino R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,
RX Buys C.H.C.M.;
RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [4]

```



RP SEQUENCE OF 222-1403 FROM N.A.  
RA Jones K., Graves T., McPherson J.;  
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
RN [5]  
RP FUNCTION:  
RC TISSUE-Liver;  
RA MEDLINE-96149249; PubMed-8552191;  
RA Liston P., Roy N., Yamal K., Lefebvre C., Balrd S., Cherton-Horvat G.,  
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RA "Suppression of apoptosis in mammalian cells by NAIP and a related  
RT family of IAP genes";  
RL Nature 379:349-353(1996).  
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
CC SIGNALS.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY  
CC NEURONS. FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN  
CC SPINAL CORD.  
CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN  
CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE 1 (SMA TYPE 1). SMAS  
CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE 1  
CC (WERDING-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE  
CC III (WOLFF-PARK-KUHLBERG-WELANDER DISEASE) BASED UPON THE AGE OF  
CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE  
CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO  
CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000  
CC NEBORN.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.  
CC -----  
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CC -----  
DR EMBL: U19251; AAC52045.1; -  
DR EMBL: U80017; AAC52047.1; -  
DR EMBL: U21913; AA64504.1; -  
DR EMBL: AC005031; AAC62261.1; -  
DR HSSP: Q13490; IOBH.  
DR Gene: HGNC:7634; BIRCL1.  
DR MIM: 600355; -  
DR InterPro: IPR001370; BIR.  
DR Pfam: PF00653; BIR; 3.  
DR SMART: SM00238; BIR; 3.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE: PS0837; NACHT; 1.  
KW Apoptosis; Repeat.  
FT REPEAT 60 127 BIR 1.  
FT REPEAT 159 227 BIR 2.  
FT REPEAT 278 345 BIR 3.  
FT DOMAIN 464 758 NACHT.  
FT CONFLICT 222 223 PK -> YR (IN REF. 4).  
FT CONFLICT 366 387 VP -> ST (IN REF. 3).  
FT CONFLICT 535 535 M -> V (IN REF. 3).  
FT CONFLICT 553 553 Y -> H (IN REF. 3).  
FT CONFLICT 1228 1231 MISSING (IN REF. 4).  
SQ SEQUENCE 1403 AA; 159613 MW; 566304C154A564 CRC64;  
Query Match 55.4%; Score 149; DB 1; Length 1403;  
Best Local Similarity 54.3%; Pred. No. 2,1e-11;  
Matches 25; Conservative 6; Mismatches 15; Indels 0; Gaps 0;  
QY 1 LARAGFYTGPDNRVACFCAGKLSNWEKPKDAMSEHRHFPNCP 46  
Db 299 LKAGLFTYTGKRDYVQCFSCGSLGWEGDDPDKHTRFCPCP 344  
RESULT 14  
BIR\_MOUSE

ID BIR\_MOUSE STANDARD; PRT; 1402 AA.  
AC 09JIB3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 1g (neuronal apoptosis  
DE inhibitory protein 7).  
GN BIRCL1 OR NAIP7.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid-10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-20414747; PubMed-10958627;  
RA Endtizi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;  
RA "Genomic sequence analysis of the mouse Naip gene array";  
RL Genome Res. 10:1095-1102(2000).  
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
CC SIGNALS.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.  
CC -----  
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CC -----  
DR EMBL: AF242433; AAF82749.1; -  
DR HSSP: Q13490; IOBH.  
DR MGD: MGI:1858256; Birc1g.  
DR InterPro: IPR001370; BIR.  
DR Pfam: PF00653; BIR; 3.  
DR SMART: SM00238; BIR; 3.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE: PS0837; NACHT; 1.  
KW Apoptosis; Repeat; Multigene family.  
FT REPEAT 60 127 BIR 1.  
FT REPEAT 159 227 BIR 2.  
FT REPEAT 278 345 BIR 3.  
FT REPEAT 464 759 NACHT.  
SQ SEQUENCE 1402 AA; 159662 MW; C1DFEBA359893E0D CRC64;  
Query Match 52.4%; Score 141; DB 1; Length 1402;  
Best Local Similarity 52.2%; Pred. No. 2,2e-10;  
Matches 24; Conservative 4; Mismatches 18; Indels 0; Gaps 0;  
QY 1 LARAGFYTGPDNRVACFCAGKLSNWEKPKDAMSEHRHFPNCP 46  
Db 181 LKAGLFTYTGKRDYVQCFSCGSLGWEGDDPDKHTRFCPCP 226  
RESULT 15  
BIR\_MOUSE  
ID BIR\_MOUSE STANDARD; PRT; 1403 AA.  
AC 09JIB5;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 1a (neuronal apoptosis  
DE inhibitory protein 1).  
GN BIRCL1 OR NAIP1 OR NAIP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid-10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yarahtl Z., Korneluk R.G., Mackenzie A.E.;



GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:57:12 ; Search time 11.235 Seconds

(without alignments)  
843,627 Million cell updates/sec

Title: US-08-569-749-7

Sequence: 1 LARAGFYTGPGDRVACFAC.....WEYKDAMSEHRHFNCF 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP rivirus:\*  
16: SP bacteriophage:\*  
17: SP archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	243	90.3	589	11	Q9SE88 rat. rat. nov.
2	243	90.3	589	11	Q9G2C6 rat. rat. nov.
3	241	89.6	374	11	Q921N0 mus. mus. nov.
4	236	87.7	602	11	Q9SE89 rat. rat. nov.
5	228	84.8	195	13	Q91A70 gall. gall. nov.
6	228	84.8	197	13	Q91A69 gall. gall. nov.
7	228	84.8	224	11	Q98642 rat. rat. nov.
8	228	84.8	324	13	Q9DDN2 gall. gall. nov.
9	228	84.8	610	13	Q9DDN2 gall. gall. nov.
10	199	74.0	628	13	Q8UMD2 gall. gall. nov.
11	190	70.6	493	13	Q8UMD2 gall. gall. nov.
12	185	68.8	496	11	Q9ESF0 gall. gall. nov.
13	185	68.8	501	11	Q9ESF0 gall. gall. nov.
14	185	68.8	501	11	Q9ESF0 gall. gall. nov.
15	155	57.6	236	4	Q96RW5 gall. gall. nov.
16	155	57.6	236	4	Q96RW5 gall. gall. nov.

17	155	57.6	236	6	Q95M72 pan. troglod
18	154	57.2	236	6	Q95M71 gor. gor.
19	152	56.5	405	13	Q8UWH2 brachydanio
20	149	55.4	1160	4	Q8TD24 gall. gall. nov.
21	144	53.5	403	5	Q8WRD9 ochlerotatu
22	143	53.2	106	4	Q96RW6 gall. gall. nov.
23	141	52.0	597	11	Q9R015 gall. gall. nov.
24	140	52.0	498	5	Q96U03 gall. gall. nov.
25	139	51.7	517	11	Q8R4U8 gall. gall. nov.
26	136	50.6	402	5	Q8T621 gall. gall. nov.
27	133.5	49.6	4845	11	Q88738 gall. gall. nov.
28	132.5	49.3	153	5	Q9VEM2 gall. gall. nov.
29	132	49.1	346	5	Q968R8 gall. gall. nov.
30	129	48.0	264	12	Q9EN27 gall. gall. nov.
31	129	48.0	438	5	Q9VUX5 gall. gall. nov.
32	127	47.2	276	12	Q8Q0L95 gall. gall. nov.
33	127	47.2	280	4	Q9HAP7 gall. gall. nov.
34	127	47.2	298	4	Q9H2A8 gall. gall. nov.
35	127	47.2	298	4	Q96CA5 gall. gall. nov.
36	126	46.8	261	12	Q9QES9 gall. gall. nov.
37	126	46.8	379	5	Q9U492 gall. gall. nov.
38	125	46.5	276	12	Q89744 gall. gall. nov.
39	123	45.7	268	12	Q91F18 gall. gall. nov.
40	123	45.7	268	12	Q9E232 gall. gall. nov.
41	123	45.7	281	12	Q9YNI8 gall. gall. nov.
42	123	45.7	313	12	Q9J827 gall. gall. nov.
43	123	45.7	377	5	Q9NU07 gall. gall. nov.
44	117	43.5	208	12	Q95770 gall. gall. nov.
45	115.5	42.9	4904	5	Q9VH01 gall. gall. nov.

## ALIGNMENTS

RESULT 1

Q9SE88 PRELIMINARY; PRT; 589 AA.

AC Q9SE88; 01-MAR-2001 (TREMBL) 16, Created)

DT 01-MAR-2001 (TREMBL) 16, Last sequence update)

DT 01-JUN-2002 (TREMBL) 16, Last annotation update)

DE Inhibitor of apoptosis protein 2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.,

RT Cloning and Characterization of the Rat Homologs of the Inhibitor of

RT Apoptosis Protein 1, 2, and 3 Genes.

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL; AF183431; AAC22971.1; -

DR HSSP; Q13490; IOBH.

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001315; CARD.

DR InterPro: IPR001841; ZNF\_Ling.

DR Pfam; PF00653; BIR; 3.

DR Pfam; PF00619; CARD; 1.

DR Pfam; PF00097; zf-C3HC4; 1.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00184; KING; 1.

DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.

DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.

DR PROSITE; PS0209; CARD; 1.

KW ZINC-FINGER.

SQ SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD285B CRC64;

Query Match 90.3%; Score 243; DB 11; Length 589;

Best Local Similarity 87.0%; Pred. No. 4.9e-23;

Matches 40; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 LARAGFYTGPDGVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46  
176 LARAGFYTGPDGVACFACGKLSNWEKDDAMSEHRRHFPNCPF 221

## RESULT 2

ID 0902C6 PRELIMINARY; PRT: 589 AA.  
AC 0902C6;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Inhibitor of apoptosis protein 2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=KIDNEY;  
RA Dong Z., Denton M., Gu S.M., Saikumar P., Venkatchalam M.A.;  
RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2.";  
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
DR EMBL; AF190020; AAF04585.1; -  
DR HSSP; O13490; IOBH.  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR001315; CARD.  
DR InterPro: IPR001841; Znf\_ring.  
DR Pfam; PF00653; BIR; 3.  
DR Pfam; PF00619; CARD; 1.  
DR SMART; SM00238; BIR; 3.  
DR SMART; SM00114; CARD; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
DR PROSITE; PS50209; CARD; 1.  
KW Zinc-finger.  
SQ SEQUENCE 589 AA; 66777 MW; E6812FEE3EA34142 CRC64;  
OY Query Match 90.3%; Score 243; DB 11; Length 589;  
Best Local Similarity 87.0%; Pred. No. 4, 9e-23;  
Matches 40; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
Db 176 LARAGFYTGPDGVACFACGKLSNWEKDDAMSEHRRHFPNCPF 221

## RESULT 3

ID 0921NO PRELIMINARY; PRT: 374 AA.  
AC 0921NO;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Similar to baculoviral IAP repeat-containing 2.  
GN BIRC2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BC013338; AAH1338.1; -  
DR MGD; MGI:1197007; Birc2.  
DR InterPro: IPR001370; BIR.  
DR Pfam; PF00653; BIR; 3.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; UNKNOWN\_3.

DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
SQ SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7E46F3 CRC64;

OY Query Match 89.6%; Score 241; DB 11; Length 374;  
Best Local Similarity 89.1%; Pred. No. 5, 3e-23;  
Matches 41; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LARAGFYTGPDGVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46  
187 LARAGFYTGPDGVACFACGKLSNWEKDDAMSEHRRHFPNCPF 232

## RESULT 4

ID 09ESE9 PRELIMINARY; PRT: 602 AA.  
AC 09ESE9;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Inhibitor of apoptosis protein 1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;  
RT "Cloning and characterization of the Rat Homologs of the Inhibitor of  
Apoptosis Protein 1, 2, and 3 Genes.";  
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
DR EMBL; AF183430; AAG22970.1; -  
DR HSSP; O13490; IOBH.  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR001315; CARD.  
DR InterPro: IPR001841; Znf\_ring.  
DR Pfam; PF00653; BIR; 3.  
DR Pfam; PF00619; CARD; 1.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR SMART; SM00238; BIR; 3.  
DR SMART; SM00114; CARD; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.  
DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
DR PROSITE; PS50209; CARD; 1.  
KW Zinc-finger.  
SQ SEQUENCE 602 AA; 67326 MW; CC91385EEA62DE5A CRC64;  
OY Query Match 87.7%; Score 236; DB 11; Length 602;  
Best Local Similarity 84.8%; Pred. No. 4e-22;  
Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
Db 189 LARAGFYTGPDGVACFACGKLSNWEKDDAMSEHRRHFPNCPF 234

## RESULT 5

ID 091A70 PRELIMINARY; PRT: 195 AA.  
AC 091A70;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Inhibitor of apoptosis 1 (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OX NCBI\_TaxId=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BREED LEHORN; TISSUE=SPLEEN;

```

RX MEDLINE-21158006; PubMed-11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
   specific genes."
RL Poult. Sci. 80:284-288(2001).
DR EMBL: AF221082; AAF35319.1; -.
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

Query Match      84.8%; Score 228; DB 13; Length 195;
Best Local Similarity 80.4%; Pred. No. 1.3e-21;
Matches 37; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNNEPKDDAMSEHRRHFPNCPF 46
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 50 LAKAGLYLTGADKVAACFTCGGOLSNNEPKDDAMSEHRRHFPNCPF 95

RESULT 6
QY 091A69 PRELIMINARY; PRT; 197 AA.
AC 091A69;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BREED FAYOUMI; TISSUE-SPLEEN;
RX MEDLINE-21158006; PubMed-11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
   specific genes."
RL Poult. Sci. 80:284-288(2001).
DR EMBL: AF221083; AAF35320.1; -.
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

Query Match      84.8%; Score 228; DB 13; Length 197;
Best Local Similarity 80.4%; Pred. No. 1.3e-21;
Matches 37; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNNEPKDDAMSEHRRHFPNCPF 46
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 51 LAKAGLYLTGADKVAACFTCGGOLSNNEPKDDAMSEHRRHFPNCPF 96

RESULT 7
QY 088642 PRELIMINARY; PRT; 224 AA.
AC 088642;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

```

```

DE Inhibitor of apoptosis protein (Fragment).
GN RIAP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-OVARY;
RA Bradley C.K., Lareu R.R., Dharmarajan A.M.;
RT "Cloning and characterization of an inhibitor of apoptosis protein
   (IAP) in the rat corpus luteum."
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF081503; AAC32497.1; -.
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
FT NON_TER 1
FT SEQUENCE 224 AA; 25209 MW; 213A52534D5E856A CRC64;

Query Match      84.8%; Score 228; DB 11; Length 224;
Best Local Similarity 80.4%; Pred. No. 1.5e-21;
Matches 37; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNNEPKDDAMSEHRRHFPNCPF 46
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 105 LKRAEYITGPDRVPCFACGKLSNNEPKDDLLSEHRRHFPNCPF 150

RESULT 8
QY 09DDN2 PRELIMINARY; PRT; 324 AA.
AC 09DDN2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Apoptosis inhibitor ch-IAP1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Pendleton C.N., Bargmann W.J., Varadarajan J., Bose H.R. Jr.;
RT "The apoptosis inhibitor ch-IAP1 is a direct transcriptional target of
   v-Rel and c-Rel."
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF311289; AAG42316.1; -.
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
FT NON_TER 324
FT SEQUENCE 324 AA; 36567 MW; 5E2B89DEAE373F3 CRC64;

Query Match      84.8%; Score 228; DB 13; Length 324;
Best Local Similarity 80.4%; Pred. No. 2.2e-21;
Matches 37; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNNEPKDDAMSEHRRHFPNCPF 46
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 196 LAKAGLYLTGADKVAACFTCGGOLSNNEPKDDAMSEHRRHFPNCPF 241

RESULT 9
QY 057319 PRELIMINARY; PRT; 610 AA.
ID 057319

```

```

AC 057319;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE Inhibitor of apoptosis protein 1 (IAP) (inhibitor of T cell apoptosis
DE PROTEIN).
GN IAP1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=EMBRYONIC FIBROBLAST;
RX MEDLINE=98038801; PubMed=9372964;
RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "Ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
RT mediator of the antiapoptotic activity of the v-Rel oncoprotein.";
RL Mol. Cell. Biol. 17:7328-7341(1997).
CC -1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
CC CELLS.
CC -1- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF
CC THE V-REL-TRANSFORMED CELLS.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE
CC SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS
CC IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
CC -1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
CC PROCESS.
CC -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
CC -1- SIMILARITY: MEMBER OF THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF
CC APOPTOSIS PROTEIN REPEAT).
CC EMBL: AF008592; AAB88044.1; -.
DR HSP: Q13490; IGBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 30 97 BIR_REPEAT 1.
FT REPEAT 176 242 BIR_REPEAT 2.
FT REPEAT 262 329 BIR_REPEAT 3.
FT ZN_FING 563 597 C3HC4-TYPE.
SQ SEQUENCE 610 AA; 68924 MW; ADF47619650B44A6 CRC64;

Query Match 84.8%; Score 228; DB 13; Length 610;
Best Local Similarity 80.4%; Pred. No. 4.4e-21;
Matches 37; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 LARAGYYIGPDRAVACFCGKLSNWEKDDAMSEHRHFNCP 46
DB 196 LKAGLYIGDADKACVCTCGQLSNWEKDDAMSEHRHFNCP 241

RESULT 10
OQUMD2 PRELIMINARY; PRT; 628 AA.
AC OQUMD2;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Iap1.
GN IAP1.

```

```

OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
RN (2)
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RX EMBL: AF442500; AL33679.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50089; zf_RING_2; 1.
SQ SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87C8A95 CRC64;

Query Match 74.0%; Score 199; DB 13; Length 628;
Best Local Similarity 69.6%; Pred. No. 2.5e-17;
Matches 32; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

OY 1 LARAGYYIGPDRAVACFCGKLSNWEKDDAMSEHRHFNCP 46
DB 207 LKAGLYIGDADKACVCTCGQLSNWEKDDAMSEHRHFNCP 252

RESULT 11
OQUMD2 PRELIMINARY; PRT; 493 AA.
AC OQUMD2;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Inhibitor of apoptosis protein 3.
GN IAP3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Identification of chicken inhibitor of apoptosis protein XIAP
RT (IAP3).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RX EMBL: AF451854; AL47170.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50089; zf_RING_2; 1.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;

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GenCore version 5.1.6-p5.4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:50:57 ; Search time 10.8353 seconds  
(without alignments)  
676.383 Million cell updates/sec

Title: US-08-569-749-5

Perfect score: 307  
Sequence: 1 CEIRMSRYSTFPAGVPVSE.....RYKFCGCGIMLDNKLGDSP 55

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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2: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT.\*  
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23: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	55	AAW13547	Human c-IAP1 repea
2	307	100.0	306	AAW02925	Angiotensin conver
3	307	100.0	618	AAW19746	Human inhibitor of
4	307	100.0	618	AAW19583	Human apoptosis in
5	307	100.0	618	AAW13545	Human c-IAP1. Hom
6	307	100.0	618	AAW69296	Human HIP-2 prote
7	307	100.0	618	AAW33998	Human cellular inh
8	307	100.0	618	ABG65665	Human inhibitor of
9	301	98.0	55	AAW13548	Human c-IAP2 repea
10	301	98.0	604	AAW19747	Human inhibitor of

11	301	98.0	604	18	AAW19582	Human apoptosis in
12	301	98.0	604	18	AAW13546	Human c-IAP2. Hom
13	301	98.0	604	19	AAW69295	Human HIP-1 prote
14	301	98.0	604	20	AAW52703	Human cellular inh
15	301	98.0	604	20	AAW33997	Human inhibitor of
16	301	98.0	604	23	ABG65664	Human cysteine pro
17	301	98.0	1141	22	AAW97837	Human APT2-MUT chl
18	301	98.0	1141	22	AAW50694	Human apoptosis in
19	291	94.8	591	23	ABG65668	Mouse inhibitor of
20	291	94.8	612	19	AAW13555	Mouse c-IAP. Mus
21	291	94.8	612	19	AAW69298	Mouse HIP-2 prot
22	284	92.5	600	19	AAW69298	Mouse apoptosis in
23	284	92.5	602	18	AAW19585	Mouse inhibitor of
24	284	92.5	602	23	ABG65667	Human apoptosis in
25	284	92.5	602	23	ABG65667	Human XIAP protein
26	159	51.8	497	18	AAW19581	Human X-linked inh
27	159	51.8	497	21	AAW69294	Human XIAP protein
28	159	51.8	497	21	AAW69294	Human inhibitor of
29	159	51.8	497	21	AAW59451	Mouse apoptosis in
30	159	51.8	497	21	AAW59451	Mouse XIAP proteol
31	153	49.8	496	18	AAW19745	Mouse inhibitor of
32	153	49.8	496	18	AAW19745	Mouse inhibitor of
33	153	49.8	496	19	AAW69297	Mouse apoptosis in
34	153	49.8	496	23	ABG65663	Mouse inhibitor of
35	145	48.9	438	17	AAW04583	Human inhibitor of
36	145	48.9	438	17	AAW04583	Human inhibitor of
37	130.5	42.5	263	23	ABW09488	Amprv baculovirus-
38	129	42.0	438	22	AAW48191	Drosophila mutant
39	127	41.4	438	22	AAW48195	Drosophila melanog
40	127	41.4	438	22	ABW67347	Drosophila melanog
41	127	41.4	438	22	AAW48188	Drosophila wild-ty
42	127	41.4	438	22	AAW48189	Drosophila mutant
43	127	41.4	438	22	AAW48190	Drosophila mutant
44	127	41.4	438	22	AAW48190	Drosophila mutant
45	127	41.4	438	22	AAW48192	Drosophila mutant

## ALIGNMENTS

RESULT 1	AAW13547	standard; Protein: 55 AA.
ID	AAW13547	
AC	AAW13547	
XX	22-JUL-1997	(first entry)
XX	Human c-IAP1 repeat 1.	
DE	IAP; inhibitor; apoptosis; RING finger domain; restinosis;	
DT	myocardial infarction; nephritis; HIV.	
KW	Homo sapiens.	
XX	W09706182-A1.	
XX	20-FEB-1997.	
PD	06-AUG-1996.	96MO-US12860.
XX	08-DEC-1995.	95US-0569749.
PR	08-AUG-1995.	95US-0512946.
XX	(TUL- ) TULARIK INC.	
PA	Goeddel DV, Rothe M.	
XX	WPI; 1997-154209/14.	
DR	Nucleic acids encoding cellular inhibitor of apoptosis proteins	
XX	useful for apoptosis regulation in cells to reduce or increase	
PT	apoptosis and for pharmacological screening	

XX PS Claim 3; Page 23; 35pp; English.  
XX  
CC The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -  
CC AAT61590/T61591) comprise a series of defined structural domain  
CC repeats and/or a RING finger domain; in particular, at least two of  
CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat  
CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)  
CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus  
CC sequences derived from these human genes.  
CC The nucleic acid is used for recombinant protein of human cellular  
CC inhibitor of apoptosis protein which modulates apoptosis  
CC regulation. The nucleic acids are useful in therapies where  
CC increased cell-specific apoptosis is desired, e.g. in restenosis,  
CC inflammatory disease states, myocardial infarction, glomerular  
CC nephritis, transplant rejection and infectious diseases, e.g. HIV.  
CC They can also be used in conditions requiring a reduction in  
CC apoptosis.  
CC  
SQ Sequence 55 AA;  
XX  
QY Query Match 100.0%; Score 307; DB 18; Length 55;  
Best Local Similarity 100.0%; Pred. No. 1.7e-35;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 CELYRMSTYTFPAGVPVSESLARAGFYTTGVNDKVKCFCCGLMDNMKLGDS 55  
1 CELYRMSTYTFPAGVPVSESLARAGFYTTGVNDKVKCFCCGLMDNMKLGDS 55  
RESULT 2  
AAU02925  
ID AAU02925 standard; Protein; 306 AA.  
XX  
AC AAU02925;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Angiotensin converting enzyme (ACEV) splice variant protein #25.  
XX  
KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;  
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;  
KW platelet-derived endothelial cell growth factor; cardiovascular disease;  
KW cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;  
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;  
KW myocardial infarction; coronary arterial thrombosis; renal disease;  
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;  
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;  
KW nonrheumatic pulmonary granulomatous disease; endothelial abnormality;  
KW vascular disorder; asbestosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200136632-A2.  
XX  
PD 25-MAY-2001.  
XX  
PF 17-NOV-2000; 2000WO-IL00766.  
XX  
PR 17-NOV-1999; 99TL-0132978.  
XX  
PR 10-DEC-1999; 99TL-0133455.  
XX  
PA (COMP-) COMPUGEN LTD.  
XX  
PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;  
XX  
DR WPI: 2001-336004/35.  
XX  
DR N-PSDB: AAS06025.  
XX  
PT Novel alternative splicing variants e.g. variant of angiotensin  
PT converting enzyme (ACEV), useful in identifying candidate compounds  
PT capable of binding to the variant and to detect anti-variant antibodies  
PT

XX PS Claim 4; Fig 25; 51pp; English.  
XX  
CC The sequence represents an angiotensin converting enzyme splice variant  
CC (ACEV) polypeptide. The polypeptides of the invention include variants of  
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,  
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase  
CC inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal  
CC polypeptide receptor 2. The polypeptides and their associated nucleic  
CC acids are useful for identification of variant sequences and detection of  
CC candidate compounds capable of binding to the molecules. The sequences of  
CC the invention can be used in the treatment and diagnosis of various  
CC disorders including cardiovascular diseases such as arteriosclerosis,  
CC myocardial infarction and coronary arterial thrombosis, renal diseases  
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,  
CC immune disorders such as immune complex nephritis, multiple sclerosis,  
CC cancer, sarcoidosis, nonrheumatic pulmonary granulomatous diseases such  
CC as asbestosis and vascular pathologies involving an endothelial  
CC abnormality such as deep vein thrombosis.  
CC  
SQ Sequence 306 AA;  
XX  
QY Query Match 100.0%; Score 307; DB 22; Length 306;  
Best Local Similarity 100.0%; Pred. No. 1.3e-34;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 45 CELYRMSTYTFPAGVPVSESLARAGFYTTGVNDKVKCFCCGLMDNMKLGDS 99  
1 CELYRMSTYTFPAGVPVSESLARAGFYTTGVNDKVKCFCCGLMDNMKLGDS 99  
RESULT 3  
AAW19746  
ID AAW19746 standard; Protein; 618 AA.  
XX  
AC AAW19746;  
XX  
DT 16-SEP-1997 (first entry)  
XX  
DE Human inhibitor of apoptosis protein homologue M1HB.  
XX  
KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; M1HB;  
KW degenerative disease; infectious disease; autoimmune disease;  
KW cancer; therapy; diagnosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 46..113  
FT /label= BIR  
FT Region 184..250  
FT /label= BIR  
FT Region 269..337  
FT /label= BIR  
FT Region 569..606  
FT /label= RING\_finger  
XX  
PN WO9723501-A1.  
XX  
PD 03-JUL-1997.  
XX  
XX 20-DEC-1996; 96WO-AU00827.  
XX  
PF 22-DEC-1995; 95AU-0007275.  
XX  
PR (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX  
PI Vaux DL;  
XX  
DR WPI: 1997-350966/32.  
XX  
DR N-PSDB: AAT72711.  
XX  
PT Isolated protein homologues of viral inhibitors of apoptosis - used  
PT

PT to modulate apoptosis for treatment of degenerative, infectious or  
 PT autoimmune diseases and cancer  
 XX  
 PS Claim 8; Page 51-54; 136pp; English.  
 XX  
 CC Mammalian IAP homologue B (MIB) (AAW19746) is a human homologue of  
 CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid  
 CC sequence was deduced from a cDNA clone (see also AAT72711) isolated  
 CC from a human foetal liver cDNA library using primers based on  
 CC human E3T sequences that resembled the BIR repeats of Oryza  
 CC pseudotsingura polyhedrosis virus IAP. IAP homologues (see also  
 CC AAW19745 and AAW19747-52) and their derivatives and chemical analogues  
 CC can be used in methods for modulating apoptosis in animal cells,  
 CC specifically for treatment, by inhibition, of degenerative and  
 CC infectious disease or, by promotion, of cancer and autoimmune  
 CC disease.  
 XX  
 XX Sequence 618 AA:

Query Match	100.0%	Score 307	DB 18	Length 618
Best Local Similarity	100.0%	Pred. No. 3e-34		
Matches	55	Conservative	0	Mismatches 0; Indels 0; Gaps 0
QY	1	CELYMNSTYSTRPACVPVSEKSLAAGTYTTCVNDKVKCECCGLMIDNNKLTDSP	55	
Db	45	CELYMNSTYSTRPACVPVSEKSLAAGTYTTCVNDKVKCECCGLMIDNNKLTDSP	99	

[illegible]

of susceptibility to apoptotic disease

Claim 27: Page 75-77; 219pp; English.

Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2 (AA119581-86) are a new class of mammalian proteins that are inhibitors of apoptosis (IAP) and which are characterised by the presence of a ring zinc finger domain (see also AA119587) and least one BIR (baculovirus IAP repeat) domain (see also AA119588). The HIAP amino acid sequences were deduced from cDNA clones (AA17038 and AA170838) from a human liver library. IAP polypeptides can be expressed in host cells (in vitro or in vivo) and used in methods for treating diseases and disorders involving apoptosis, esp. in a human diagnosed as HIV-positive or as having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or an ischaemic injury, selected from myocardial infarction, stroke, reperfusion injury, or a toxin-induced liver disease.

Query Match	100.0%;	Score 307;	DB 18;	Length 618;
Best Local Similarity	100.0%;	Pred. No. 3e-34;		
Matches	55;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

```

Oy      1 CELYRMSTSTSTFPAGVPVSESLARAGFYTYGVNDKVKCECCGLMLDNWKLGDSP 55
         |||||
Db      45 CELYRMSTSTSTFPAGVPVSESLARAGFYTYGVNDKVKCECCGLMLDNWKLGDSP 99

```

CC	AAW13545	standard; Protein: 618 AA.
XX	AAW13545	
XX	AAW13545	
AC	AAW13545	
XX	22-JUL-1997	(first entry)
DT		
XX		
DE	Human c-IAP1.	
XX		
KW	IAP, inhibitor; apoptosis; RING finger domain; reelinosis;	
KW	myocardial infarction; nephritis; HIV.	
XX		
OS	Homo sapiens.	
XX		
PN	W09706182-A1.	
XX		
PD	20-FEB-1997.	
XX		
PF	06-AUG-1996; 96WO-US12860.	
XX		
PR	08-DEC-1995; 95US-0569749.	
PR	08-AUG-1995; 95US-0512946.	
XX		
PA	(TULA-) TULARIK INC.	
PI		
XX	Goeddel DV, Rothe M;	
XX	WPI: 1997-154209/14.	
DR	N-PSDB; AAT61590.	
XX		
PT	Nucleic acids encoding cellular inhibitor of apoptosis proteins	
PT	useful for apoptosis regulation in cells to reduce or increase	
PT	apoptosis and for pharmacological screening	
XX		
PS	Disclosure; Page 18-20; 35pp; English.	
XX		
CC	The human cellular inhibitor of apoptosis proteins (C-IAP1/2 -	
CC	AAW1590/T61591) comprise a series of defined structural domain	
CC	repeats and/or a RING finger domain; in particular, at least two of	
CC	a first domain repeat (AAW13547 or AAW13548), a second domain repeat	
CC	(AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)	
CC	and/or a RING finger domain (AAW13553 or AAW13554), or a consensus	
CC	sequences derived from these human genes.	

CC The nucleic acid is used for recombinant prodn. of human cellular  
 CC inhibitor of apoptosis protein which modulates apoptosis  
 CC regulation. The nucleic acids are useful in therapies where  
 CC increased cell-specific apoptosis is desired, e.g. in restitutions,  
 CC inflammatory disease states, myocardial infarction, glomerular  
 CC nephritis, transplant rejection and infectious diseases, e.g. HIV.  
 CC They can also be used in conditions requiring a reduction in  
 CC apoptosis.  
 CC  
 XX Sequence 618 AA;  
 SO  
 Query Match 100.0%; Score 307; DB 18; Length 618;  
 Best Local Similarity 100.0%; Pred. No. 3e-34;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSYSTFPAGVPVSRSLARAGFYTTGVNDKVKCCGGLMDNKLGDSP 55  
 DB 45 CELYRMSYSTFPAGVPVSRSLARAGFYTTGVNDKVKCCGGLMDNKLGDSP 99

## RESULT 6

AAW69296  
 ID AAW69296 standard; Protein; 618 AA.

XX AAW69296;  
 AC  
 XX  
 DT 13-NOV-1998 (first entry)  
 DE Human HIAP-2 protein.  
 XX  
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
 KW proliferative disease; IAP; therapy; cancer; human; HIAP-2 protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9835693-A2.  
 PD 20-AUG-1998.  
 XX  
 PF 13-FEB-1998; 98WO-1B00781.  
 XX  
 PR 13-FEB-1997; 97US-0800929.  
 XX  
 PA (UYOR-) UNIV OTTAWA.  
 XX  
 PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;  
 PI Tsang B;  
 XX  
 DR WPI, 1998-467164/40.  
 DR N-PSDB; AAV55040.  
 XX  
 PT Inducing apoptosis in proliferative mammalian cells with inhibitor  
 PT of IAP or NAIP polypeptide - also methods for prognosis based on  
 PT presence of IAP and NAIP, specifically applied to cancers involving  
 PT p53 mutations  
 XX  
 PS Disclosure; Flg 3; 147pp; English.

CC This sequence is the human HIAP-2 protein, which is a inhibitor of  
 CC apoptosis protein (IAP), and can be used in the method of the invention.  
 CC The method is for enhancing apoptosis in cells from a mammal with  
 CC proliferative disease by treatment with a compound that inhibits  
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
 CC compounds are used to treat proliferative diseases, specially cancers of  
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
 CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,  
 CC rectum, cervix or endometrium, particularly to increase their sensitivity  
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
 CC detected in many cancers and are associated with poor prognosis,  
 CC resistance to chemotherapeutic agents and mutations in p53 (it is  
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
 CC genes). Transgenic animals are used for testing the effects of antisense  
 CC oligonucleotides and for screening for the inhibitors.

XX  
 SO Sequence 618 AA;

Query Match 100.0%; Score 307; DB 19; Length 618;  
 Best Local Similarity 100.0%; Pred. No. 3e-34;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSYSTFPAGVPVSRSLARAGFYTTGVNDKVKCCGGLMDNKLGDSP 55  
 DB 45 CELYRMSYSTFPAGVPVSRSLARAGFYTTGVNDKVKCCGGLMDNKLGDSP 99

## RESULT 7

AA333998  
 ID AAY333998 standard; Protein; 618 AA.

XX AAY333998;  
 AC  
 XX  
 DT 26-NOV-1999 (first entry)

DE Human cellular inhibitor of apoptosis-1 sequence.

XX  
 KW Cellular inhibitor of Apoptosis-1; antisense; diagnostic; therapeutic;  
 KW c-IAP-1; prophylaxis; infection; inflammation; tumor formation.  
 XX

OS Homo sapiens.

PN US5958772-A.

PD 28-SEP-1999;

PF 03-DEC-1998; 98US-0205204.

PR 03-DEC-1998; 98US-0205204.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowsebert LM, Ackermann ET;

DR WPI: 1999-561047/47.

DR N-PSDB; AA222143.

XX  
 PT Antisense compounds complementary to Cellular inhibitor of Apoptosis-1  
 PT useful for e.g. diagnostics, therapeutics, and as research reagents -  
 XX  
 PS Example 13; Columns 41-46; 32pp; English.

CC The invention provides antisense compounds of 8-30 nucleotides that  
 CC inhibit the expression of human Cellular inhibitor of Apoptosis-1  
 CC (c-IAP-1). The antisense compounds may be used for diagnostics,  
 CC therapeutics (for modulating the expression of c-IAP-1), prophylaxis  
 CC (e.g. to prevent or delay infection, inflammation, or tumor formation),  
 CC as research reagents (e.g. to distinguish between members of a biological  
 CC pathway) and in kits. The present sequence represents the human cellular  
 CC inhibitor of apoptosis-1.  
 CC  
 XX

SO Sequence 618 AA;

Query Match 100.0%; Score 307; DB 20; Length 618;  
 Best Local Similarity 100.0%; Pred. No. 3e-34;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSYSTFPAGVPVSRSLARAGFYTTGVNDKVKCCGGLMDNKLGDSP 55  
 DB 45 CELYRMSYSTFPAGVPVSRSLARAGFYTTGVNDKVKCCGGLMDNKLGDSP 99

## RESULT 8

ABG65665  
 ID ABG65665 standard; Protein; 618 AA.

XX ABG65665;  
 AC  
 XX

DT 26-AUG-2002 (first entry)

XX Human inhibitor of apoptosis, HIAP2.

DE Human; antisense; inhibitor of apoptosis; HIAP1, HIAP2; XIAP;

KW cytostatic cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;

KW pancreatic cancer; embryonic development; viral pathogenesis;

KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;

KW lupus erythematosus; herpes virus infection; pox virus infection;

KW adenovirus infection; proliferative disease.

OS Homo sapiens.

XX WO200226968-A2.

PN 04-APR-2002.

PD 27-SEP-2001; 2001WO-CA01379.

PF 28-SEP-2000; 2000US-0672717.

PR (UYOT-) UNIV OTTAWA.

PA (AEGE-) AEGERA THERAPEUTICS INC.

XX Korneiluk RG, Lacasse E, Baird S, Holcik M, Young S;

PI WPI; 2002-479562/51.

DR N-PSDB; ABR93871.

XX Novel antisense inhibitor of apoptosis nucleic acid useful for

PT enhancing apoptosis in a cell, for treating cancer and other

PT proliferative diseases -

PS Disclosure; Fig 3; 135pp; English.

XX The invention relates to an inhibitor of apoptosis (IAP) antisense

CC nucleic acid (I) that inhibits IAP biological activity, regardless of

CC length of the antisense nucleic acid, the IAP proteins may be mouse

CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical

CC composition comprising a mammalian IAP antisense molecule and a method of

CC enhancing apoptosis in a cell, comprising administering a negative

CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP

CC antisense inhibitor is useful for enhancing apoptosis in a cell in a

CC mammal diagnosed with a proliferative disease. The method is useful for

CC treating a patient diagnosed with a proliferative disease like cancer.

CC The IAP antisense molecule is useful to treat, ameliorate, improve,

CC sustain or prevent proliferative diseases (e.g. ovarian cancer,

CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or

CC conditions where apoptosis is involved or implicated (e.g. embryonic

CC development, viral pathogenesis, autoimmune disorders, neurodegenerative

CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes

CC virus, pox virus and adenovirus). The present sequence is a human IAP

CC protein sequence.

XX

SQ Sequence 618 AA:

Query Match 100.0%; Score 307; DB 23; Length 618;

Best Local Similarity 100.0%; Pred. No. 3e-34;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CELYRMSYSTPAGVPSERSIARAGFYTGNDVKCFCCGLMDNMRKLGDS 55

DB 45 CELYRMSYSTPAGVPSERSIARAGFYTGNDVKCFCCGLMDNMRKLGDS 99

RESULT 9

AAW13548

ID AAW13548 standard; Protein; 55 AA.

XX

AC AAW13548;

XX

DT 22-JUL-1997 (first entry)

XX

DE Human c-IAP2 repeat 1.

XX IAP; inhibitor; apoptosis; RING finger domain; restinosis;

KW myocardial infarction; nephritis; HIV.

XX

OS Homo sapiens.

XX WO9706182-A1.

PN 20-FEB-1997.

PD 06-AUG-1996; 96WO-US12860.

PF 08-DEC-1995; 95US-0569749.

PR 08-AUG-1995; 95US-0512946.

XX

PA (TULA-) TULARIK INC.

XX Goeddel DV, Rothe M;

PI WPI; 1997-154209/14.

DR

XX Nucleic acids encoding cellular inhibitor of apoptosis proteins -

PT useful for apoptosis regulation in cells to reduce or increase

PT apoptosis and for pharmacological screening

PS Claim 3; Page 24; 35pp; English.

XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -

CC AAT61596/761591) comprise a series of defined structural domain

CC repeats and/or a RING finger domain; in particular, at least two of

CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat

CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)

CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus

CC sequences derived from these human genes.

CC The nucleic acid is used for recombinant prodn. of human cellular

CC inhibitor of apoptosis protein which modulates apoptosis

CC regulation. The nucleic acids are useful in therapies where

CC increased cell-specific apoptosis is desired, e.g. in restinosis,

CC inflammatory disease states, myocardial infarction, glomerular

CC nephritis, transplant rejection and infectious diseases, e.g. HIV.

CC They can also be used in conditions requiring a reduction in

CC apoptosis.

XX

SQ Sequence 55 AA:

Query Match 98.0%; Score 301; DB 18; Length 55;

Best Local Similarity 98.2%; Pred. No. 1.2e-34;

Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRMSYSTPAGVPSERSIARAGFYTGNDVKCFCCGLMDNMRKLGDS 55

DB 1 CELYRMSYSTPAGVPSERSIARAGFYTGNDVKCFCCGLMDNMRKLGDS 55

RESULT 10

AAW19747

ID AAW19747 standard; Protein; 604 AA.

XX

AC AAW19747;

XX

DT 16-SEP-1997 (first entry)

XX

DE Human inhibitor of apoptosis protein homologue MHC.

XX

KW inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MHC;

KW degenerative disease; infectious disease; autoimmune disease;

KW cancer; therapy; diagnosis.

XX

OS Homo sapiens.

XX

FT Key Location/Qualifiers

FT Region 29..97

```
FT FT /label= BIR
FT Region 169..236
FT /label= BIR
FT Region 255..323
FT /label= BIR
FT Region 556..593
FT /label= RING_finger
XX PN MO9723501-A1.
XX PD 03-JUL-1997.
XX PF 20-DEC-1996; 96WO-AU00827.
XX PR 22-DEC-1995; 95AU-0007275.
XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX PI Vaux DL;
XX DR WPI: 1997-350966/32.
XX DR N-PSDB; AAT72712.
XX PT Isolated protein homologues of viral inhibitors of apoptosis - used
XX PT to modulate apoptosis for treatment of degenerative, infectious or
XX PT autoimmune diseases and cancer
XX PS Claim 9; Page 58-62; 136pp; English.
XX CC Mammalian IAP homologue C (MIHC) (AAW19747) is a human homologue of
XX CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid
XX CC sequence was deduced from a cDNA clone (see also AAT72712) isolated
XX CC from a human foetal liver cDNA library using primers based on
XX CC human E3F sequences that resembled the BIR repeats of Oryza
XX CC pseudotsugata polynucleotide virus IAP. IAP homologues (see also
XX CC AAW19743-46 and AAW19748-52) and their derivatives and chemical
XX CC analogues can be used in methods for modulating apoptosis in animal
XX CC cells, specifically for treatment, by inhibition, of degenerative
XX CC and infectious disease or, by promotion, of cancer and autoimmune
XX CC disease.
XX SQ Sequence 604 AA;
SQ Query Match 98.0%; Score 301; DB 18; Length 604;
Best Local Similarity 98.2%; Pred. No. 2e-33;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTYGVNDKVKCCCGIMLDNMKLGDS 55
DB 28 CELYRMSTYSTFPAGVPSERSLARAGFYTYGVNDKVKCCCGIMLDNMKRGDSP 82
RESULT 11
AAW19582
ID AAW19582 standard; Protein; 604 AA.
XX AC AAW19582;
XX DT 02-SEP-1997 (first entry)
XX DE Human apoptosis inhibitor HIAP-1.
XX DE Apoptosis inhibitor; HIAP-1; HIV; AIDS; neurodegeneration;
XX DE myelodysplastic syndrome; ischaemia; myocardial infarction; stroke;
XX DE reperfusion injury; toxin-induced liver disease; gene therapy;
XX KM diagnosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Domain 29..96
FT /label= BIR-1
FT Domain 169..235
```

```
FT FT /label= BIR-2
FT Domain 255..322
FT /label= BIR-3
FT Domain 546..591
FT /label= RING_finger
XX PN MO9706255-A2.
XX PD 20-FEB-1997.
XX PF 05-AUG-1996; 96WO-IB01022.
XX PR 22-DEC-1995; 95US-0576956.
XX PR 04-AUG-1995; 95US-0511485.
XX PA (UYOT-) UNIV OTTAWA.
XX PI Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX DR WPI: 1997-154262/14.
XX DR N-PSDB; AAT70837.
XX PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
XX PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
XX PT of susceptibility to apoptotic disease
XX PS Claim 27; Page 72-74; 219pp; English.
XX CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
XX CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
XX CC are inhibitors of apoptosis (IAP) and which are characterised by
XX CC the presence of a ring zinc finger domain (see also AAW19587) and at
XX CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
XX CC The HIAP amino acid sequences were deduced from cDNA clones (AAT70837
XX CC and AAT70838) from a human liver library. IAP polypeptides can be
XX CC expressed in host cells (in vitro or in vivo) and used in methods
XX CC for treating diseases and disorders involving apoptosis, esp. in a
XX CC human diagnosed as HIV-positive or as having AIDS, a
XX CC neurodegenerative disease, a myelodysplastic syndrome or an
XX CC ischemic injury, selected from myocardial infarction, stroke,
XX CC reperfusion injury, or a toxin-induced liver disease.
XX SQ Sequence 604 AA;
SQ Query Match 98.0%; Score 301; DB 18; Length 604;
Best Local Similarity 98.2%; Pred. No. 2e-33;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTYGVNDKVKCCCGIMLDNMKLGDS 55
DB 28 CELYRMSTYSTFPAGVPSERSLARAGFYTYGVNDKVKCCCGIMLDNMKRGDSP 82
RESULT 12
AAW13546
ID AAW13546 standard; Protein; 604 AA.
XX AC AAW13546;
XX DT 22-JUL-1997 (first entry)
XX DE Human c-IAP2.
XX DE IAP; inhibitor; apoptosis; RING finger domain; restinosis;
XX DE myocardial infarction; nephritis; HIV.
XX OS Homo sapiens.
XX PN MO9706182-A1.
XX PD 20-FEB-1997.
XX PR 06-AUG-1996; 96WO-US12860.
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XX 08-DEC-1995; 95US-0569749.
PR 08-AUG-1995; 95US-0512946.
XX
XX (TULA-) TULARIK INC.
XX
XX Goeddel DV, Rothe M.
XX
XX WPI; 1997-154209/14.
DR N-PSDB; AAT61591.
XX
XX Nucleic acids encoding cellular inhibitor of apoptosis proteins
XX useful for apoptosis regulation in cells to reduce or increase
XX apoptosis and for pharmacological screening
XX
XX
XX Disclosure: Page 21-23; 35pp; English.
XX
XX The human cellular inhibitor of apoptosis proteins (C-IAP1/2 -
XX AAG1590/761591) comprise a series of defined structural domain
XX repeats and/or a RING finger domain; in particular, at least two of
XX a first domain repeat (AAW13547 or AAW13548), a second domain repeat
XX (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
XX and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
XX sequences derived from these human genes.
XX The nucleic acid is used for recombinant prodn. of human cellular
XX inhibitor of apoptosis protein which modulates apoptosis
XX regulation. The nucleic acids are useful in therapies where
XX increased cell-specific apoptosis is desired, e.g. in restitosis,
XX inflammatory disease states, myocardial infarction, glomerular
XX nephritis, transplant rejection and infectious diseases, e.g. HIV.
XX They can also be used in conditions requiring a reduction in
XX apoptosis.
XX
XX Sequence 604 AA:
XX
XX Query Match 98.0%; Score 301; DB 16; Length 604;
XX Best Local Similarity 98.2%; Pred. No. 2e-33;
XX Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 CELYRMSTYSTRPAGVPVSESLARAGFYTGVDKVCFCGGLMDWKKLGDSP 55
XX |||||
XX 28 CELYRMSTYSTRPAGVPVSESLARAGFYTGVDKVCFCGGLMDWKKRGDSP 82
XX
XX RESULT 13
XX AAW69295
XX ID AAW69295 standard; Protein; 604 AA.
XX
XX AAW69295;
XX
XX 13-NOV-1998 (first entry)
XX
XX Human HIAP-1 protein.
XX
XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
XX proliferative disease; IAP; therapy; cancer; human; HIAP-1 protein.
XX
XX Homo sapiens.
XX
XX WO9835693-A2.
XX
XX 20-AUG-1998.
XX
XX 13-FEB-1998; 98WO-IB00781.
XX
XX 13-FEB-1997; 97US-0800929.
XX
XX (UYOT-) UNIV OTTAWA.
XX
XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
XX Tsang B;
XX WPI; 1998-467164/40.
XX

```

```

DR N-PSDB; AAV55039.
XX
XX Inducing apoptosis in proliferative mammalian cells with inhibitor
XX of IAP or NAIP polypeptide - also methods for prognosis based on
XX presence of IAP and NAIP, specifically applied to cancers involving
XX p53 mutations
XX
XX Disclosure: Fig 2; 147pp; English.
XX
XX This sequence is the human HIAP-1 protein, which is a inhibitor of
XX apoptosis protein (IAP), and can be used in the method of the invention.
XX The method is for enhancing apoptosis in cells from a mammal with
XX proliferative disease by treatment with a compound that inhibits
XX biological activity of an IAP or NAIP polypeptide. The inhibitory
XX compounds are used to treat proliferative diseases, specially cancers of
XX ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
XX liver nasopharynx, thyroid, central nervous system, prostate, colon,
XX rectum, cervix or endometrium, particularly to increase their sensitivity
XX to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
XX detected in many cancers and are associated with poor prognosis,
XX resistance to chemotherapeutic agents and mutations in p53 (it is
XX suggested that wild-type p53 suppresses transcription of the IAP or NAIP
XX genes). Transgenic animals are used for testing the effects of antisense
XX oligonucleotides and for screening for the inhibitors.
XX
XX Sequence 604 AA:
XX
XX Query Match 98.0%; Score 301; DB 19; Length 604;
XX Best Local Similarity 98.2%; Pred. No. 2e-33;
XX Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 CELYRMSTYSTRPAGVPVSESLARAGFYTGVDKVCFCGGLMDWKKLGDSP 55
XX |||||
XX 28 CELYRMSTYSTRPAGVPVSESLARAGFYTGVDKVCFCGGLMDWKKRGDSP 82
XX
XX RESULT 14
XX AAV52703
XX ID AAV52703 standard; Protein; 604 AA.
XX
XX AAV52703;
XX
XX 26-JAN-2000 (first entry)
XX
XX Human cellular inhibitor of apoptosis-2 protein.
XX
XX Identification; genetic target; gene modulation; human;
XX antisense oligonucleotide; phosphorothioate; target validation;
XX nucleotide sequence-based technology; antisense drug discovery.
XX
XX Homo sapiens.
XX
XX WO9953101-A1.
XX
XX 21-OCT-1999.
XX
XX 13-APR-1999; 99WO-US08268.
XX
XX 13-APR-1998; 98US-0081483.
XX
XX 28-APR-1998; 98US-0067638.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowseart LM, Baker BF, McNeil J, Freiler SM, Sasmor HM, Brooks DG;
XX Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
XX WPI; 1999-620446/53.
XX
XX N-PSDB; AA241005.
XX
XX Identifying compounds which modulate expression of nucleic acids, used
XX to provide compounds having defined physical, chemical or bioactive
XX properties, e.g. antisense activity
XX

```

PS Example 20; Page 197-202; 264pp; English.  
 CC A method has been developed of defining a set of compounds that modulate  
 CC the expression of a target nucleic acid (tNA) sequence via binding of  
 CC the compounds with the tNA sequence. The method comprises generating a  
 CC library of virtual compounds in silico according to defined criteria,  
 CC and evaluating in silico the binding of the virtual compounds with the  
 CC tNA according to defined criteria. Also described are: (1) a method of  
 CC defining a set of oligonucleotides (ONS) that modulate the expression of  
 CC a tNA sequence via binding of the ONS with the tNA sequence comprising:  
 CC generating a library of virtual compounds in silico according to defined  
 CC criteria, and evaluating in silico the binding of the virtual ONS with  
 CC the tNA according to defined criteria; and (2) a method of defining a  
 CC set of compounds that modulate the expression of a tNA sequence via  
 CC binding of the compounds with the tNA. The methods can be used for the  
 CC generation and identification of synthetic compounds having defined  
 CC physical, chemical or bioactive properties. Information gathered from  
 CC assays of such compounds is used to identify nucleic acid sequences that  
 CC are tractable to a variety of nucleotide sequence-based technologies,  
 CC e.g. antisense drug discovery and target validation. AA240852 to  
 CC AA241220, and AAY52701 to AAY52706, represent sequences used in the  
 CC exemplification of the present invention.

SQ Sequence 604 AA;

Query Match 98.0%; Score 301; DB 20; Length 604;  
 Best Local Similarity 98.2%; Pred. No. 2e-33; 1; Indels 0; Gaps 0;  
 Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNWKRGDSP 55  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 28 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNWKRGDSP 82

RESULT 15  
 AAY33997

ID AAY33997 standard; Protein; 604 AA.

AC AAY33997;

DT 26-NOV-1999 (first entry)

DE Human cellular inhibitor of apoptosis-2 sequence.

KM Cellular inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;  
 KM c-IAP-2; prophylaxis; infection; inflammation; tumor formation.

OS Homo sapiens.

PN US5958771-A.

PD 28-SEP-1999.

PF 03-DEC-1998; 98US-0205144.

PR 03-DEC-1998; 98US-0205144.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowsett LM, Ackermann EJ;

DR WPI; 1999-561046/47.

DR N-PSDB; AA222096.

PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2  
 useful for e.g. diagnostics, therapeutics, and as research reagents -

PS Example 13; Columns 45-50; 33pp; English.

CC The invention provides antisense compounds of 8-30 nucleotides that  
 CC inhibit the expression of human Cellular Inhibitor of Apoptosis-2  
 CC (c-IAP-2). The antisense compounds may be used for diagnostics,  
 CC therapeutics (for modulating the expression of c-IAP-2), prophylaxis

CC (e.g. to prevent or delay infection, inflammation, or tumor formation),  
 CC as research reagents (e.g. to distinguish between members of a biological  
 CC pathway) and in kits. The present sequence represents the human cellular  
 CC inhibitor of apoptosis-2.

SQ Sequence 604 AA;

Query Match 98.0%; Score 301; DB 20; Length 604;  
 Best Local Similarity 98.2%; Pred. No. 2e-33; 1; Indels 0; Gaps 0;  
 Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNWKRGDSP 55  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 28 CELYRMSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNWKRGDSP 82

Search completed: May 5, 2003, 16:01:58  
 Job time : 11.8353 secs



GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:02:07 ; Search time 6.77995 Seconds.

(without alignments)  
699.970 Million cell updates/sec

Title: US-08-569-749-5

Perfect score: 307  
Sequence: 1 CELRMSYSTPAGVPSERSLARAGFYTGVDNKKVCCGGLMDNKKLADSP 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PTI\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/PCURS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	306	10	US-09-778-927A-62
2	307	100.0	618	9	US-09-201-936-8
3	307	100.0	618	10	US-09-974-582-8
4	301	98.0	604	9	US-09-201-936-6
5	301	98.0	604	10	US-09-974-582-6
6	298	97.1	68	9	US-09-201-936-19
7	292	95.1	68	9	US-09-201-936-18
8	291	94.8	591	9	US-09-201-936-42
9	291	94.8	612	10	US-09-974-582-14
10	284	92.5	600	10	US-09-974-582-12
11	284	92.5	602	9	US-09-201-936-40
12	159	51.8	68	9	US-09-965-967-17
13	159	51.8	110	9	US-09-965-967-22
14	159	51.8	497	10	US-09-201-936-4
15	159	51.8	497	10	US-09-974-582-4
16	153	49.8	68	9	US-09-201-936-16
17	153	49.8	496	9	US-09-201-936-10
18	153	49.8	496	10	US-09-974-592-10
19	150	48.9	438	1	US-08-464-588-2

20	139	45.3	110	9	US-09-965-967-21	Sequence 21, Appl
21	138	45.0	68	9	US-09-201-936-27	Sequence 27, Appl
22	133	43.3	68	9	US-09-201-936-26	Sequence 26, Appl
23	132	43.0	68	9	US-09-201-936-28	Sequence 28, Appl
24	132	43.0	68	9	US-10-041-859-18	Sequence 18, Appl
25	132	43.0	172	9	US-10-041-859-12	Sequence 12, Appl
26	130	42.3	68	9	US-09-201-936-21	Sequence 21, Appl
27	128	41.7	68	9	US-09-201-936-20	Sequence 20, Appl
28	127	41.4	68	9	US-10-041-859-19	Sequence 19, Appl
29	127	41.4	109	9	US-09-965-967-30	Sequence 30, Appl
30	127	41.4	172	9	US-10-041-859-13	Sequence 13, Appl
31	125	40.7	1403	8	US-08-913-322-22	Sequence 22, Appl
32	125	40.7	1403	8	US-08-913-322-24	Sequence 24, Appl
33	120.5	39.3	67	9	US-09-201-936-22	Sequence 22, Appl
34	115	37.5	68	9	US-10-041-859-14	Sequence 14, Appl
35	115	37.5	172	9	US-10-041-859-8	Sequence 8, Appl
36	115	37.5	346	9	US-10-041-859-2	Sequence 2, Appl
37	114.5	37.3	67	9	US-09-201-936-23	Sequence 23, Appl
38	111	36.2	66	9	US-09-201-936-24	Sequence 24, Appl
39	111	36.2	66	9	US-09-201-936-25	Sequence 25, Appl
40	111	36.2	107	9	US-09-965-967-20	Sequence 20, Appl
41	111	36.2	278	9	US-09-964-899-39	Sequence 39, Appl
42	108.5	35.3	109	9	US-09-965-967-19	Sequence 19, Appl
43	107	34.9	68	9	US-10-041-859-16	Sequence 16, Appl
44	107	34.9	172	9	US-10-041-859-10	Sequence 10, Appl
45	106	34.5	68	9	US-10-041-859-15	Sequence 15, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-778-927A-62
; Sequence 62, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Ram et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; FILE REFERENCE: 2786-0160P
; CURRENT FILING DATE: 2001-02-08
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)-(306)
; OTHER INFORMATION: Xaa - any amino acid, unknown, or other
US-09-778-927A-62
Query Match          100.0%; Score 307; DB 10; Length 306;
Best Local Similarity 100.0%; Pred. No. 2.8e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CELRMSYSTPAGVPSERSLARAGFYTGVDNKKVCCGGLMDNKKLADSP 55
DB 45 CELRMSYSTPAGVPSERSLARAGFYTGVDNKKVCCGGLMDNKKLADSP 99
RESULT 2
US-09-201-936-8
; Sequence 8, Application US/09201936
; PUBLIC INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
```

```

: APPLICANT: Mackenzie, Alexander E.
: APPLICANT: Liston, Stephen
: TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
: FILE REFERENCE: 07891/003003
: CURRENT FILING DATE: 1998-12-01
: EARLIER APPLICATION NUMBER: 09/011,356
: EARLIER FILING DATE: 1998-02-04
: EARLIER APPLICATION NUMBER: PCT/IB96/01022
: EARLIER FILING DATE: 1996-08-05
: EARLIER APPLICATION NUMBER: 08/576,956
: EARLIER FILING DATE: 1995-12-22
: EARLIER APPLICATION NUMBER: 08/511,485
: EARLIER FILING DATE: 1995-08-04
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 8
: LENGTH: 618
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-201-936-8

Query Match
Best Local Similarity 100.0%; Score 307; DB 9; Length 618;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCCCGMLDNWKLGDSP 55
Db 45 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCCCGMLDNWKLGDSP 99
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RESULT 3
US-09-974-592-8
: Sequence 8, Application US/09974592
: Patent No. US20020120121A1
: GENERAL INFORMATION:
: APPLICANT: Korneluk, Robert G
: APPLICANT: Mackenzie, Alexander E
: APPLICANT: Liston, Peter
: APPLICANT: Baird, Stephen
: APPLICANT: Tsang, Benjamin K
: APPLICANT: Pratt, Christine
: TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
: TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
: TITLE OF INVENTION: DISEASE
: FILE REFERENCE: 07891/009004
: CURRENT APPLICATION NUMBER: US/09/974,592
: CURRENT FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: US 09/617,053
: PRIOR FILING DATE: 2000-07-14
: PRIOR APPLICATION NUMBER: US 08/800,929
: PRIOR FILING DATE: 1997-02-13
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 618
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-974-592-8
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OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCCCGMLDNWKLGDSP 55
Db 45 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCCCGMLDNWKLGDSP 99
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RESULT 4
US-09-201-936-6
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: Sequence 6, Application US/09201936
: Publication No. US20020187946A1
: GENERAL INFORMATION:
: APPLICANT: Korneluk, Robert G.
: APPLICANT: Mackenzie, Alexander E.
: APPLICANT: Baird, Stephen
: APPLICANT: Liston, Peter
: TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
: FILE REFERENCE: 07891/003003
: CURRENT APPLICATION NUMBER: US/09/201,936
: CURRENT FILING DATE: 1998-12-01
: EARLIER APPLICATION NUMBER: 09/011,356
: EARLIER FILING DATE: 1998-02-04
: EARLIER APPLICATION NUMBER: PCT/IB96/01022
: EARLIER FILING DATE: 1996-08-05
: EARLIER APPLICATION NUMBER: 08/576,956
: EARLIER FILING DATE: 1995-12-22
: EARLIER APPLICATION NUMBER: 08/511,485
: EARLIER FILING DATE: 1995-08-04
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 6
: LENGTH: 604
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-201-936-6

Query Match
Best Local Similarity 98.2%; Score 301; DB 9; Length 604;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCCCGMLDNWKLGDSP 55
Db 28 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCCCGMLDNWKLGDSP 82
```

```

RESULT 5
US-09-974-592-6
: Sequence 6, Application US/09974592
: Patent No. US20020120121A1
: GENERAL INFORMATION:
: APPLICANT: Korneluk, Robert G
: APPLICANT: Mackenzie, Alexander E
: APPLICANT: Liston, Peter
: APPLICANT: Baird, Stephen
: APPLICANT: Tsang, Benjamin K
: APPLICANT: Pratt, Christine
: TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
: TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
: TITLE OF INVENTION: DISEASE
: FILE REFERENCE: 07891/009004
: CURRENT APPLICATION NUMBER: US/09/974,592
: CURRENT FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: US 09/617,053
: PRIOR FILING DATE: 2000-07-14
: PRIOR APPLICATION NUMBER: US 08/800,929
: PRIOR FILING DATE: 1997-02-13
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 604
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-974-592-6
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OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCCCGMLDNWKLGDSP 55
Db 28 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCCCGMLDNWKLGDSP 82
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RESULT 6
US-09-201-936-19
; Sequence 19, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/1B96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-19

Query Match          97.1%; Score 298; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 8.2e-13;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  ELRYMSTYSTPAGVPSERSLARAGFYTTGVNDKVCFCGGLMDNKRIGDSP 55
Db      1  ELRYMSTYSTPAGVPSERSLARAGFYTTGVNDKVCFCGGLMDNKRIGDSP 54

RESULT 7
US-09-201-936-18
; Sequence 18, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/1B96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-18

Query Match          95.1%; Score 292; DB 9; Length 68;
Best Local Similarity 98.1%; Pred. No. 5.2e-32;
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Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  ELRYMSTYSTPAGVPSERSLARAGFYTTGVNDKVCFCGGLMDNKRIGDSP 55
Db      1  ELRYMSTYSTPAGVPSERSLARAGFYTTGVNDKVCFCGGLMDNKRIGDSP 54

RESULT 8
US-09-201-936-42
; Sequence 42, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/1B96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-42

Query Match          94.8%; Score 291; DB 9; Length 591;
Best Local Similarity 94.5%; Pred. No. 8.3e-31;
Matches 52; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  CELRYMSTYSTPAGVPSERSLARAGFYTTGVNDKVCFCGGLMDNKRIGDSP 55
Db      24  CELRYMSTYSTPAGVPSERSLARAGFYTTGVNDKVCFCGGLMDNKRIGDSP 78

RESULT 9
US-09-974-592-14
; Sequence 14, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K.
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; EARLIER FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Mus musculus
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US-09-974-592-14

Query Match 94.8%; Score 291; DB 10; Length 612;  
Best Local Similarity 94.5%; Pred. No. 8,7e-31;  
Matches 52; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CELYRMSTYTFPAGVPSERSLARAGFYTTGVNDKVCFCGGLMDNMKLGSP 55  
DB 45 CELYRMSTYTFPAGVPSERSLARAGFYTTGVNDKVCFCGGLMDNMKLGSP 99

RESULT 10  
US-09-974-592-12  
Sequence 12, Application US/09974592  
Patent No. US20020120121A1

GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K.  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 07891/009004  
CURRENT APPLICATION NUMBER: US/09/974,592  
CURRENT FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: US 09/617,053  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 600  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-974-592-12

Query Match 92.5%; Score 284; DB 10; Length 600;  
Best Local Similarity 90.9%; Pred. No. 7,4e-30;  
Matches 50; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CELYRMSTYTFPAGVPSERSLARAGFYTTGVNDKVCFCGGLMDNMKLGSP 55  
DB 26 CELYRMSTYTFPAGVPSERSLARAGFYTTGVNDKVCFCGGLMDNMKLGSP 80

RESULT 11  
US-09-201-936-40  
Sequence 40, Application US/09201936  
Patent No. US20020187946A1

GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
APPLICANT: Liston, Peter  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
TITLE OF INVENTION: PROBES AND DETECTION METHODS  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
CURRENT FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 40  
LENGTH: 602  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-201-936-40

Query Match 92.5%; Score 284; DB 9; Length 602;  
Best Local Similarity 90.9%; Pred. No. 7,4e-30;  
Matches 50; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CELYRMSTYTFPAGVPSERSLARAGFYTTGVNDKVCFCGGLMDNMKLGSP 55  
DB 28 CELYRMSTYTFPAGVPSERSLARAGFYTTGVNDKVCFCGGLMDNMKLGSP 82

RESULT 12  
US-09-201-936-17  
Sequence 17, Application US/09201936  
Patent No. US20020187946A1

GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
TITLE OF INVENTION: PROBES AND DETECTION METHODS  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
CURRENT FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 17  
LENGTH: 68  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-201-936-17

Query Match 51.8%; Score 159; DB 9; Length 68;  
Best Local Similarity 52.8%; Pred. No. 3,8e-14;  
Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

OY 2 ELYRMSTYTFPAGVPSERSLARAGFYTTGVNDKVCFCGGLMDNMKLGDS 54  
DB 1 EFNRLTFANFPSPGSPVSTLARAGFYTTGEBDYTRCFSCAAVVRKQXGDS 53

RESULT 13  
US-09-965-967-22  
Sequence 22, Application US/09965967  
Patent No. US20020177557A1

GENERAL INFORMATION:  
APPLICANT: Shi, Yigong  
TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis  
FILE REFERENCE: PU-0031 (01-1739-1)  
CURRENT APPLICATION NUMBER: US/09/965,967  
CURRENT FILING DATE: 2001-09-28  
PRIOR APPLICATION NUMBER: 60/236,574  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/256,830  
PRIOR FILING DATE: 2000-12-20  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 110  
TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-965-967-22

Query Match
Best Local Similarity 51.8%; Score 159; DB 3; Length 110;
Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 2 ELYRMSTYTFPGVPSERSLARAGFYTGVDKVCFCGGLMDNMKLGDS 54
DB 16 EFNRLKTFANFPGSPVSASTLARAGFLYTGEGDTCFSCHAADVDMQYGDS 68

RESULT 14
US-09-201-936-4
; Sequence 4, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneiluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-201-936-4

Query Match
Best Local Similarity 51.8%; Score 159; DB 9; Length 497;
Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 2 ELYRMSTYTFPGVPSERSLARAGFYTGVDKVCFCGGLMDNMKLGDS 54
DB 26 EFNRLKTFANFPGSPVSASTLARAGFLYTGEGDTCFSCHAADVDMQYGDS 78

RESULT 15
US-09-974-592-4
; Sequence 4, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneiluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K.
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-974-592-4

Query Match
Best Local Similarity 51.8%; Score 159; DB 10; Length 497;
Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 2 ELYRMSTYTFPGVPSERSLARAGFYTGVDKVCFCGGLMDNMKLGDS 54
DB 26 EFNRLKTFANFPGSPVSASTLARAGFLYTGEGDTCFSCHAADVDMQYGDS 78

Search completed: May 5, 2003, 16:11:04
Job time : 7.7795 secs
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GenCore version 5.1.4\_P5\_4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003; 15:58:42 ; Search time 6.01959 Seconds

(without alignments)  
878.365 Million cell updates/sec

Title: US-08-569-749-5

Sequence: 1 CELYRMSTYSTFPAGVPVSE.....KVCFCGGLMDNWKLGDSP 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	618	2	S68450 apoptosis inhibito
2	301	98.0	604	2	S68449 apoptosis inhibito
3	159	51.8	497	2	S69544 apoptosis inhibito
4	140	45.6	358	2	JC5964 apoptosis inhibito
5	132	43.0	268	2	T10304 inhibitor of apopt
6	132	43.0	268	2	A53989 apoptosis-inhibiti
7	125	40.7	1232	2	A55478 neuronal apoptosis
8	122	39.7	1447	2	T42628 neuronal apoptosis
9	119	38.8	208	2	T03183 probable apoptosis
10	117	38.1	298	2	JC7568 kidney inhibitor o
11	103.5	33.7	275	2	A45679 inhibitor-of-apopt
12	103	33.6	150	2	T28409 ORF MSV248 probabl
13	102	33.2	496	2	S68452 apoptosis inhibito
14	102	33.2	497	2	S69545 apoptosis inhibito
15	93	30.3	275	2	T10310 apoptosis-inhibiti
16	86.5	28.2	292	2	T41772 - Bomby
17	83.5	27.2	155	2	D36828 orf13 protein - Au
18	82	26.7	155	2	T30489 apoptosis inhibito
19	72.5	23.6	997	2	T43523 cut17 protein - fi
20	71.5	23.3	4845	2	T31067 BIR repeat contain
21	65.5	21.3	234	2	T30427 probable apoptosis
22	61	19.9	329	2	T28407 ORF MSV242 probabl
23	60	19.5	1401	2	T17452 Werner syndrome pr
24	60	19.5	1401	2	T30247 Werner syndrome pr
25	59.5	19.4	337	2	T27615 hypothetical prote
26	59	19.2	733	2	T04070 hypothetical prote
27	58	18.9	733	2	B72272 ion-sulfur cluste
28	57.5	18.7	616	2	A55796 ecarin precursor -
29	57	18.6	187	2	B98183 3-methyl-adenine D

30	57	18.6	187	2	F86029 3-methyladenine DN
31	57	18.6	707	2	T40070 origin recognition
32	57	18.6	1930	2	F86200 protein f12k11.17
33	56.5	18.4	433	2	AG1044 anaerobic C4-dicar
34	56	18.2	249	2	H72858 apoptosis inhibito
35	55.5	18.1	506	2	G90430 conserved hypothet
36	55	17.9	249	2	T41814 IAP2 orf17 - Bomby
37	55	17.9	422	2	G90259 hypothetical prote
38	55	17.9	422	2	H90271 hypothetical prote
39	55	17.9	422	2	H90275 hypothetical prote
40	55	17.9	422	2	H90501 hypothetical prote
41	55	17.9	422	2	B90327 hypothetical prote
42	55	17.9	932	2	H86325 hypothetical prote
43	55	17.9	1435	2	T01075 polypeptide - hepa
44	54.5	17.8	155	2	T37471 apoptosis inhibito
45	54.5	17.8	410	2	T49266 hypothetical prote

#### ALIGNMENTS

##### RESULT 1

S68450 apoptosis inhibitor hlap-2 - human

C:Species: Homo sapiens (man)

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 21-Jul-2000

C:Accession: S68450

R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha

Nature 379, 349-353, 1996

A:Title: Suppression of apoptosis in mammalian cells by NARP and a related family of

A:Reference number: A58182; MUID:96149249; PMID:8552191

A:Accession: S68450

A:Molecule type: mRNA

A:Status: nucleic acid sequence not shown

A:Residues: 1-618 <LIS>

A:Cross-references: EMBL:U45879; NID:G1184317; PIDN:AC50372.1; PID:G1184318

C:Function:

A:Description: apoptotic suppressor

C:Superfamily: RING finger homology

C:Keywords: apoptosis; zinc finger

F:567-611/Domain: RING finger homology <RNG>

Query Match	Score	307	DB 2	Length	618
Best Local Similarity	100.0%				
Matches	55	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0

##### RESULT 2

S68449 apoptosis inhibitor hlap-1 - human

C:Species: Homo sapiens (man)

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 21-Jul-2000

C:Accession: S68449

R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha

Nature 379, 349-353, 1996

A:Title: Suppression of apoptosis in mammalian cells by NARP and a related family of

A:Reference number: A58182; MUID:96149249; PMID:8552191

A:Accession: S68449

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-604 <LIS>

A:Cross-references: EMBL:U45878; NID:G1184315; PIDN:AC50371.1; PID:G1184316

C:Function:

A:Description: apoptotic suppressor

C:Superfamily: RING finger homology

C:Keywords: apoptosis; zinc finger

F:553-597/Domain: RING finger homology <RNG>

Query Match 98.0%, Score 301, DB 2, Length 604;



```

A:Cross-references: GB:U19251
C:Genetics:
A:Gene: GDB:SMA#; SMA
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A:Map position: 5q12.2-5q13
C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
E:94-110/Domain: transmembrane #status predicted <TM1>
F:470-477/Region: nucleotide-binding motif A (P-loop)
F:479-486/Domain: transmembrane #status predicted <TM2>
F:476/Binding site: ATP (Lys) #status predicted
F:618,652,823,923,1035/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match          40.7%; Score 125; DB 2; Length 1232;
Best Local Similarity 40.7%; Pred. No. 1e-07;
Matches 22; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Oy      2  ELYRSTSTSPAGVPVSESRSLARAGFYTYGVNDKVKFCFCGLMDNNKRLDSP 55
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      278  EELRSTSRKDPRESAVGAALAKAGLEFYTGIKLDIVQCFSGCGCLEKRWQEDDP 331

```

RESULT 8  
T42628  
neuronal apoptosis inhibitory protein 2 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000  
C:Accession: T42628  
R:Yaraghi, Z.; Diez, E.; Gros, P.; Mackenzie, A.  
Mamm. Genome 10, 761-763, 1999  
A:Title: CDNA cloning and the 5'genomic organization of Naip2, a candidate gene for mur2a  
A:Reference number: Z22179; M0UD:99315342; PMID:10384056  
A:Accession: T42628  
A:Status: preliminary; translated from GB/EMBL/DBJr  
A:Molecule type: mRNA  
A:Residues: 1-1447 <YAR>  
C:Cross-references: EMBL:AF102871; NID:g3860228; P:ID:g3860229; PIDN:AAC73002.1  
C:Genetics:  
A:Gene: Naip2

	Query Match	39.7%	Score 122;	DB 2;	Length 1447;
	Best Local Similarity	40.7%;	Pred. No. 2.9e-07;		
Matches	22: Conservative	10;	Mismatches	22;	Indels 0; Gaps 0.
Oy	2	ELYKRSSTVTPAGCVPVSESLARAGFYITTCGVNDKYKCCGCGGLMDNKKLGSP	55		
Db	278	ELRLDRTDKDWHEPSPGALEALVKYKGLFYTCTGRDRIIVQCSGGCKEAKNEGNP	331		

RESULT 9  
T03183  
Probable apoptosis inhibitor - Chilo iridescent virus  
C:Species: Chilo iridescent virus  
C:Date: 24-Mar-1999 #sequence:revision 24-Mar-1999 #text-change 02-Sep-2000  
C:Accession: T03183  
R:Bahr, U.; Tildona, C.A.; Darai, G.  
Virus Genes 15, 235-245, 1997  
A:Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101  
A:Reference number: Z14834; M01D:96141693; PMID:9482585  
A:Accession: T03183  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: DNA  
A:Residues: 1-208 <BAH>  
A:Cross-references: EMBL:AF005334; NID:g2738385; PIDN:AA894461.1; PID:g2738454  
C:Superfamily: RING finger homology  
C:Superfamily: RING finger homology <RRN>  
C:159-202/Domain: RING finger homology

[illegible]

RESULT 10  
JC7568  
Kidney inhibitor of apoptosis protein - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001  
C:Accession: JC7568  
R:Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.  
Biochem. Biophys. Res. Commun. 279, 820-831, 2000  
A>Title: KIAp, a novel member of the inhibitor of apoptosis protein family.  
A:Reference number: JC7568; MUID: 21092523; PMID:11162435  
A:Contents: Fetal kidney  
A:Accession: JC7568  
A:Molecule type: mRNA  
A:Residues: 1-298 <LIN>  
C:Comment: This protein, a new member of the inhibitor of apoptosis protein family, p

C:Genetics:  
A:Gene: kiap  
A:Map position: 20q13.3  
C:Keywords: apoptosis

Query Match 38.1%; Score 117; DB 2; Length 298;  
 Best Local Similarity 42.6%; Pred. No. 1.8e-07;  
 Matches 23; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

RESULT 11  
A45679  
inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV  
C:Species: Cydia pomonella granulosis virus CpGV  
C:Date: 21-Sep-1993 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000  
C:Accession: A45679  
R:Crook, N.E.; Clem, R.J.; Miller, L.K.  
J. Virol. 67, 2168-2174, 1993  
A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.  
A:Reference number: A45679; MIMD:93188168; PMID:8445726  
A:Accession: A45679  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-275 <CRO>  
A:Cross-references: GB:J05494; NID:q289583; PIDD:AAA3835.1; PID: q289584  
A:Note: Sequence extracted from NCBI backbone (NCBIN:127014, NCBIPI:127015)  
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match	33.7%	Score	103.5	DB 2	Length	275
Best Local Similarity	35.2%	Pred. NO.	1.4e-05			
Matches	19	Conservative	14	Mismatches	20	Indels
						Gaps
QY	2	EYRNRSTSTPAGVPSERSRLARGFYITGNDKVCRCGCLMDNKKLDSF	55			
DB	7	EVRNTEKRWVSF-LSPETAKNGFYITGLGSDERCAFCVCEIWMRKEGGDP	59			

```

RESULT 12
T28409
ORF MSV48 probable inhibitor of apoptosis protein (IAP) - Melanoplus sangulipes ent
C:Species: Melanoplus sangulipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T28409
R:Alfonso, C.L.; Tullman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sangulipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612; PMID:9847359
A:Accession: T28409
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-150 <AFO>

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GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:51:32 ; Search time 2.28111 Seconds

(without alignments)  
1000.040 Million cell updates/sec

Title: US-08-569-749-5

Perfect score: 307  
Sequence: 1 CEIXRMSYTFPAGVSE.....KYACFCGLMDMKLGDSP 55

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	618	BIR3_HUMAN	Q13490 homo sapien
2	301	98.0	604	BIR2_HUMAN	Q13489 homo sapien
3	291	94.8	612	BIR3_MOUSE	Q62210 mus musculu
4	284	92.5	600	BIR2_MOUSE	Q08863 mus musculu
5	247	80.5	611	BIR_CHICK	Q90660 gallus galli
6	159	51.8	497	BIR4_HUMAN	P88170 homo sapien
7	153	49.8	496	BIR4_MOUSE	Q60989 mus musculu
8	152	49.5	496	BIR4_RAT	Q91016 rattus norv
9	140	45.6	358	PIAP_PIG	Q62640 sus scrofa
10	134	43.6	1402	BIR3_MOUSE	Q911b3 mus musculu
11	134	43.6	1403	BIR2_MOUSE	Q91016 mus musculu
12	133	43.3	1403	BIR3_MOUSE	Q911b3 mus musculu
13	132	43.0	268	IAP3_NPYOP	P41437 oryza pseu
14	127	41.4	438	IAP1_DROME	Q24306 drosophila
15	125	40.7	1403	BIR1_HUMAN	Q13075 homo sapien
16	122	39.7	1447	BIRB_MOUSE	Q93944 mus musculu
17	119	38.8	239	ZEP_TRV6	P47732 chilo iride
18	117	38.1	298	BIR7_HUMAN	Q96ca3 homo sapien
19	111	36.2	236	BIR8_HUMAN	Q96p09 homo sapien
20	109	35.5	1403	BIR4_MOUSE	Q9gw43 mus musculu
21	108	35.2	236	BIR8_PANTR	Q95m72 pan troglod
22	106	34.5	236	BIR8_GORGO	Q95m71 gorilla gor
23	103.5	33.7	275	IAP_GVCP	P41436 cydia pomon
24	102	33.2	498	IAP2_DROME	Q24307 drosophila
25	93	30.3	275	IAP1_NPYOP	Q10296 oryza pseu
26	83.5	27.2	286	IAP1_NPVAC	P41435 autographa
27	75	24.4	224	IAPL_ASFB7	Q65138 african swi
28	73.5	23.9	142	BIR5_HUMAN	Q14064 homo sapien
29	72.5	23.6	997	BIR1_SCHPO	Q9nt09 homo sapien
30	71.5	23.3	4829	BIR6_HUMAN	Q9nt09 homo sapien
31	70.5	23.0	140	BIR5_MOUSE	Q70201 mus musculu
32	68.5	22.3	224	IAPL_ASFC3	Q11451 african swi
33	68.5	22.3	224	IAPL_ASFC4	Q12407 african swi

## ALIGNMENTS

RESULT 1	STANDARD:	PRT:	618 AA.
BIR3_HUMAN			
AC Q13490; Q16516;			
DT 01-NOV-1997 (Rel. 35, Created)			
DT 01-NOV-1997 (Rel. 35, Last sequence update)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DE Baculoviral IAP repeat-containing protein 3 (inhibitor of apoptosis protein 2) (HIAF2) (HIAF-2) (C-IAP1) (TNFR2-TRAF signaling complex protein 2) (IAP homolog B).			
DE BIR3 OR API2 OR IAP2 OR MIH8.			
GN Homo sapiens (Human).			
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX NCBI_Taxid=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=96128127; PubMed=8548810;			
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;			
RT "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";			
RL Cell 83:1243-1252(1995).			
RN [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=96149249; PubMed=8552191;			
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,			
RT Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;			
RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";			
RL Nature 379:349-353(1996).			
RN [3]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=96209843; PubMed=8643514;			
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;			
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";			
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).			
RN [4]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=96209843; PubMed=8643514;			
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;			
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";			
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).			
RN [5]			
RP STRUCTURE BY NMR OF 266-363.			
RX MEDLINE=99312054; PubMed=10404221;			
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;			
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP) repeat.";			
RL Nat. Struct. Biol. 6:648-651(1999).			
CC -I- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).			

34	68.5	22.3	224	1	IAPL_ASFM1	Q11452 african swi
35	68.5	22.3	238	1	IAPL_ASFM2	Q11453 african swi
36	61.5	20.0	142	1	BIR5_RAT	Q91hy7 rattus norv
37	60	19.5	1401	1	WRN_MOUSE	Q09053 mus musculu
38	57	18.6	707	1	ORC1_SCHPO	P54789 schizosacch
39	56	18.2	249	1	IAP2_NPVAC	P41454 autographa
40	56	18.2	1432	1	WRN_HUMAN	Q14191 homo sapien
41	54.5	17.8	458	1	YMW6_CAEEL	P34508 caenorhabdi
42	54.5	17.8	954	1	BIR1_YEAST	P47134 saccharomyc
43	54.5	17.8	1192	1	METH_MYCTU	Q33259 mycobacteri
44	53.5	17.4	949	1	IF2_HELPF	Q9zm46 helicobacte
45	53.5	17.4	1025	1	HTRA_FUGRU	Q42611 frugu rubrip

```

CC CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC CC inhibit apoptotic suppressor activity.
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
CC CC AND PANCREAS. LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
CC CC LEUKOCYTES.
CC CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
CC CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/BIRC3ID239.html".
CC CC -----
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CC CC -----
DR DR EMBL: L49431; AAC41942.1; -
DR DR EMBL: U45879; AAC50372.1; -
DR DR EMBL: U37547; AAC50508.1; -
DR DR EMBL: BC016174; AAH16174.1; -
DR DR PDB: 1OBN: 20-OCT-99.
DR DR GeneW: HGNC:590; BIRC2.
DR DR MIM: 601721.
DR DR InterPro: IPR001370; BIR.
DR DR InterPro: IPR001315; CARD.
DR DR InterPro: IPR001841; Znf_ring.
DR DR Pfam: PF00097; zf-C3HC4.1.
DR DR Pfam: PF00619; CARD.1.
DR DR Pfam: PF00653; BIR.1.
DR DR SMART: SM00236; BIR.3.
DR DR SMART: SM00184; CARD.1.
DR DR SMART: SM00184; RING.1.
DR DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR DR PROSITE: PS0209; CARD.1.
DR DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR DR PROSITE: PS00508; ZF_RING_2; 1.
DR DR Apoptosis; zinc-finger; Repeat; 3D-structure.
DR DR REPEAT 46 113 BIR 1.
DR DR REPEAT 184 250 BIR 2.
DR DR REPEAT 269 336 BIR 3.
DR DR DOMAIN 453 543 CARD.
DR DR ZN_FING 571 606 RING-TYPE.
DR DR CONFLICT 157 157 S -> P (IN REF. 2).
DR DR CONFLICT 308 308 C -> G (IN REF. 2).
DR DR CONFLICT 414 414 Q -> L (IN REF. 2).
DR DR CONFLICT 514 514 L -> W (IN REF. 2).
DR DR SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;
SQ
Query Match 100.0%; Score 307; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 6,6e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DE DE protein 1) (IAP homolog C).
GN GN BIRC2 OR API1 OR IAP1 OR MICH.
OS OS Homo sapiens (Human).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX OX NCBI_TaxID=9606;
RN RN [1]
RP RP SEQUENCE FROM N.A.
RX RX MEDLINE=96128127; PubMed=8548810;
RA RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RL RL to baculoviral inhibitor of apoptosis proteins."
RN RN [2]
RP RP SEQUENCE FROM N.A.
RX RX MEDLINE=96128127; PubMed=8548810;
RA RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RL RL to baculoviral inhibitor of apoptosis proteins."
RN RN [3]
RP RP SEQUENCE FROM N.A.
RX RX MEDLINE=96209843; PubMed=8643514;
RA RA Uren A.G., Pakusch M., Hawkins C.J., Puls R.L., Vaux D.L.;
RT RT "Cloning and expression of apoptosis inhibitory protein homologs that
RL RL function to inhibit apoptosis and/or bind tumor necrosis factor
RN RN receptor-associated factors."
RL RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN RN [4]
RP RP SEQUENCE FROM N.A.
RX RX MEDLINE=99252096; PubMed=10233894;
RA RA Horrevorts A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
RT RT ten Cate J.W., Pannekoek H.;
RL RL "Vascular endothelial genes that are responsive to tumor necrosis
RN RN factor-alpha in vitro are expressed in atherosclerotic lesions,
RT RT including inhibitor of apoptosis protein-1, stannin, and two novel
RL RL genes."
RN RN Blood 93:3418-3431(1999).
RN RN [5]
RP RP SEQUENCE OF 362-441 FROM N.A.
RX RX MEDLINE=20519161; PubMed=11066071;
RA RA Baens M., Steyels A., Dierlam J., De Wolf-Peeters C., Harynen P.;
RT RT "Structure of the MIF gene and molecular characterization of the
RL RL genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone
RN RN B-cell lymphomas of MALT type."
RT RT Genes Chromosomes Cancer 29:281-291(2000).
RN RN "FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
RT RT WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
RN RN FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
RT RT NECROSIS FACTOR RECEPTOR 2 (TNFR2).
RN RN -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC CC inhibit apoptotic suppressor activity.
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN
CC CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES.
CC CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
CC CC -1- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
CC CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid
CC CC tissue). This translocation is found in approximately 50% of
CC CC cytogenetically abnormal low-grade MALT lymphoma and involves
CC CC MALT1 and BIRC2.
CC CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC CC -----
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CC -----
DR EMBL; L49432; AAC41943.1; -
DR EMBL; U458748; AAC50371.1; -
DR EMBL; U37546; AAC50507.1; -
DR EMBL; AF070674; AAC83232.1; -
DR EMBL; AF178945; AAC09369.1; -
DR HSSP; Q13490; IQBH.
DR Genew; HGNC:591; BIRC3.
DR MIM; 601712; -
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat; Chromosomal translocation.
KT REPEAT 29 96 BIR 1.
KT REPEAT 169 235 BIR 2.
KT REPEAT 255 322 BIR 3.
KT DOMAIN 439 529 CARD.
KT ZN_FING 557 592 CARD.
KT SITE 442 443 RING-TYPE.
KT BREAKPOINT FOR TRANSLOCATION TO FORK
KT BIRC2-MALT1.
KT CONFLICT 18 18 N -> Y (IN REF. 4).
KT CONFLICT 119 119 N -> H (IN REF. 2).
KT CONFLICT 153 153 D -> E (IN REF. 2).
KT CONFLICT 163 163 H -> P (IN REF. 2).
KT CONFLICT 165 165 A -> P (IN REF. 2).
KT CONFLICT 191 191 F -> R (IN REF. 2).
KT CONFLICT 364 364 F -> L (IN REF. 2).
KT CONFLICT 552 552 Q -> P (IN REF. 2).
KT SEQUENCE 604 AA; 68371 MW; 8581A00BA9A4A7 CRC64;

Query Match 98.0%; Score 301; DB 1; Length 604;
Best Local Similarity 98.2%; Pred. No. 4e-32;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

OY 1 CELYMSYSTRPAACVPYSERSLARGFYTYGVNDKVKCFCCGLMDNKKLDSP 55
Db 28 CELYMSYSTRPAACVPYSERSLARGFYTYGVNDKVKCFCCGLMDNKKRDSP 82

RESULT 3
BIR3_MOUSE
BIR3_MOUSE STANDARD: PRT; 612 AA.
AC Q62210; Q08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
DE protein 2) (MARP2).
GN BIRC3 OR API2 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810;
RA Roche M., Pan M.-G., Henzel W.J., Ayres T.M., Ccedel D.V.;
RT "The TRAF2-TRAF signaling complex contains two novel proteins related
to baculoviral inhibitor of apoptosis proteins."

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RL Cell 83:1243-1252(1995).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.:
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
  1 and 2 genes."
RL Genomics 46:195-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROOMIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR).
CC -1- SUBUNIT: Interacts with SMAC and with PR55; these interactions
CC inhibit apoptotic suppressor activity (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
DR EMBL; L49433; AAC42078.1; -.
DR EMBL; U88909; AAC53532.1; -.
DR HSSP; Q13490; IOBH.
DR MGD; MGI:1197009; Birc3.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00653; BIR; 3.
DR SMART; SMO0238; BIR; 3.
DR SMART; SMO0114; CARD; 1.
DR SMART; SMO0184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS00518; zf_RING_1; FALSE_NEG.
DR PROSITE; PS50089; zf_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN_FING 565 600 RING-TYPE.
FT CONFLICT 380 380 E -> K (IN REF. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match 94.8% Score 291; DB 1; Length 612;
Best Local Similarity 94.5%; Pred. No. 8.5e-31;
Matches 52; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CELYKSTYSTRPAGVPSERSLARAGFYTGVDNKKVKCFCCGLMDNNKLDSP 55
DB 45 CELYKSTYSTRPAGVPSERSLARAGFYTGVDNKKVKCFCCGLMDNNKLDSP 99

RESULT 4
ID BIR2_MOUSE STANDARD: PRT: 600 AA.
AC 008863;
DC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

```

DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis  
GN protein 1) (MIAP-1).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN NCBI\_TaxID=10090;  
RP [1]  
RC SEQUENCE FROM N.A.  
RX TISSUE-Skeletal muscle;  
RA MEDLINE=98110590; PubMed=9441758;  
RT Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;  
RT "Genomic characterization of the mouse inhibitor of apoptosis protein  
RT 1 and 2 genes."  
RT Genomics 46:495-503(1997).  
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).  
CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions  
CC inhibit apoptotic suppressor activity (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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CC -----  
DR EMBL; U88908; AAC53531.1; -  
DR HSSP; Q13490; IQBH.  
DR MGD; MGI:1197007; BIRC2.  
DR InterPro; IPR001370; BIR.  
DR InterPro; IPR001315; CARD.  
DR InterPro; IPR001841; Znf\_fing.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR Pfam; PF00653; BIR; 3.  
DR SMART; SM00238; BIR; 3.  
DR SMART; SM00114; CARD; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE; PS0209; CARD; 1.  
DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE; PS0089; ZF\_RING\_2; 1.  
KW Apoptosis; Zinc-finger; Repeat.  
FT REPEAT 27 94 BIR 1.  
FT REPEAT 167 233 BIR 2.  
FT REPEAT 253 320 BIR 3.  
FT DOMAIN 436 525 CARD.  
FT ZN\_FING 553 588 RING-TYPE.  
SQ SEQUENCE 600 AA; 67198 MW; AD7F73E6849317D; CRC64;  
  
Query Match 92.5%; Score 284; DB 1; Length 600;  
Best Local Similarity 90.9%; Pred. No. 7e-30;  
Matches 50; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 CELYRSTSTPPAGVPSERSLARAGFYTGVDKVCPCCGGLMDNKLGDSP 55  
DB 26 CELYRSTSTPPAGVPSERSLARAGFYTGVDKVCPCCGGLMDNKLGDSP 80  
RESULT 5  
BIR\_CHICK  
ID BIR\_CHICK STANDARD; PRT; 611 AA.

AC 090660;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Inhibitor of apoptosis protein (IAP) (inhibitor of T cell apoptosis  
DE protein).  
GN ITA.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
RN NCBI\_TaxID=9031;  
RP [1]  
RC SEQUENCE FROM N.A.  
RX TISSUE-Spleen;  
RA MEDLINE=97101112; PubMed=8945639;  
RT Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;  
RT "ITA, a vertebrate homologue of IAP that is expressed in T  
RT lymphocytes."  
RT DNA Cell Biol. 15:981-988(1996).  
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.  
CC -1- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN  
CC BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.  
CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF  
CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.  
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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CC -----  
DR EMBL; U27466; AAB48118.1; -  
DR HSSP; Q13490; IQBH.  
DR InterPro; IPR001370; BIR.  
DR InterPro; IPR001315; CARD.  
DR InterPro; IPR001841; Znf\_fing.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR Pfam; PF00653; BIR; 3.  
DR SMART; SM00238; BIR; 3.  
DR SMART; SM00114; CARD; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE; PS0209; CARD; 1.  
DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE; PS0089; ZF\_RING\_2; 1.  
KW Apoptosis; Zinc-finger; Repeat; Nuclear protein.  
FT REPEAT 30 97 BIR 1.  
FT REPEAT 176 242 BIR 2.  
FT REPEAT 262 329 BIR 3.  
FT DOMAIN 446 536 CARD.  
FT ZN\_FING 564 599 RING-TYPE.  
SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD; CRC64;  
  
Query Match 80.5%; Score 247; DB 1; Length 611;  
Best Local Similarity 81.5%; Pred. No. 5.6e-25;  
Matches 44; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 CELYRSTSTPPAGVPSERSLARAGFYTGVDKVCPCCGGLMDNKLGDSP 54  
DB 29 CELYRSTSTPPAGVPSERSLARAGFYTGVDKVCPCCGGLMDNKLGDSP 82  
RESULT 6

ID	BIR4_HUMAN	STANDARD;	PRT;	497 AA.
AC	P98170: Q9NQ14;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)			
DE	(IAP-like protein) (HILP)			
GN	BIRC4 OR API3 OR IAP3 OR XIAP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fetal brain;			
RX	MDLINE=96149249; PubMed=8552191;			
RA	Liston P., Roy N., Tamai K., Lelebyre C., Baird S., Chertton-Horvat G.			
RA	Parahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;			
RT	"Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";			
RL	Nature 379:349-353(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fetal heart;			
RX	MDLINE=96256286; PubMed=8654366;			
RA	Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., Van Dongen J.L.,			
RA	Giffillan M.C., Shfels H., Hardick J.M., Thompson C.B.;			
RT	"A conserved family of cellular genes related to the baculovirus iap gene and encoding apoptosis inhibitors.";			
RL	EMBO J. 15:2685-2694(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Graham D.;			
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	FUNCTION.			
RX	MDLINE=97373959; PubMed=9230442;			
RA	Deveraux Q.L., Takehashi R., Salvesen G.S., Reed J.C.;			
RT	"X-linked IAP is a direct inhibitor of cell-death proteases.";			
RL	Nature 388:300-304(1997).			
RN	[5]			
RP	WOTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.			
RX	MDLINE=21634829; PubMed=11604410;			
RA	Verhaegen A.M., Silke J., Ekert P.G., Pakusch M., Kaufmann H.;			
RA	Connolly L.M., Day C.L., Tikoo A., Burke R., Wöbel C., Moritz R.L.;			
RA	Simpson R.J., Vaux D.V.;			
RT	"IAP promotes cell death through its serine protease activity and its ability to antagonize inhibitor of apoptosis proteins.";			
RL	J. Biol. Chem. 277:445-454(2002).			
RN	[6]			
RP	STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.			
RX	MDLINE=21020961; PubMed=11140637;			
RA	Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T.;			
RA	Herrmann J., Wu J.C., Fesik S.W.;			
RT	"Structural basis for binding of Smac/Diablo to the XIAP BIR3 domain.";			
RL	Nature 408:1004-1008(2000).			
CC	-1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9			
CC	-1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions			
CC	inhibit apoptotic suppressor activity.			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-1- TISSUE SPECIFICITY: UBIQUITOUS, EXCEPT PERIPHERAL BLOOD			
CC	LEUCOCYTES.			
CC	-1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3			
CC	and -7, while the third BIR is involved in caspase-9 inhibition.			
CC	The interactions with SMAC and PRSS25 are mediated by the second			
CC	and third BIR domains.			
CC	-1- SIMILARITY: BELONGS TO THE IAP FAMILY.			
CC	-1- SIMILARITY: CONTAINS 3 BIR REPEATS.			
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
CC	-----			



```

RC TISSUE=Arcta; PubMed-9501011;
RA MEDLINE-98162622;
RT Stehlik C., de Martin R., Binder B.R., Lipp J.;
RT "Cytokine induced expression of porcine inhibitor of apoptosis
RL protein (Iap) family member is regulated by NF-kappa B.";
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -1 SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1 SIMILARITY: CONTAINS 2 CARD REPEATS.
CC -1 SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL; U79142; AAC39171.1; -.
DR HSSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR01841; ZnF_Fing.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00653; BIR; 2.
DR SMART; SMO0238; BIR; 2.
DR SMART; SMO0114; CARD; 1.
DR SMART; SMO0184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Apoptosis; zinc-finger; Repeat.
FT REPEAT 4 70 BIR 1.
FT REPEAT 90 157 BIR 2.
FT DOMAIN 193 283 CARD.
FT ZN_FING 311 346 RING-TYPE.
SQ SEQUENCE 358 AA; 40977 MW; EB2268FA9A6190A1 CRC64;
Query Match 45.6%; Score 140; DB 1; Length 358;
Best Local Similarity 49.0%; Pred. No. 4.8e-11;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;
QY 5 RMSTSTEPAGVPSERSLARAGFYTYGVNPKVKFCGGLMDNNKLGDSP 55
Db 1 : : : || | ||||| 1 : : |||||
13 RFKTFCKMNPSSIPVHPBQLASGFYYMGHSDYKCFCCDGGJCRCHSGDDP 143
RESULT 10
ID BIRG_MOUSE STANDARD; PRT; 1402 AA.
GC 09JIB3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis
DE Inhibitory protein 7).
GN BIRCIG OR NAIp7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20414747; PubMed-10958627;
RA Endrizzi M.G., Hadjiloto V., Growney J.D., Miller W., Dietrich W.F.;
RT "Genomic fine analysis of the mouse Nalp gene array.";
EL Genome Res. 10:1095-1102(2000).
CC -1 FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
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CC -I SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -I SIMILARITY: CONTAINS 1 NACHT DOMAIN
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CC -----
DR EMBL; AF242433; AAF82749.1; -
DR HSSP; O13490; IOBH.
DR MGD; MG1:1858256; Birclg.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS01043; BIR_REPEAT_2; 3.
DR PROSITE; PS50837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT FT FT
FT FT FT
FT FT FT
FO SEQUENCE 1402 AA; 159662 MW; 1CDFSBA359893EOD CRC64;

Query Match 43.6%; Score 134; DR 1; Length 1402;
Best Local Similarity 46.3%; Pred. NO. 1.2e-09;
Matches 25; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

OY 2 ELRYNRSTYSPPAGVPSERSLARAGFYTYGVNDKRCFCGGLMDNKLDSNP 55
   1 11 : : 1 1 : : 1111111 1 1 11 1 1 : : 1 1 1
Db 278 BELRDMEKDPQESPVGEVLVRAGFYTGKDIVCFSCGGCLEKWAEGDDP 331

RESULT 11
BIRE_MOUSE STANDARD; PRT; 1403 AA.
ID BIRE_MOUSE
AC Q9R016; Q9R029; P81703; O09122; O09121;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1e (Neuronal apoptosis
DE inhibitory protein 5).
DE BIRCIE OR NAIP5 OR NAIP-R53.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
RA "The mouse Nalp gene cluster on Chromosome 13 encodes several distinct
RA functional transcripts.";
RL Mannu. Genome 10:1032-1035(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=129/SvJ;
RC MEDLINE=99431676; PubMed=10486205;
RA Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,
RA Kunkel L.M., Miller W., Dietrich W.F.;
RA "Comparative sequence analysis of the mouse and human Igml/SMA
RA Interval.";
RT Genomics 60:137-151(1999).
RN [3]
RP SEQUENCE OF 82-168 FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=97131520; PubMed=8975718;
RA Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
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RT      within the lgnt critical interval and contains multiple copies of Naip
RT      exon 5."
RL      Genomics 38:405-417(1996).
CC      -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC      SIGNALS.
CC      -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC      -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: AF135492; AAD56764.1; -.
DR      EMBL: AF131205; AAD56760.1; -.
DR      HSSP: Q13490; 10BH.
DR      MGD: MGI:1298220; Bircle.
DR      InterPro: IPR001370; BIR.
DR      Pfam: PF00653; BIR; 3.
DR      SMART: SM00238; BIR; 3.
DR      PROSITE: PS01282; BIR_REPEAT_1; 2.
DR      PROSITE: PS50143; BIR_REPEAT_2; 3.
DR      PROSITE: PS50837; NACHT; 1.
DR      KMW: Apoptosis; Repeat; Multigene family.
FT      REPEAT 60
FT      REPEAT 127
FT      REPEAT 159
FT      REPEAT 227
FT      REPEAT 278
FT      DOMAIN 345
FT      DOMAIN 759
FT      NACHT.
FT      CONFLICT 92
FT      CONFLICT 144
FT      CONFLICT 242
FT      CONFLICT 472
FT      CONFLICT 516
FT      CONFLICT 521
FT      CONFLICT 533
FT      CONFLICT 538
FT      CONFLICT 1092
FT      CONFLICT 1129
FT      CONFLICT 1137
FT      CONFLICT 1242
FT      CONFLICT 1276
FT      CONFLICT 1403 AA; 159695 MW; B27F645043BCE42 CRC64;
SQ      SEQUENCE
Query Match
Best Local Similarity 46.3%; Score 134; DB 1; Length 1403;
Matches 25; Conservative 6; Mismatches 23; Indels 0; Gaps 0;
QY      2 ELYRMSTYSTFPAGVPSERSLARAGFYTYGVNDKYKCFCCGGLMDNWKIGDSP 55
DB      278 EELRMDFKMDPQSPVGFALVRAGFYTGKKDIYRCFCGGLKMAEGDDP 331
RESULT 12
BIR_MOUSE
ID      BIR_MOUSE
AC      99186; P81704; O09122; O09121;
DT      16-OCT-2001 (Rel. 40; Created)
DT      16-OCT-2001 (Rel. 40; Last sequence update)
DT      15-JUN-2002 (Rel. 41; Last annotation update)
DE      Baculoviral IAP repeat-containing protein 1f (Neuronal apoptosis
DE      inhibitory protein 5)
GN      BIRCLF OR NAIP6 OR NAIP-RS4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
MEDLINE=20414747; PubMed=10958627;

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RA      Endrizzi M.G., Hadjiozoto V., Growney J.D., Miller W., Dietrich W.F.;
RA      "Genomic sequence analysis of the mouse Naip gene array.";
RL      Genome Res. 10:1095-1102(2000).
RN      [2]
RP      SEQUENCE OF 82-168 FROM N.A.
RC      STRAIN=129/Svj.
RX      MEDLINE=97131520; PubMed=8975718;
RA      Scharf J.M., Danton D., Fritsella A., Bruno S., Beggs A.H.,
RA      Kunzel L.M., Dietrich W.F.;
RT      "The mouse region syntenic for human spinal muscular atrophy lies
RT      within the lgnt critical interval and contains multiple copies of Naip
RT      exon 5."
RL      Genomics 38:405-417(1996).
CC      -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC      SIGNALS.
CC      -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC      -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: AF242431; AAF82751.1; -.
DR      EMBL: U66327; AAC52975.1; -.
DR      HSSP: Q13490; 10BH.
DR      MGD: MGI:1298222; Birc1f.
DR      InterPro: IPR001370; BIR.
DR      Pfam: PF00653; BIR; 3.
DR      SMART: SM00238; BIR; 3.
DR      PROSITE: PS01282; BIR_REPEAT_1; 2.
DR      PROSITE: PS50143; BIR_REPEAT_2; 3.
DR      PROSITE: PS50837; NACHT; 1.
DR      KMW: Apoptosis; Repeat; Multigene family.
FT      REPEAT 60
FT      REPEAT 127
FT      REPEAT 159
FT      REPEAT 227
FT      REPEAT 278
FT      DOMAIN 345
FT      DOMAIN 759
FT      NACHT.
FT      CONFLICT 92
FT      CONFLICT 144
FT      CONFLICT 242
FT      CONFLICT 472
FT      CONFLICT 516
FT      CONFLICT 521
FT      CONFLICT 533
FT      CONFLICT 538
FT      CONFLICT 1092
FT      CONFLICT 1129
FT      CONFLICT 1137
FT      CONFLICT 1242
FT      CONFLICT 1276
FT      CONFLICT 1403 AA; 159823 MW; 9D4912503358C4B9 CRC64;
SQ      SEQUENCE
Query Match
Best Local Similarity 46.3%; Score 133; DB 1; Length 1403;
Matches 25; Conservative 6; Mismatches 23; Indels 0; Gaps 0;
QY      2 ELYRMSTYSTFPAGVPSERSLARAGFYTYGVNDKYKCFCCGGLMDNWKIGDSP 55
DB      278 EELRMDFKMDPQSPVGFALVRAGFYTGKKDIYRCFCGGLKMAEGDDP 331
RESULT 13
IAP3_NPVOP
ID      IAP3_NPVOP
AC      P41437;
DT      01-NOV-1995 (Rel. 32; Created)
DT      01-NOV-1995 (Rel. 32; Last sequence update)
DT      16-OCT-2001 (Rel. 40; Last annotation update)
DE      Apoptosis inhibitor 3 (IAP-3).
GN      IAP3 OR IAP.
OS      Oryzias pseudotsugata multicapsid polyhedrosis virus (OPMVNV).
OC      Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC      Nucleopolyhedrovirus.
OX      NCBI_TaxID=164623;
RN      [1]
RP      SEQUENCE FROM N.A.
MEDLINE=94187094; PubMed=8139034;
RA      Birbaun M.J., Clem R.J., Miller L.K.;
RA      "An apoptosis-inhibiting gene from a nuclear polyhedrosis virus
RT      encoding a polypeptide with Cys/His sequence motifs.";
RL      J. Virol. 68:2521-2528(1994).
RN      [2]

```

RP SEQUENCE FROM N.A.  
 RX MEDLINE=97271300; PubMed=9126251;  
 RA Abrams C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,  
 RA Rohmann G.F.;  
 RT "The sequence of the Oryza pseudotsugata multinucleocapsid nuclear  
 RT polyhedrosis virus genome";  
 RL Virology 229:381-399(1997).  
 CC -1- FUNCTION: ACS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY  
 CC PREVENTING VIRAL STIMULATION OF APOPTOSIS.  
 CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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 CC -----  
 DR EMBL: L22564; AAC02610.1; -  
 DR EMBL: U75930; AAC59034.1; -  
 DR HSSP: Q13490; IOBH.  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001841; znf\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR Pfam: PF00653; BIR; 2.  
 DR SMART; SM00238; BIR; 2.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE; PS50143; BIR\_REPEAT\_2; 2.  
 DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 DR Apoptosis; Zinc-finger; Repeat.  
 KW REPEAT 18 84 BIR 1.  
 FT REPEAT 111 178 BIR 2.  
 FT ZN\_FING 221 256 RING-TYPE.  
 SO SEQUENCE 268 AA; 30076 MW; DF89175FDE85A708 CRC64;  
 Query Match 43.0%; Score 132; DB 1; Length 268;  
 Best Local Similarity 42.6%; Pred. No. 4,1e-10;  
 Matches 23; Conservative 10; Mismatches 21; Indels 0; Gaps 0;  
 QY 2 ELRYRSTVTPAGYVRSRLRAGFYTYGVNDKRCFCGCLMDNMTLGGSP 55  
 DB 111 EAARLTFEAMRNLRKQKPEELAEAGFFTYGGDKTRCFCHGGLKDWEPDAP 164  
 RESULT 14  
 ID IAP1\_DROME STANDARD: PRT: 438 AA.  
 AC Q24306;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Apoptosis 1 inhibitor (inhibitor of apoptosis 1) (DIAP1) (Thread  
 DE protein).  
 GN IAP1 OR TH.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye imaginal disk;  
 RX MEDLINE=96128128; PubMed=8548811;  
 RA Hay B.A., Wasserman D.A., Rubin G.M.;  
 RT "Drosophila homologs of baculovirus inhibitor of apoptosis proteins  
 RT function to block cell death";  
 RL Cell 83:1233-1262(1995).  
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND  
 CC HID-DEPENDENT CELL DEATH IN THE EYE.

CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -----  
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 CC -----  
 DR EMBL: L49440; AAC41609.1; -  
 DR HSSP: Q13490; IOBH.  
 DR Flybase: FBgn0003691; th.  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001841; znf\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR Pfam: PF00653; BIR; 2.  
 DR SMART; SM00238; BIR; 2.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE; PS50143; BIR\_REPEAT\_2; 2.  
 DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 DR Apoptosis; Zinc-finger; Repeat.  
 KW REPEAT 44 110 BIR 1.  
 FT REPEAT 226 293 BIR 2.  
 FT ZN\_FING 391 426 RING-TYPE.  
 SO SEQUENCE 438 AA; 48098 MW; A6C22C8EDF5AEF29 CRC64;  
 Query Match 41.4%; Score 127; DB 1; Length 438;  
 Best Local Similarity 42.6%; Pred. No. 3,1e-09;  
 Matches 23; Conservative 8; Mismatches 23; Indels 0; Gaps 0;  
 QY 2 ELRYRSTVTPAGYVRSRLRAGFYTYGVNDKRCFCGCLMDNMTLGGSP 55  
 DB 226 EAARLTFEAMRNLRKQKPEELAEAGFFTYGGDKTRCFCHGGLMDNNDNEP 279  
 RESULT 15  
 ID BIR1\_HUMAN STANDARD: PRT: 1403 AA.  
 AC Q13075; Q13730; Q99796; O75857;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis  
 DE inhibitory protein).  
 GN BIR1 OR NAIP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fetal brain;  
 RX MEDLINE=95112344; PubMed=7813013;  
 RA Roy N., Mahadevan M.S., McLean M., Shuttler G., Yaraqhi Z.,  
 RA Farahani R., Balid S., Besner-Johnston A., Lefebvre C., Kang X.,  
 RA Salih M., Aubry R., Tamai K., Guan X., Ioannou P., Crawford T.O.,  
 RA de Jong P.J., Suh L., Ikeda J., Korneluk R.G., Mackenzie A.;  
 RT "The gene for neuronal apoptosis inhibitory protein is partially  
 RT deleted in individuals with spinal muscular atrophy";  
 RL Cell 80:167-178(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND REVISIONS.  
 RC TISSUE=Brain;  
 RX MEDLINE=98163755; PubMed=9503025;  
 RA Chen Q., Balid S.D., Mahadevan M., Besner-Johnston A., Farahani R.,  
 RA Xuan J.-Y., Kang X., Lefebvre C., Ikeda J.E., Korneluk R.G.,  
 RA Mackenzie A.E.;  
 RT "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular

RT atrophy candidate genes SMN and NARP.";  
RL Genomics 48:121-127(1998).  
RN [3]  
RP SEQUENCE OF 386-623 FROM N.A.  
RA der Steege G., Draaljeers T.G., Grootscholten P.M., Oslina J.,  
RA Anzeveno R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,  
RA Buys C.H.C.M.;  
RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 222-1403 FROM N.A.  
RA Jones K., Graves T., McPherson J.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP FUNCTION.  
RC TISSUE=Liver;  
RX MEDLINE=9619249; PubMed=8552191;  
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,  
RA Farhant R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RT "Suppression of apoptosis in mammalian cells by NARP and a related  
RT family of IAP genes".  
RL Nature 379:349-353(1996).  
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
CC SIGNALS.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY  
CC NEURONS. FOUND IN LIVER AND PLACENTA, AMT. IN A LESSER EXTENT IN  
CC SPINAL CORD.  
CC -1- DISEASE: MUTATED OR DELETED FORMS OF NARP HAVE BEEN FOUND IN  
CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE I). SMAS  
CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE I  
CC (MERINIG-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE  
CC III (WOLFF-PARK-KUGELBERG-WELANDER DISEASE) BASED UPON THE AGE OF  
CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE  
CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO  
CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000  
CC NEWBORNS.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.  
CC -----\*-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----\*-----  
DR EMBL: U19251; AAC52045.1; -;  
DR EMBL: U80017; AAC52047.1; -;  
DR EMBL: U21913; AAA64504.1; -;  
DR EMBL: AC005031; AAC62261.1; -;  
DR HSSP: O13490; IOBH.  
DR Genew: HGNC:7634; BIRC1.  
DR MIM: 600355; -;  
DR InterPro: IPR001370; BIR.  
DR Pfam: PF00653; BIR; 3.  
DR SMART: SMO0238; BIR; 3.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE: PS0837; NACHT; 1.  
KW Apoptosis; Repeat.  
FT REPEAT 60 127 BIR 1.  
FT REPEAT 159 227 BIR 2.  
FT REPEAT 278 345 BIR 3.  
FT DOMAIN 464 758 NACHT.  
FT 222 223 PK -> YR (IN REF. 1).  
FT 386 387 VP -> ST (IN REF. 3).  
FT 535 535 M -> V (IN REF. 3).  
FT 553 553 Y -> H (IN REF. 3).  
FT 1228 1231 MISSING (IN REF. 4).  
SQ SEQUENCE 1403 AA: 159613 MW: 566304C154DA5E64 CRC64;

Query Match 40.7%; Score 125; DB 1; Length 1403;  
Best Local Similarity 40.7%; Pred. No. 1.8e-08;

Matches 22; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

OY 2 ELTRMSTYSTFPAGVPSERSLARAGTYTGVDKVKCFCCGLMDNWKLGDSF 55  
DB 278 EELRLDSFKDWPRESAVGVAALAKAGLFTYGRINDIVOCFSCGCGCLERKWDGDDP 331

Search completed: May 5, 2003, 16:02:42  
Job time: 4.28111 secs

GenCore version 5.1.4-D5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 15:57:12 ; Search time 13.4332 Seconds

(Without alignments)  
843.627 Million cell updates/sec

Title: US-08-569-749-5

Perfect score: 307  
Sequence: 1 CELMRSTYRFPAGVPSE.....KVKFCGGLMDNKLGDSP 55

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 20604715 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*

1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.virus:\*  
13: sp.vertibrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298	97.1	602	11 Q9SES9	Q9SES9 rattus norv
2	291	94.8	589	11 Q9SES8	Q9SES8 rattus norv
3	291	94.8	589	11 Q9QZC6	Q9QZC6 rattus norv
4	281	91.5	374	11 Q921N0	Q921N0 mus musculu
5	247	80.5	324	11 Q9DDN2	Q9DDN2 gallus galli
6	247	80.5	610	13 Q57319	Q57319 gallus galli
7	191	62.2	628	13 Q8UWD2	Q8UWD2 brachydanio
8	157	51.1	493	13 Q8UVP8	Q8UVP8 gallus galli
9	155	50.5	495	11 Q8UWH2	Q8UWH2 brachydanio
10	152	49.5	496	11 Q9ESF0	Q9ESF0 rattus norv
11	152	49.5	501	11 Q9EC05	Q9EC05 rattus norv
12	152	49.5	501	11 Q9EC04	Q9EC04 rattus norv
13	145	47.2	264	12 Q9EN27	Q9EN27 amsacta moe
14	143	46.6	195	13 Q91A70	Q91A70 gallus galli
15	143	46.6	197	13 Q91A69	Q91A69 gallus galli
16	140	45.6	281	12 Q9YN18	Q9YN18 choristoneu

17	136	44.3	276	12 Q8Q195	Q8Q195 mamestra co
18	136	44.3	517	11 Q8R408	Q8R408 rattus norv
19	134	43.6	597	11 Q9R015	Q9R015 mus musculu
20	131	42.7	224	11 Q88642	Q88642 rattus norv
21	131	42.7	243	12 Q91EW1	Q91EW1 cydia pomon
22	127	41.4	438	5 Q9VUX5	Q9VUX5 drosophila
23	125	40.7	1160	4 Q8RDZ4	Q8RDZ4 homo sapien
24	122	38.7	403	5 Q8WRD9	Q8WRD9 oclerotatu
25	119	38.8	208	12 Q55770	Q55770 chilo iride
26	117	38.1	280	4 Q9HAP7	Q9HAP7 homo sapien
27	117	38.1	298	4 Q9H2A8	Q9H2A8 homo sapien
28	117	38.1	298	4 Q96CA5	Q96CA5 homo sapien
29	115	37.5	346	5 Q968T8	Q968T8 bombyx mori
30	115	37.5	402	5 Q8T621	Q8T621 aedes albop
31	113.5	37.0	153	5 Q9VEM2	Q9VEM2 drosophila
32	111	36.2	236	4 Q96RW5	Q96RW5 homo sapien
33	111	36.2	236	4 Q96P09	Q96P09 homo sapien
34	111	36.2	313	12 Q9J827	Q9J827 spodoptera
35	108	35.2	236	6 Q95M72	Q95M72 pan troglod
36	107	34.9	379	5 Q8Y492	Q8Y492 trichoplusi
37	106	34.5	106	4 Q96RW6	Q96RW6 homo sapien
38	106	34.5	236	6 Q95M71	Q95M71 gorilla gor
39	106	34.5	377	5 Q9NJ07	Q9NJ07 spodoptera
40	105.5	34.4	276	12 Q89744	Q89744 buzura supp
41	104	33.9	109	6 Q8WNY4	Q8WNY4 bos taurus
42	103	33.6	150	12 Q9YV74	Q9YV74 melanoplus
43	103	33.6	261	12 Q9QES9	Q9QES9 epiphyas po
44	102	33.2	498	5 Q96U03	Q96U03 drosophila
45	101	32.9	268	12 Q9E232	Q9E232 helicoverpa

## ALIGNMENTS

RESULT 1  
ID Q9SES9 PRELIMINARY: PRT: 602 AA.  
AC Q9SES9;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Inhibitor of apoptosis protein 1.  
DE Rattus norvegicus (Rat).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;  
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of  
RT Apoptosis Protein 1, 2, and 3 Genes.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
DR EMBL; AF183430; AAG22970.1; -  
DR HSSP; Q13490; IOBH.  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR001315; CARD.  
DR InterPro: IPR001841; Znf\_ring.  
DR Pfam; PF00653; BIR; 3.  
DR Pfam; PF00619; CARD; 1.  
DR SMART; PF00097; zf-C3HC4; 1.  
DR SMART; SM00238; BIR; 3.  
DR SMART; SM00114; CARD; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.  
DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
DR PROSITE; PS50209; CARD; 1.  
KW Zinc-finger.  
SQ SEQUENCE 602 AA: 67326 MW; CC91385EFA62DE5A CRC64;  
Query Match 97.1%; Score 298; DB 11; Length 602;  
Best Local Similarity 96.4%; Pred. No. 1.2e-31;  
Matches 53; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 1 CELYRMSTYTFPAGVPSERSLARAGFYTTGVNDKYKCCGGLMDNMKLGSP 55
DB 28 CELYRMSTYTFPAGVPSERSLARAGFYTTGVNDKYKCCGGLMDNMKRGDSP 82

RESULT 2
OQ92C6 PRELIMINARY; PRT; 589 AA.
AC OQ92C6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF183431; AAG22971.1; -.
DR HSSP: 013490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00997; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR Zinc-finger.
KW ZINC-FINGER.
SQ SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD285B CRC64;

Query Match 94.8%; Score 291; DB 11; Length 589;
Best Local Similarity 94.5%; Pred. No. 1.1e-30;
Matches 52; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CELYRMSTYTFPAGVPSERSLARAGFYTTGVNDKYKCCGGLMDNMKLGSP 55
DB 24 CELYRMSTYSAFPRGVPVPSERSLARAGFYTTGVNDKYKCCGGLMDNMKRGDSP 78

RESULT 3
OQ92C6 PRELIMINARY; PRT; 589 AA.
AC OQ92C6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Dong Z., Denton M., Gu S.M., Satkumar P., Venkateshram M.A.;
RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF190020; AAF04585.1; -.
DR HSSP: 013490; 10BH.
DR InterPro: IPR001370; BIR.

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DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00997; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR Zinc-finger.
SQ SEQUENCE 589 AA; 66777 MW; E6812FEE3EA34142 CRC64;

Query Match 94.8%; Score 291; DB 11; Length 589;
Best Local Similarity 94.5%; Pred. No. 1.1e-30;
Matches 52; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CELYRMSTYTFPAGVPSERSLARAGFYTTGVNDKYKCCGGLMDNMKLGSP 55
DB 24 CELYRMSTYSAFPRGVPVPSERSLARAGFYTTGVNDKYKCCGGLMDNMKRGDSP 78

RESULT 4
OQ921N0 PRELIMINARY; PRT; 374 AA.
AC OQ921N0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Similar to baculoviral IAP repeat-containing 2.
GN BIRC2.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011338; AAH1338.1; -.
DR MGD: MGI:1197007; Birc2.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
SQ SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7E46F3 CRC64;

Query Match 91.5%; Score 281; DB 11; Length 374;
Best Local Similarity 90.9%; Pred. No. 1.4e-29;
Matches 50; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CELYRMSTYTFPAGVPSERSLARAGFYTTGVNDKYKCCGGLMDNMKLGSP 55
DB 26 CELYRMSTYSAFPRGVPVPSERSLARAGFYTTGVNDKYKCCGGLMDNMKRGDSP 80

RESULT 5
OQ9DDN2 PRELIMINARY; PRT; 324 AA.
AC OQ9DDN2;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE Apoptosis inhibitor ch-IAP1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCB1_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Pendleton C.N., Bargmann W.J., Varadarajan J., Bose H.R. Jr.;

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RT "The apoptosis inhibitor ch-IAP1 is a direct transcriptional target of v-Rel and c-Rel."

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF311289; AAC42316.1; -

DR HSSP: Q13490; IQBH.

DR InterPro: IPR001370; BIR.

DR Pfam: PF00653; BIR; 3.

DR SMART: SM00238; BIR; 3.

DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.

DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.

FT NON\_TER 324

SO SEQUENCE 324 AA; 36567 MW; 5E2B89DEAE3733F3 CRC64;

Query Match 80.5%; Score 247; DB 13; Length 324;  
Best Local Similarity 81.5%; Pred. No. 4.7e-25;  
Matches 44; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CELYRMSTYSPFAGVPSERSLARAGFYTGVDKVKCFCCGMLDWMKIGDS 54  
DB 29 CELYRMSTSTFPVNVPSERRLARAGFYTGVDKVKCFSCGLVLDNMQPGDN 82

RESULT 6  
057319 PRELIMINARY; PRT; 610 AA.

AC 057319;

DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)

DE Inhibitor of apoptosis protein 1 (IAP) (Inhibitor of T cell apoptosis PROTEIN).

GN IAP1.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI\_TaxID=9031;

OX [1]

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-WHITE LEGHORN; TISSUE-EMBRYONIC FIBROBLAST;

RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;

RT "Ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a mediator of the antiapoptotic activity of the v-Rel oncoprotein."

RT Mol. Cell. Biol. 17:7328-7341(1997).

RL -1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED CELLS.

CC -1- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF THE V-REL-TRANSFORMED CELLS.

CC -1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE SPLEEN, THYMUS, BURS, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS IN TESTIS, BRAIN, AND SKELETAL MUSCLE.

CC -1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION PROCESS.

CC -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.

CC -1- SIMILARITY: MEMBER OF THE IAP FAMILY.

CC -1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF APOPTOSIS PROTEIN REPEAT).

CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

CC EMBL: AF008592; AAB88044.1; -

DR HSSP: Q13490; IQBH.

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001315; CARD.

DR InterPro: IPR001841; Znf\_ring.

DR Pfam: PF00653; BIR; 3.

DR Pfam: PF00619; CARD; 1.

DR Pfam: PF00097; zf-C3HC4; 1.

DR SMART: SM00238; BIR; 3.

DR SMART: SM00114; CARD; 1.

DR SMART: SM00184; RING; 1.

DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.

DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.

DR PROSITE: PS50209; CARD; 1.

KM Apoptosis; Zinc-finger; Repeat.

FT REPEAT 30 97 BIR\_REPEAT 1.

FT REPEAT 176 242 BIR\_REPEAT 2.

FT REPEAT 262 329 BIR\_REPEAT 3.

FT ZN\_FING 563 597 C3HC4-TYPE.

SO SEQUENCE 610 AA; 68924 MW; ADF47619650B44A6 CRC64;

Query Match 80.5%; Score 247; DB 13; Length 610;  
Best Local Similarity 81.5%; Pred. No. 9.6e-25;  
Matches 44; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CELYRMSTYSPFAGVPSERSLARAGFYTGVDKVKCFCCGMLDWMKIGDS 54  
DB 29 CELYRMSTSTFPVNVPSERRLARAGFYTGVDKVKCFSCGLVLDNMQPGDN 82

RESULT 7  
080WD2 PRELIMINARY; PRT; 628 AA.

ID 080WD2;

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)

DE Iap1.

GN Iap1.

OS Brachydanio rerio (Zebrafish) (Zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

OC NCBI\_TaxID=7955;

OX [1]

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=20373792; PubMed=10917738;

RA Inohara N., Nunez G.;

RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."

RT Cell Death Differ. 7:509-510(2000).

RL [2]

RN [2]

RP SEQUENCE FROM N.A.

RA Inohara N., Nunez G.;

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF442500; AL33679.1; -

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001315; CARD.

DR InterPro: IPR001841; Znf\_ring.

DR Pfam: PF00653; BIR; 3.

DR Pfam: PF00619; CARD; 1.

DR Pfam: PF00097; zf-C3HC4; 1.

DR SMART: SM00238; BIR; 3.

DR SMART: SM00114; CARD; 1.

DR SMART: SM00184; RING; 1.

DR PROSITE: PS01282; BIR\_REPEAT\_1; UNKNOWN\_2.

DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.

DR PROSITE: PS50209; CARD; 1.

DR PROSITE: PS50089; ZF\_RING\_2; 1.

SO SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87CBA95 CRC64;

Query Match 62.2%; Score 191; DB 13; Length 628;  
Best Local Similarity 61.1%; Pred. No. 3.6e-17;  
Matches 33; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 2 ELYRMSTYSPFAGVPSERSLARAGFYTGVDKVKCFCCGMLDWMKIGDSP 55  
DB 29 ELYRMSTYSPFAGVPSERSLARAGFYTGVDKVKCFSCGLVLDNMQPGDN 82

RESULT 8  
080VP8 PRELIMINARY; PRT; 493 AA.

ID 080VP8;

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)

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DE Inhibitor of apoptosis protein 3.
GN IAP3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Identification of chicken inhibitor of apoptosis protein XIAP
  (IAP3).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF451854; AAL47170.1; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;

Query Match 51.1%; Score 157; DB 13; Length 493;
Best Local Similarity 54.7%; Pred. No. 1,1e-12;
Matches 29; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 2 ELYKSTSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNMKLCDS 54
DQ 26 EHYRIGTFEPHDCPVASALARAGFYTGEDKVCFCFCHVYEGWEPDS 78

RESULT 9
ID Q8UWH2 PRELIMINARY; PRT; 405 AA.
AC Q8UWH2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE XIAP.
OS Brachydonto rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20373792; PubMed-10917738;
RA Itohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
  zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Itohara N., Nunez G.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF439767; AAL32047.1; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS50143; BIR_REPEAT_1; 3.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 405 AA; 45564 MW; A366E3342D83BECAB CRC64;

Query Match 50.5%; Score 155; DB 13; Length 405;
Best Local Similarity 51.0%; Pred. No. 1,6e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

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QY 5 RMSTSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNMKLCDS 55
DQ 140 RLSTFNMPPADSPVPEDLAEAGMTYIGIDNVQCFCCGGGLSGWEGCDDP 190

RESULT 10
ID Q9ESFO PRELIMINARY; PRT; 496 AA.
AC Q9ESFO;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
  Apoptosis Protein 1, 2, and 3 Genes.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF183429; AAG22969.1; -
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
KW Zinc-finger.
SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AE5B798 CRC64;

Query Match 49.5%; Score 152; DB 11; Length 496;
Best Local Similarity 50.9%; Pred. No. 5e-12;
Matches 27; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 2 ELYKSTSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNMKLCDS 54
DQ 26 EFNRLKTFANPPSSPASATLARAGFYTGEDTVCCFCHAAVDRWOYXDS 78

RESULT 11
ID Q9EQ05 PRELIMINARY; PRT; 501 AA.
AC Q9EQ05;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-WISTAR; TISSUE-Ovary;
RA Lareu R., Bradley C.K., Iacher M., Ellis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
  protein in the rat corpus luteum.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF304333; AAG41192.1; -
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.

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GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:59:02 ; Search time 3.26267 Seconds

(Without alignments)  
432.866 Million cell updates/sec

Title: US-08-569-749-9

Perfect score: 1 PEOLASAGFTYVGRNDVYK.....CMESGDDPWVHAHAFPRCE 48

Sequence: 295

Scoring table: BIOSUM62

Gap: 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

1: Issued\_Patents\_AA:\*  
2: /cgn2\_6/ptodata/1/1aa/5A.COMB.pap:\*  
3: /cgn2\_6/ptodata/1/1aa/5B.COMB.pap:\*  
4: /cgn2\_6/ptodata/1/1aa/6A.COMB.pap:\*  
5: /cgn2\_6/ptodata/1/1aa/6B.COMB.pap:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfilest.pap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	295	100.0	48	4	US-08-569-749-9
2	295	100.0	48	5	PCT-US96-12860-9
3	295	100.0	438	5	PCT-US95-05922A-2
4	295	100.0	618	4	US-08-569-749-2
5	295	100.0	618	4	US-09-069-023-29
6	295	100.0	618	5	PCT-US96-12860-2
7	283	95.9	68	2	US-08-511-485-27
8	283	95.9	618	2	US-08-511-485-8
9	283	95.9	618	3	US-09-212-971-8
10	283	95.9	618	4	US-08-800-929A-8
11	283	95.9	618	4	US-09-617-053A-8
12	282	95.6	48	4	US-08-569-749-10
13	282	95.6	68	5	PCT-US96-12860-10
14	282	95.6	604	2	US-08-511-485-26
15	282	95.6	604	3	US-08-511-485-6
16	282	95.6	604	2	US-09-212-971-6
17	282	95.6	604	4	US-08-800-929A-6
18	282	95.6	604	4	US-08-569-749-4
19	282	95.6	604	4	US-09-617-053A-6
20	282	95.6	604	5	PCT-US96-12860-4
21	282	95.6	612	3	US-09-212-971-14
22	282	95.6	612	4	US-08-800-929A-14
23	282	95.6	612	4	US-08-569-749-14
24	282	95.6	612	4	US-09-617-053A-14
25	282	95.6	612	4	PCT-US96-12860-14
26	268	90.8	600	3	US-09-212-971-12
27	268	90.8	600	4	US-08-800-929A-12

28	268	90.8	600	4	US-09-617-053A-12	Sequence 12, Appl
29	231	78.3	50	4	US-08-975-080-21	Sequence 31, Appl
30	230	78.0	50	4	US-08-975-080-22	Sequence 22, Appl
31	230	78.0	50	4	US-08-975-080-30	Sequence 30, Appl
32	198	67.1	68	2	US-08-511-485-28	Sequence 28, Appl
33	198	67.1	268	3	US-08-836-134-22	Sequence 22, Appl
34	198	67.1	268	4	US-09-493-784-22	Sequence 22, Appl
35	187	63.4	50	4	US-08-975-080-21	Sequence 21, Appl
36	182	61.7	68	2	US-08-511-485-29	Sequence 29, Appl
37	182	61.7	275	3	US-08-836-134-21	Sequence 12, Appl
38	182	61.7	275	3	US-08-836-134-21	Sequence 21, Appl
39	182	61.7	275	4	US-09-493-784-21	Sequence 21, Appl
40	178	60.3	1151	3	US-08-836-134-23	Sequence 23, Appl
41	178	60.3	1151	3	US-09-493-784-23	Sequence 23, Appl
42	178	60.3	1232	3	US-08-836-134-2	Sequence 2, Appl
43	178	60.3	1232	4	US-09-493-784-2	Sequence 2, Appl
44	174	59.0	66	2	US-08-511-485-25	Sequence 25, Appl
45	174	59.0	236	4	US-09-239-867-4	Sequence 4, Appl

#### ALIGNMENTS

RESULT 1  
US-08-569-749-9  
Sequence 9, Application US/08569749  
Patent No. 6187557  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Goeddel, David V  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brenner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-9

Query Match 100.0%; Score 295; DB 4; Length 48;  
Best Local Similarity 100.0%; Pred. No. 3.7e-30;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEOLASAGFTYVGRNDVYKFCFCDDGLRCWESGDDPWVHAHAFPRCE 48  
DB 1 PEOLASAGFTYVGRNDVYKFCFCDDGLRCWESGDDPWVHAHAFPRCE 48

RESULT 2  
PCT-US96-12860-9  
Sequence 9, Application PC/US9612860  
GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-9  
Query Match 100.0%; Score 295; DB 5; Length 48;  
Best Local Similarity 100.0%; Pred. No. 3.7e-30;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PEOIASGFTYVGRNDVKFCDCDGLRCWESGDDPWVEHAKMPRCE 48  
Db 1 PEOIASGFTYVGRNDVKFCDCDGLRCWESGDDPWVEHAKMPRCE 48  
RESULT 3  
PCT-US95-05922A-2  
Sequence 2, Application PC/US9505922A  
GENERAL INFORMATION:  
APPLICANT: HE, ET AL.  
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARBELL, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05922A

FILING DATE: 11 MAY 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-292  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 438 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
PCT-US95-05922A-2  
Query Match 100.0%; Score 295; DB 5; Length 438;  
Best Local Similarity 100.0%; Pred. No. 4.1e-29;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PEOIASGFTYVGRNDVKFCDCDGLRCWESGDDPWVEHAKMPRCE 48  
Db 107 PEOIASGFTYVGRNDVKFCDCDGLRCWESGDDPWVEHAKMPRCE 154  
RESULT 4  
US-08-569-749-2  
Sequence 2, Application US/08569749  
Patent No. 6187557  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-2  
Query Match 100.0%; Score 295; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 6e-29;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVKKCCCGGLRCWESGDDPWVEHAKWPRCE 48  
DB 287 PEOLASAGFYVGRNDVKKCCCGGLRCWESGDDPWVEHAKWPRCE 334

## RESULT 5

US-09-069-023-29  
Sequence 29, Application US/09069023A  
Patent No. 6348573  
GENERAL INFORMATION:  
APPLICANT: Nunez, Gabriel  
APPLICANT: Inohara, Naohiro  
APPLICANT: Koseki, Takeyoshi  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
FILE REFERENCE: UM-03333  
CURRENT APPLICATION NUMBER: US/09/069,023A  
CURRENT FILING DATE: 1998-04-27  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-069-023-29

Query Match 100.0%; Score 295; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 6e-29;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVKKCCCGGLRCWESGDDPWVEHAKWPRCE 48  
DB 287 PEOLASAGFYVGRNDVKKCCCGGLRCWESGDDPWVEHAKWPRCE 334

## RESULT 6

PCT-US96-12860-2  
Sequence 2, Application PC/TUS9612860  
GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOERBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749 -  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-2

Query Match 100.0%; Score 295; DB 5; Length 618;  
Best Local Similarity 100.0%; Pred. No. 6e-29;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVKKCCCGGLRCWESGDDPWVEHAKWPRCE 48  
DB 287 PEOLASAGFYVGRNDVKKCCCGGLRCWESGDDPWVEHAKWPRCE 334

## RESULT 7

US-08-511-485-27  
Sequence 27, Application US/08511485  
Patent No. 5919912  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,485  
FILING DATE: 04-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-511-485-27

Query Match 95.98%; Score 283; DB 2; Length 68;  
Best Local Similarity 97.98%; Pred. No. 1.7e-28;  
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVKKCCCGGLRCWESGDDPWVEHAKWPRCE 48  
DB 19 PEOLASAGFYVGRNDVKKCCCGGLRCWESGDDPWVEHAKWPRCE 66

## RESULT 8

US-08-511-485-8  
Sequence 8, Application US/08511485  
Patent No. 5919912  
GENERAL INFORMATION:

```

; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-511-485-8

Query Match          95.9%; Score 283; DB 2; Length 618;
Best Local Similarity 97.9%; Pred. No. 1.9e-27;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PEQLASAGFYVGRNDVRCFCDCGGLRCWESGDDPWVHAHWPCE 48
Db 287 PEQLASAGFYVGRNDVRCFCDCGGLRCWESGDDPWVHAHWPCE 334

RESULT 9
US-09-212-971-8
; Sequence 8, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-212-971-8

Query Match          95.9%; Score 283; DB 3; Length 618;
Best Local Similarity 97.9%; Pred. No. 1.9e-27;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PEQLASAGFYVGRNDVRCFCDCGGLRCWESGDDPWVHAHWPCE 48
Db 287 PEQLASAGFYVGRNDVRCFCDCGGLRCWESGDDPWVHAHWPCE 334

RESULT 10
US-08-800-929A-8
; Sequence 8, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Ebling LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-800-929A-8

Query Match          95.9%; Score 283; DB 4; Length 618;
Best Local Similarity 97.9%; Pred. No. 1.9e-27;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PEQLASAGFYVGRNDVRCFCDCGGLRCWESGDDPWVHAHWPCE 48
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Db 287 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAKWPFRC 334

RESULT 11

US-09-617-053A-8

Sequence 8, Application US/09617053A  
Patent No. 6300492  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 07891/009003  
CURRENT APPLICATION NUMBER: US/09/617,053A  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-617-053A-8

Query Match 95.9%; Score 283; DB 4; Length 618;  
Best Local Similarity .97.9%; Pred. No. 1.9e-27;  
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAKWPFRC 48

Db 287 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAKWPFRC 334

RESULT 12

US-08-569-749-10

Sequence 10, Application US/08569749  
Patent No. 6187557  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Goeddel, David V  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 48 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-10

Query Match 95.6%; Score 282; DB 4; Length 48;  
Best Local Similarity 93.8%; Pred. No. 1.6e-28;  
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAKWPFRC 48

Db 1 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAKWPFRC 48

RESULT 13

PCT-US96-12860-10

Sequence 10, Application PC/TUS9612860  
GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)398-3249  
TELEFAX: (415)781-1989  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-10

Query Match 95.6%; Score 282; DB 5; Length 48;  
Best Local Similarity 93.8%; Pred. No. 1.6e-28;  
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAKWPFRC 48

Db 1 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAKWPFRC 48

RESULT 14  
US-08-511-485-26  
Sequence 26, Application US/08511485  
Patent No. 5919912  
GENERAL INFORMATION:

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; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-8906
; TELEFAX: 617/542-5070
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-511-485-26

Query Match          95.6%; Score 282; DB 2; Length 68;
Best Local Similarity 93.8%; Pred. No. 2.3e-28;
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PQLASAGFYVYGRNDVVKFCFCDDGLRCMESGDDPVPVHAKEFPCE 48
DB 19 PQLASAGFYVYGRNDVVKFCFCDDGLRCMESGDDPVPVHAKEFPCE 66

RESULT 15
US-08-511-485-6
; Sequence 6, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
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; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-8906
; TELEFAX: 617/542-5070
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 604 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-511-485-6

Query Match          95.6%; Score 282; DB 2; Length 604;
Best Local Similarity 93.8%; Pred. No. 2.4e-27;
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PQLASAGFYVYGRNDVVKFCFCDDGLRCMESGDDPVPVHAKEFPCE 48
DB 273 PQLASAGFYVYGRNDVVKFCFCDDGLRCMESGDDPVPVHAKEFPCE 320

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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

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(without alignments)  
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Title: US-08-569-749-9

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	295	100.0	48	AAW13551	Human c-IAP1 repeat
2	295	100.0	48	AAW04563	Human c-IAP2 repeat
3	295	100.0	48	AAW19746	Human c-IAP1 repeat
4	295	100.0	48	AAW13545	Human c-IAP1 repeat
5	295	100.0	48	AAW33998	Human c-IAP1 repeat
6	283	95.9	48	AAW19583	Human c-IAP1 repeat
7	283	95.9	48	AAW69296	Human c-IAP1 repeat
8	283	95.9	48	ABG56565	Human c-IAP2 repeat
9	282	95.6	48	AAW13552	Human c-IAP2 repeat
10	282	95.6	60	AAW19747	Human c-IAP2 repeat

11	282	95.6	60	AAW19582	Human c-IAP2 repeat
12	282	95.6	60	AAW13546	Human c-IAP2 repeat
13	282	95.6	60	AAW69295	Human c-IAP1 repeat
14	282	95.6	60	AAW52703	Human c-IAP1 repeat
15	282	95.6	60	AAW33997	Human c-IAP1 repeat
16	282	95.6	60	ABG56564	Human c-IAP1 repeat
17	282	95.6	60	AAW13555	Human c-IAP1 repeat
18	282	95.6	60	AAW69299	Human c-IAP1 repeat
19	282	95.6	60	AAW52703	Human c-IAP1 repeat
20	282	95.6	60	AAW52703	Human c-IAP1 repeat
21	276	93.6	59	AAW19586	Human c-IAP1 repeat
22	276	93.6	59	ABG56568	Human c-IAP1 repeat
23	268	90.8	60	AAW69298	Human c-IAP1 repeat
24	262	88.8	60	ABG56567	Human c-IAP1 repeat
25	258	87.5	60	AAW19585	Human c-IAP1 repeat
26	258	87.5	60	AAW19585	Human c-IAP1 repeat
27	195	66.1	20	ABG27363	Human c-IAP1 repeat
28	195	66.1	20	AAW52707	Human c-IAP1 repeat
29	195	66.1	22	AAW52707	Human c-IAP1 repeat
30	195	66.1	22	AAW52707	Human c-IAP1 repeat
31	195	66.1	22	AAW52707	Human c-IAP1 repeat
32	195	66.1	22	AAW52707	Human c-IAP1 repeat
33	195	66.1	22	AAW52707	Human c-IAP1 repeat
34	195	66.1	22	AAW52707	Human c-IAP1 repeat
35	195	66.1	22	AAW52707	Human c-IAP1 repeat
36	188	63.7	37	AAE07881	Human c-IAP1 repeat
37	185	62.7	25	AAE09458	Human c-IAP1 repeat
38	184	62.4	26	ABG09488	Human c-IAP1 repeat
39	178	60.3	12	AAW52707	Human c-IAP1 repeat
40	178	60.3	12	AAW52707	Human c-IAP1 repeat
41	178	60.3	12	AAW52707	Human c-IAP1 repeat
42	178	60.3	12	AAW52707	Human c-IAP1 repeat
43	178	60.3	12	AAW52707	Human c-IAP1 repeat
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#### ALIGNMENTS

RESULT 1	AAW13551	standard; Protein: 48 AA.
ID	AAW13551	
AC	AAW13551	
DT	22-JUL-1997	(first entry)
XX	XX	
DE	Human c-IAP1 repeat 3.	
KW	IAP; Inhibitor; apoptosis; RING finger domain; restinosis;	
KW	myocardial infarction; nephritis; HIV.	
XX	XX	
OS	Homo sapiens.	
PN	W09706182-A1.	
XX	XX	
PD	20-FEB-1997.	
XX	XX	
PF	06-AUG-1996; 96MO-DS12860.	
XX	XX	
PR	08-DEC-1995; 95US-0569749.	
PR	08-AUG-1995; 95US-0512946.	
XX	XX	
PA	(TUL- ) TULARIK INC.	
PI	Goeddel DV, Rothe M;	
XX	XX	
DR	WPI; 1997-154209/14.	
XX	XX	
PT	Nucleic acids encoding cellular inhibitor of apoptosis proteins	
PT	useful for apoptosis regulation in cells to reduce or increase	
PT	apoptosis and for pharmacological screening	



CC	lines. Recombinant hIAP-1 can be produced in prokaryotic or
CC	eukaryotic host cells, or expressed in vivo. It can also be used
CC	to screen for modulators of hIAP-1 activity.
XX	
SQ	Sequence 438 AA:
Query Match	100.0%; Score 295; DB 17; Length 438;
Best Local Similarity	100.0%; Pred. No.6.8e-28;
Matches 48; Conservative	0; Mismatches 0; Indels 0; Gaps
OY	1 PEOLASGFYYVGRNDVKCFCCDGGIRCWESGDDPWEHAKWPRCE 48       Db 107 PEOLASGFYYVGRNDVKCFCCDGGIRCWESGDDPWEHAKWPRCE 154
RESULT 3	
AAM19746	
ID AAM19746 standard; Protein; 618 AA.	
AC AAM19746;	
XX	
DT 16-SEP-1997 (first entry)	
DE Human inhibitor of apoptosis protein homologue MIHB.	
XX	
KM Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHB;	
KW degenerative disease; infectious disease; autoimmune disease; cancer; therapy; diagnosis.	
XX	
OS Homo sapiens.	
XX	
FH Key Location/Qualifiers	
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FT /label= BIR	
FT Region 184..250	
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FT Region 569..606	
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XX	
PN W09723501-A1.	
XX	
PD 03-JUL-1997.	
XX	
PF 20-DEC-1996; 96WO-AU00827.	
XX	
PR 22-DEC-1995; 95AU-0007275.	
XX	
PA (AMRA-) AMRAD OPERATIONS PTY LTD.	
XX	
Vaux DL;	
DR WPI; 1997-350966/32.	
RR N-PSDB; AAT72711.	
PT Isolated protein homologues of viral inhibitors of apoptosis - used	
PT to modulate apoptosis for treatment of degenerative, infectious or	
PT autoimmune diseases and cancer	
XX	
PS Claim 8; Page 51-54; 136pp; English.	
XX	
CC Mammalian IAP homologue B (MIHB) (AAM19746) is a human homologue of	
CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid	
CC sequence was deduced from a cDNA clone (see also AAT72711) isolated	
CC from a human foetal liver cDNA library using primers based on	
CC human EST sequences that resembled the BIR repeats of Oryza	
CC pseudotsugata polyhedrosis virus IAP. IAP homologues (see also	
CC AAM19745 and AAM19747-52) and their derivatives and chemical analogues	
CC can be used in methods for modulating apoptosis in animal cells,	
CC specifically for treatment, by inhibition, of degenerative and	
CC infectious disease or, by promotion, of cancer and autoimmune	
CC disease.	



OS	Homo sapiens.
XX	
FH	Key
FT	Domain
FT	Location/Qualifiers 46..113
FT	/label= BIR-1
FT	Domain
FT	184..250
FT	/label= BIR-2
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FT	/label= BIR-3
FT	Domain
FT	560..605
FT	/label= Ring_zinc_finger
XX	
PN	W09706255-A2.
PD	20-FEB-1997.
XX	
PE	05-AUG-1996;
XX	96WO-IB01022.
XX	22-DEC-1995;
PR	95US-0576956.
PR	04-AUG-1995;
XX	95US-0511485.
PA	(UYOT-) UNIV OTTAWA.
XX	
PI	Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX	
DR	WPI; 1997-154262/14.
DR	N-PSDB; AAT70838.
XX	
PT	Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT	to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
PT	of susceptibility to apoptotic disease
PS	Claim 27; Page 75-77; 219pp; English.
XX	
CC	Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC	M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC	are inhibitors of apoptosis (IAP) and which are characterised by
CC	the presence of a ring zinc finger domain (see also AAW19587) and at
CC	least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC	The HIAP amino acid sequences were deduced from cDNA clones (AAT70837
CC	and AAT70838) from a human liver library. IAP polypeptides can be
CC	expressed in host cells (in vitro or in vivo) and used in methods
CC	for treating diseases and disorders involving apoptosis, esp. in a
CC	human diagnosed as HIV-positive or as having AIDS, a
CC	neurodegenerative disease, a myelodysplastic syndrome or an
CC	ischemic injury, selected from myocardial infarction, stroke,
CC	reperfusion injury, or a toxin-induced liver disease.
XX	
SQ	Sequence 618 AA;
Query Match	95.9%; Score 283; DB 18; Length 618;
Best Local Similarity	97.9%; Pred. NO. 2.9e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0.	
OY	1 PEOLASAGFYVGRNDVKKCFCCDDGLGKWCESGDPPWEHAHPFRC 48
D287	PEQLASAGFYVGRNDVKKCFCCDDGLGKWCESGDPPWEHAHPFRC 334
RESULT 7	
ID	AAW69296
AC	AAW69296 standard; Protein; 618 AA.
DT	13-NOV-1998 (first entry)
DE	Human HIAP-2 protein.
KM	Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide; proliferative disease; IAP; therapy; cancer; human; HIAP-2 protein.
XX	Homo sapiens.

[illegible]

XX 27-SEP-2001; 2001WO-CA01379.  
 PF 28-SEP-2000; 2000US-0672717.  
 XX  
 XX  
 PA (UYOT-) UNIV OTTAWA.  
 XX (ABGE-) ABERGIA THERAPEUTICS INC.  
 XX  
 XX Korneiluk RG, Lacasse E, Baird S, Holcik M, Young S;  
 PI MPI: 2002-479562/51.  
 DR N-PSDB: ABK93871.  
 XX  
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for  
 PF enhancing apoptosis in a cell, for treating cancer and other  
 PT proliferative diseases  
 XX  
 XX Disclosure: Fig 3; 135pp; English.  
 PS  
 XX The invention relates to an inhibitor of apoptosis (IAP) antisense  
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of  
 CC length of the antisense nucleic acid, the IAP proteins may be mouse  
 CC or human XIAP, HAPI or HIAP2. Also included are a pharmaceutical  
 CC composition comprising a mammalian IAP antisense molecule and a method of  
 CC enhancing apoptosis in a cell, comprising administering a negative  
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
 CC mammal diagnosed with a proliferative disease. The method is useful for  
 CC treating a patient diagnosed with a proliferative disease like cancer.  
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
 CC conditions where apoptosis is involved or implicated (e.g. embryonic  
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
 CC virus, pox virus and adenovirus). The present sequence is a human IAP  
 CC protein sequence.  
 XX  
 XX Sequence 618 AA;  
 SQ  
 Query Match 95.9%; Score 283; DB 23; Length 618;  
 Best Local Similarity 97.9%; Pred. No. 2.9e-26;  
 Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 PEQLASAGFYVGRNDVYKFCGCCDGLRCWESGDDPWVHAHWPFRCE 48  
 DB 287 PEQLASAGFYVGRNDVYKFCGCCDGLRCWESGDDPWVHAHWPFRCE 334  
 RESULT 9  
 AAM13552  
 ID AAM13552 standard; Protein: 48 AA.  
 XX  
 XX AAM13552;  
 AC  
 XX  
 XX 22-JUL-1997 (first entry)  
 DT  
 XX  
 XX Human c-IAP2 repeat 3.  
 DE  
 XX IAP; Inhibitor; apoptosis; RING finger domain; Westinosis;  
 KW myocardial infarction; nephritis; HIV.  
 XX  
 XX Homo sapiens.  
 OS  
 XX W09706182-A1.  
 PN  
 XX 20-FEB-1997.  
 PD  
 XX 06-AUG-1996; 96WO-US12860.  
 PF  
 XX 08-DEC-1995; 95US-0569749.  
 PR 08-AUG-1995; 95US-0512946.  
 XX

PA (TULA-) TULARIK INC.  
 XX  
 XX Goeddel DV, Rothe M;  
 PI  
 XX MPI: 1997-154209/14.  
 DR  
 XX  
 XX Nucleic acids encoding cellular inhibitor of apoptosis proteins  
 PT useful for apoptosis regulation in cells to reduce or increase  
 PT apoptosis and for pharmacological screening  
 XX  
 XX Claim 3; Page 25; 35pp; English.  
 PS  
 XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -  
 CC AAM61590/761591) comprise a series of defined structural domain  
 CC repeats and/or a RING finger domain; in particular, at least two of  
 CC a first domain repeat (AAM13547 or AAM13548), a second domain repeat  
 CC (AAM13549 or AAM13550), and a third domain repeat (AAM13551 or AAM13552)  
 CC and/or a RING finger domain (AAM13553 or AAM13554), or a consensus  
 CC sequences derived from these human genes.  
 CC The nucleic acid is used for recombinant prodn. of human cellular  
 CC inhibitor of apoptosis protein which modulates apoptosis  
 CC regulation. The nucleic acids are useful in therapies where  
 CC increased cell-specific apoptosis is desired, e.g. in Westinosis,  
 CC inflammatory disease states, myocardial infarction, glomerular  
 CC nephritis, transplant rejection and infectious diseases, e.g. HIV.  
 CC They can also be used in conditions requiring a reduction in  
 CC apoptosis.  
 XX  
 XX Sequence 48 AA;  
 SQ  
 Query Match 95.6%; Score 282; DB 18; Length 48;  
 Best Local Similarity 93.8%; Pred. No. 2.7e-27;  
 Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 PEQLASAGFYVGRNDVYKFCGCCDGLRCWESGDDPWVHAHWPFRCE 48  
 DB 1 PEQLASAGFYVGRNDVYKFCGCCDGLRCWESGDDPWVHAHWPFRCE 48  
 RESULT 10  
 AAM19747  
 ID AAM19747 standard; Protein: 604 AA.  
 XX  
 XX AAM19747;  
 AC  
 XX  
 XX 16-SEP-1997 (first entry)  
 DT  
 XX  
 XX Human inhibitor of apoptosis protein homologue MIRC.  
 DE  
 XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIRC;  
 KW degenerative disease; infectious disease; autoimmune disease;  
 KW cancer; therapy; diagnosis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Region 29..97  
 FT Region /label= BIR  
 FT Region 169..236  
 FT Region /label= BIR  
 FT Region 255..323  
 FT Region /label= BIR  
 FT Region 556..593  
 FT Region /label= RING\_finger  
 PN  
 XX W09723501-A1.  
 PD  
 XX 03-JUL-1997.  
 PF  
 XX 20-DEC-1996; 96WO-AU00827.  
 PR 22-DEC-1995; 95AU-0007275.  
 XX

PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX  
XX Vaux DL;  
XX  
XX WPI, 1997-350966/32.  
DR N-PSDB; AAT72712.  
XX  
XX Isolated protein homologues of viral inhibitors of apoptosis - used  
PT to modulate apoptosis for treatment of degenerative, infectious or  
PT autoimmune diseases and cancer  
XX  
XX Claim 9; Page 58-62; 136pp; English.  
XX  
XX Mammalian IAP homologue C (MIHC) (AAW19747) is a human homologue of  
CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid  
CC sequence was deduced from a cDNA clone (see also AAT72712) isolated  
CC from a human foetal liver cDNA library using primers based on  
CC human EST sequences that resembled the BIR repeats of Oryza  
CC pseudotsuguta polyhedrosis virus IAP. IAP homologues (see also  
CC AAW19745-46 and AAW19748-52) and their derivatives and chemical  
CC analogues can be used in methods for modulating apoptosis in animal  
CC cells, specifically for treatment, by inhibition, of degenerative  
CC and infectious disease or, by promotion, of cancer and autoimmune  
CC disease.  
XX  
XX Sequence 604 AA;  
SQ  
Query Match 95.6%; Score 282; DB 18; Length 604;  
Best Local Similarity 93.8%; Pred. No. 3.7e-26;  
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 1 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAHAKWPPCE 48  
||||| :|||||  
DB 273 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAHAKWPPCE 320  
RESULT 11  
AAW19582  
ID AAW19582 standard; Protein; 604 AA.  
XX  
XX AAW19582;  
AC  
XX  
XX 02-SEP-1997 (first entry)  
DT  
XX  
XX Human apoptosis inhibitor HIAP-1.  
DE  
XX  
XX Apoptosis inhibitor; HIAP-1; HIV; AIDS; neurodegeneration;  
KW myelodysplastic syndrome; ischemia; myocardial infarction; stroke;  
KW reperfusion injury; toxin-induced liver disease; gene therapy;  
diagnosis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Domain 29..96  
FT /label= BIR-1  
FT 169..235  
FT /label= BIR-2  
FT 255..322  
FT /label= BIR-3  
FT 346..591  
FT /label= Ring\_zinc\_finger  
FT  
XX  
XX WO9706255-A2.  
PN  
XX  
XX 20-FEB-1997.  
PD  
XX  
XX 05-AUG-1996; 96WO-IB01022.  
PF  
XX  
XX 22-DEC-1995; 95US-0576956.  
PR  
XX 04-AUG-1995; 95US-0511485.  
XX  
XX (UYOT-) UNIV OTTAWA.  
PA

XX  
XX Baird S, Korneluk RG, Liston P, Mackenzie AE;  
XX  
XX WPI, 1997-154262/14.  
DR N-PSDB; AAT70837.  
XX  
XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used  
PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection  
PT of susceptibility to apoptotic disease  
XX  
XX Claim 27; Page 72-74; 219pp; English.  
XX  
XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and  
CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that  
CC are inhibitors of apoptosis (IAP) and which are characterised by  
CC the presence of a ring zinc finger domain (see also AAW19587) and at  
CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).  
CC The HIAP amino acid sequences were deduced from cDNA clones (AAT70837  
CC and AAT70838) from a human liver library. IAP polypeptides can be  
CC expressed in host cells (in vitro or in vivo) and used in methods  
CC for treating diseases and disorders involving apoptosis, esp. in a  
CC human diagnosed as HIV-positive or as having AIDS, a  
CC neurodegenerative disease, a myelodysplastic syndrome or an  
CC ischemic injury, selected from myocardial infarction, stroke,  
CC reperfusion injury, or a toxin-induced liver disease.  
XX  
XX Sequence 604 AA;  
SQ  
Query Match 95.6%; Score 282; DB 18; Length 604;  
Best Local Similarity 93.8%; Pred. No. 3.7e-26;  
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 1 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAHAKWPPCE 48  
||||| :|||||  
DB 273 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAHAKWPPCE 320  
RESULT 12  
AAW13546  
ID AAW13546 standard; Protein; 604 AA.  
XX  
XX AAW13546;  
AC  
XX  
XX 22-JUL-1997 (first entry)  
DT  
XX  
XX Human C-IAP2.  
DE  
XX  
XX IAP; inhibitor; apoptosis; RING finger domain; restinosis;  
KW myocardial infarction; nephritis; HIV.  
KW  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9706182-A1.  
PN  
XX  
XX 20-FEB-1997.  
PD  
XX  
XX 06-AUG-1996; 96WO-US12860.  
PF  
XX  
XX 08-DEC-1995; 95US-0569749.  
PR  
XX 08-AUG-1995; 95US-0512946.  
XX  
XX (TUL-) TULARIK INC.  
PA  
XX  
XX Goeddel DV, Rothe M;  
XX  
XX WPI, 1997-154209/14.  
DR N-PSDB; AAT61591.  
XX  
XX Nucleic acids encoding cellular inhibitor of apoptosis proteins  
PT useful for apoptosis regulation in cells to reduce or increase  
PT apoptosis and for pharmacological screening  
XX  
XX Disclosure; Page 21-23; 35pp; English.  
PS

XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -  
 CC AAT61590/761591) comprise a series of defined structural domain  
 CC repeats and/or a RING finger domain; in particular, at least two of  
 CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat  
 CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)  
 CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus  
 CC sequences derived from these human genes.  
 CC The nucleic acid is used for recombinant prodn. of human cellular  
 CC inhibitor of apoptosis protein which modulates apoptosis  
 CC regulation. The nucleic acids are useful in therapies where  
 CC increased cell-specific apoptosis is desired, e.g. in restinosis,  
 CC inflammatory disease states, myocardial infarction, glomerular  
 CC nephritis, transplant rejection and infectious diseases, e.g. HIV.  
 CC They can also be used in conditions requiring a reduction in  
 CC apoptosis.  
 CC  
 SQ Sequence 604 AA;  
 Query Match 95.6%; Score 282; DB 1c; Length 604;  
 Best Local Similarity 93.8%; Pred. No. 3.7e-26;  
 Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVHAHAKMPRCE 48  
 DB 273 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVHAHAKMPRCE 320  
 RESULT 13  
 ID AAW69295 standard; Protein: 604 AA.  
 AC AAW69295;  
 XX 13-NOV-1998 (first entry)  
 DT  
 DE Human HIAP-1 protein.  
 DE  
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
 KW proliferative disease; IAP; therapy; cancer; human; HIAP-1 protein.  
 OS Homo sapiens.  
 OS  
 XX WO9835693-A2.  
 PN 20-AUG-1998.  
 PD  
 XX 13-FEB-1998; 98WO-1B00781.  
 PF  
 XX 13-FEB-1997; 97US-0800929.  
 PR  
 XX (UYOT-) UNIV OTTAWA.  
 PA  
 XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;  
 PI Tsang B;  
 PI WPI: 1998-467164/40.  
 DR N-PSDB: AAV35039.  
 DR  
 XX  
 PT Inducing apoptosis in proliferative mammalian cells with inhibitor  
 PT of IAP or NAIP polypeptide - also methods for prognosis based on  
 PT presence of IAP and NAIP, specifically applied to cancers involving  
 PT p53 mutations  
 PT  
 PS Disclosure; Fig 2; 147pp; English.  
 PS  
 XX This sequence is the human HIAP-1 protein, which is a inhibitor of  
 CC apoptosis protein (IAP), and can be used in the method of the invention.  
 CC The method is for enhancing apoptosis in cells from a mammal with  
 CC proliferative disease by treatment with a compound that inhibits  
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
 CC compounds are used to treat proliferative diseases, specially cancers of  
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,

CC liver nasopharynx, thyroid, central nervous system, prostate, colon,  
 CC rectum, cervix or endometrium, particularly to increase their sensitivity  
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
 CC detected in many cancers and are associated with poor prognosis,  
 CC resistance to chemotherapeutic agents and mutations in p53 (it is  
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
 CC genes). Transgenic animals are used for testing the effects of antisense  
 CC oligonucleotides and for screening for the inhibitors.  
 CC  
 SQ Sequence 604 AA;  
 Query Match 95.6%; Score 282; DB 19; Length 604;  
 Best Local Similarity 93.8%; Pred. No. 3.7e-26;  
 Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVHAHAKMPRCE 48  
 DB 273 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVHAHAKMPRCE 320  
 RESULT 14  
 ID AAY52703 standard; Protein: 604 AA.  
 AC AAY52703;  
 XX 26-JAN-2000 (first entry)  
 DT  
 DE Human cellular inhibitor of apoptosis-2 protein.  
 DE  
 KW Identification; genetic target; gene modulation; human,  
 KW antisense oligonucleotide; phosphorothioate; target validation;  
 KW nucleotide sequence-based technology; antisense drug discovery.  
 OS Homo sapiens.  
 OS  
 XX WO9953101-A1.  
 PN 21-OCT-1999.  
 PD  
 XX 13-APR-1999; 99WO-US08268.  
 PF  
 XX 13-APR-1998; 98US-0081483.  
 PR 28-APR-1998; 98US-0067638.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Cowseart LM, Baker BF, McNeil J, Freiler SM, Saemor HM, Brooks DG;  
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;  
 DR WPI: 1999-620446/53.  
 DR N-PSDB: AAZ41005.  
 DR  
 XX  
 PT Identifying compounds which modulate expression of nucleic acids, used  
 PT to provide compounds having defined physical, chemical or bioactive  
 PT properties, e.g. antisense activity  
 PT  
 PS Example 20; Page 197-202; 264pp; English.  
 PS  
 XX A method has been developed of defining a set of compounds that modulate  
 CC the expression of a target nucleic acid (tNA) sequence via binding of  
 CC the compounds with the tNA sequence. The method comprises generating a  
 CC library of virtual compounds in silico according to defined criteria,  
 CC and evaluating in silico the binding of the virtual compounds with the  
 CC tNA according to defined criteria. Also described are: (1) a method of  
 CC defining a set of oligonucleotides (ONS) that modulate the expression of  
 CC a tNA sequence via binding of the ONS with the tNA sequence comprising  
 CC generating a library of virtual compounds in silico according to defined  
 CC criteria, and evaluating in silico the binding of the virtual ONS with  
 CC the tNA according to defined criteria; and (2) a method of defining a  
 CC set of compounds that modulate the expression of a tNA sequence via  
 CC binding of the compounds with the tNA. The methods can be used for the  
 CC generation and identification of synthetic compounds having defined

CC physical, chemical or bioactive properties. Information gathered from  
 CC assays of such compounds is used to identify nucleic acid sequences that  
 CC are tractable to a variety of nucleotide sequence-based technologies,  
 CC e.g. antisense drug discovery and target validation. AAZ40852 to  
 CC AAZ41220, and AAY52701 to AAY52706, represent sequences used in the  
 CC exemplification of the present invention.

XX  
 SQ Sequence 604 AA;

Query Match 95.6%; Score 282; DB 30; Length 604;  
 Best Local Similarity 93.8%; Pred. No. 3.7e-26;  
 Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAHAKMPFCE 48  
 |||||  
 Db 273 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAHAKMPFCE 320

RESULT 15

AY3397  
 ID AAY33997 standard; Protein; 604 AA.

AC AAY33997;

DT 26-NOV-1999 (first entry)

DE Human cellular inhibitor of apoptosis-2 sequence.

KW Cellular inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;  
 C-IAP-2; prophylaxis; infection; inflammation; tumor formation.

OS Homo sapiens.

PN US5958771-A.

PD 28-SEP-1999.

PF 03-DEC-1998; 98US-0205144.

PR 03-DEC-1998; 98US-0205144.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowser LM, Ackermann EJ;

DR WPI: 1999-561046/47.

DR N-PSDB; AAZ22096.

PT Antisense compounds complementary to Cellular inhibitor of Apoptosis-2  
 useful for e.g. diagnostics, therapeutics, and as research reagents

PS Example 13; Columns 45-50; 33pp; English.

CC The invention provides antisense compounds of 8-30 nucleotides that  
 CC inhibit the expression of human Cellular inhibitor of Apoptosis-2  
 CC (C-IAP-2). The antisense compounds may be used for diagnostics,  
 CC therapeutics (for modulating the expression of C-IAP-2), prophylaxis  
 CC (e.g. to prevent or delay infection, inflammation, or tumor formation),  
 CC as research reagents (e.g. to distinguish between members of a biological  
 CC pathway) and in kits. The present sequence represents the human cellular  
 CC inhibitor of apoptosis-2.

XX  
 SQ Sequence 604 AA;

Query Match 95.6%; Score 282; DB 30; Length 604;  
 Best Local Similarity 93.8%; Pred. No. 3.7e-26;  
 Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAHAKMPFCE 48  
 |||||  
 Db 273 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAHAKMPFCE 320

Search completed: May 5, 2003, 16:02:02  
 Job time : 10.4562 secs

GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 15:58:42 ; Search time 5.25346 Seconds

(without alignments)  
878.365 Million cell updates/sec

Title: US-08-569-749-9

Perfect score: 295

Sequence: 1 PEQLASAGFYVGRNDVRC.....CWISGDDPWVHAHAKMPRCE 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	95.9	618	2 S68450	apoptosis inhibito
2	282	95.6	358	2 JC5964	apoptosis inhibito
3	282	95.6	604	2 S68449	apoptosis inhibito
4	198	67.1	268	2 T10304	inhibitor of apopt
5	198	67.1	268	2 A53989	apoptosis-inhibiti
6	195	66.1	298	2 JC7368	kidney inhibitor o
7	183	62.0	1447	2 T42628	neuronal apoptosis
8	182	61.7	275	2 A45679	inhibitor-of-apopt
9	178	60.3	1232	2 A55478	neuronal apoptosis
10	174	59.0	497	2 S69544	apoptosis inhibito
11	156	52.9	496	2 S68452	apoptosis inhibito
12	156	52.9	497	2 S69545	apoptosis inhibito
13	119	40.3	150	2 T28409	ORF MSV248 probabl
14	118	39.8	286	2 D36828	orif13 protein - Au
15	117.5	39.0	4845	2 T31067	BIR repeat contain
16	115	39.0	292	2 T41772	TAPl orf27 - Bomby
17	111	37.6	275	2 T10310	apoptosis-inhibiti
18	110	37.3	208	2 T03183	cut17 protein - fi
19	104	35.3	997	2 T43523	apoptosis inhibito
20	100	33.9	155	2 T30489	apoptosis inhibito
21	79	26.8	155	2 T37471	apoptosis inhibito
22	77	26.1	308	2 T37474	apoptosis inhibito
23	71	24.1	234	2 T30427	probable apoptosis
24	64.5	21.9	329	2 T28403	ORF MSV242 probabl
25	64.5	21.9	772	2 D96504	protein F9C16.25.1
26	62	21.0	287	2 T05358	hypothetical prote
27	58.5	19.8	743	2 T02147	hypothetical prote
28	58	19.7	556	2 A32466	numb protein - fru
29	57.5	19.5	156	2 A48886	8-oxo-7,8-dihydrog

30	57.5	19.5	555	2 B49918	schC protein - Str
31	56.5	19.2	485	2 E89859	D-alanine-D-alanyl
32	56	19.0	65	2 A38739	metallothionein -
33	56	19.0	281	2 T13340	probable lysin - S
34	56	19.0	436	2 F88499	protein K0467.4 [1
35	55.5	18.8	703	2 T04191	hypothetical prote
36	55.5	18.8	1536	1 R6BYS3	regulatory protein
37	55	18.6	92	2 S34802	embryonic abunda
38	55	18.6	92	2 S71372	embryonic abunda
39	55	18.6	625	2 T01929	probable cellulase
40	55	18.6	954	2 S57108	hypothetical prote
41	55	18.6	3229	2 S27852	probable cell-surf
42	54.5	18.5	249	2 H72858	apoptosis inhibito
43	54.5	18.5	249	2 T41814	TAPl orf17 - Bomby
44	54.5	18.5	415	2 C71467	probable tyrosine
45	54.5	18.5	547	2 A36046	collagen alpha cha

## ALIGNMENTS

RESULT 1  
S68450  
apoptosis inhibitor hlap-2 - human  
C:Species: Homo sapiens (man)  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 21-Jul-2000  
C:Accession: S68450  
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Chertton-Horvat, G.; Faraha  
Nature 379:349-353, 1996  
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of  
A:Reference number: A58182; MUID:96149249; PMID:8552191  
A:Accession: S68450  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-618 <LIS>  
A:Cross-references: EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g1184318  
C:Function:  
A:Description: apoptotic suppressor  
C:Superfamily: RING finger homology  
C:Keywords: apoptosis; zinc finger  
F:567-611/Domain: RING finger homology <RNG>

Query Match 95.98; Score 283; DB 2; Length 618;  
Best Local Similarity 97.98; Pred. No. 1.7e-25;  
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEQLASAGFYVGRNDVRCDCGGLRCWESGDDPWVHAHAKMPRCE 48  
DB 287 PEQLASAGFYVGRNDVRCDCGGLRCWESGDDPWVHAHAKMPRCE 334

## RESULT 2

JC5964

apoptosis inhibitor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 02-Sep-2000

C:Accession: JC5964

R:Stehlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.

Biochem. Biophys. Res. Commun. 243, 827-832, 1998

A:Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (Iap)

A:Reference number: JC5964; MUID:98162622; PMID:9501011

A:Accession: JC5964

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: GB:U79142; NID:g2957174; PIDN:AAC39171.1; PID:g2957175

F:307-351/Domain: RING finger homology <RRN>

Query Match 95.68; Score 282; DB 2; Length 358;  
Best Local Similarity 93.88; Pred. No. 1.3e-25;  
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;





RESULT 8  
A:Accession: A45679  
Inhibitor of apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV  
C:Species: Cydia pomonella granulosis virus CpGV  
C>Date: 21-Sep-1993 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000  
C:Accession: A45679  
R:Crack, N.E.; Clem, R.J.; Miller, L.K.  
J. Virol. 67, 2168-2174, 1993  
A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.  
A:Reference number: A45679; MUID:93188168; PMID:8445726  
A:Accession: A45679  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-275 <CNO>  
A:Cross-references: GB:I05494; NID:g289563; PIDN:AA43835.1; PID:g289584  
A:Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBI:P127015)  
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 61.7%; Score 182; DB 2; Length 275;  
Best Local Similarity 59.6%; Pred. No. 5.3e-14;  
Matches 28; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAHKMPFRC 47  
||||| : : : : : ||||| : : : : : ||| : : : : : |||  
Db 126 PEOMADAGFYTGDKTKCFCDGGLKMDPEVPMQHVSMFDRC 172

RESULT 9  
A:Accession: A55478  
neural apoptosis inhibitory protein - human  
N:Alternate names: NAIP  
C:Species: Homo sapiens (man)  
C>Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 02-Feb-2001  
R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shuter, G.; Yaraaghi, Z.; Farahani, R.; Baird, S.  
Cell 80, 167-178, 1995  
A:Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in Ind1  
Cell 80, 167-178, 1995  
A:Reference number: A55478; MUID:95112344; PMID:7813013  
A:Accession: A55478  
A:Molecule type: mRNA  
A:Residues: 1-1232 <ROY>  
A:Cross-references: GB:U19251  
C:Genetics:  
A:Gene: GDB:SMAE, SMA  
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300  
A:Map position: 5q12.2-5q13  
C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prot  
F:94-110/Domain: transmembrane #status predicted <TM1>  
F:470-477/Region: nucleotide-binding motif A (P-loop)  
F:479-486/Domain: transmembrane #status predicted <TM2>  
F:476/Binding site: ATP (lys) #status predicted  
F:618,632,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 60.3%; Score 178; DB 2; Length 1232;  
Best Local Similarity 60.4%; Pred. No. 6.3e-13;  
Matches 29; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAHKMPFRC 48  
||||| : : : : : ||||| : : : : : ||||| : : : : : |||||  
Db 178 PCVISEAGFYTGKODVYQCFSCGCGCLGNWEGDDPWVHAHKMPFRC 225

RESULT 10  
A:Accession: S69544  
apoptosis inhibitor IAP homolog - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Nov-2000  
C:Accession: S69544; S68451  
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C.  
EMBO J. 15, 2685-2694, 1996  
A:Title: A conserved family of cellular genes related to the baculovirus IAP gene and en

A:Reference number: S69544; MUID:96256286; PMID:8654366  
A:Accession: S69544  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-497 <DDC>  
A:Cross-references: EMBL:U32974; NID:g1016687; PIDN:AAC50518.1; PID:g1016688  
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Chertion-Horvat, G.; Faraha  
Nature 379, 349-353, 1996  
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of  
A:Reference number: A58182; MUID:96149249; PMID:8552191  
A:Accession: S68451  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>  
A:Cross-references: EMBL:U45880; NID:g1184319; PIDN:AAC50373.1; PID:g1184320  
C:Genetics:  
A:Gene: ILP  
C:Function:  
A:Description: apoptotic suppressor  
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology  
C:Keywords: apoptosis; zinc finger  
F:446-490/Domain: RING finger homology <RRN>

Query Match 59.0%; Score 174; DB 2; Length 497;  
Best Local Similarity 59.6%; Pred. No. 8.1e-13;  
Matches 28; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

OY 2 EQLASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAHKMPFRC 48  
||||| : : : : : ||||| : : : : : ||| : : : : : |||  
Db 282 EQLARAGFYALGEGDKVCFHCGGGLTDMKPSDEPMQHVSMFDRC 328

RESULT 11  
A:Accession: S68452  
apoptosis inhibitor IAP - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 17-Nov-2000  
C:Accession: S68452; S78528  
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Chertion-Horvat, G.; Faraha  
Nature 379, 349-353, 1996  
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of  
A:Reference number: A58182; MUID:96149249; PMID:8552191  
A:Accession: S68452  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-496 <LIS>  
A:Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314  
R:Baird, S.D.  
submitted to the EMBL Data Library, January 1996  
A:Reference number: S78528  
A:Accession: S78528  
A:Molecule type: mRNA  
A:Residues: 1-36, 'AT', 37, 'K', 39, 'L', 41-44, 'H', 46-58, 'Q', 60-412, 'A', 414-427, 'A', 429-49  
A:Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314  
C:Genetics:  
A:Cross-references: Flybase:FBgn0015247  
C:Function:  
A:Description: apoptotic suppressor  
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology  
C:Keywords: apoptosis; zinc finger  
F:445-489/Domain: RING finger homology <RNG>

Query Match 52.9%; Score 156; DB 2; Length 496;  
Best Local Similarity 55.6%; Pred. No. 1e-10;  
Matches 25; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 4 LASAGFYVGRNDVYKCFCCDGLRCWESGDDPWVHAHKMPFRC 48  
||||| : : : : : ||||| : : : : : ||||| : : : : : |||||  
Db 231 LAQAGLYTQKIGDVRCHFCNIGLRSMQKEDPWVHAHKMPFRCQ 275

RESULT 12  
A:Accession: S69545

A:apoptosis inhibitor iap homolog - fruit fly (*Drosophila melanogaster*)  
 C:Species: *Drosophila melanogaster*  
 C>Date: 06-dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
 C/Accession: S69545  
 R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gillfillan, M.C.  
 EMBL J. 15, 2685-2694, 1996  
 A:Title: A conserved family of cellular genes related to the baculovirus iap gene and enhancer  
 A:Reference number: S69544; MUID:56256286; PMID:8654366  
 A:Accession: S69545  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-497 <DDCC>  
 A:Cross-references: EMBL:U32373; NID:g1019116; PIDN:AAC47155.1; PID:g1019117  
 C:Genetics:  
 A:Gene: i1p  
 C:Superfamily: apoptosis inhibitor iap homolog; RING finger homology  
 F:446-490/Domain: RING finger homology <RRN>

Query Match	52.9%;	Score 156;	DB 2;	Length 497;
Best Local Similarity	55.6%;	Pred. NO. 1e-10;		
Matches 25; Conservative	6;	Mismatches 14;	Indels 0;	Gaps 0;

QY 4 LASAGFYVGRNDVKKFCDCDGLRCWESGDDPVEHAKWIPRCE 48  
 || || || | : || | : || || || || || : ||  
 Db 233 LAQAGLYYQKIGDQVRCFHCNIGRLSRWQEKDEPVEHAKWSPKCQ 277

RESULT 13

C:Species: Melanoplus sanguinipes entomom  
C:Date: 21-Jan-2000 #sequence=revision 21-Jan 2000 #text\_change 21-Jul-2000  
C:Date: 21-Jan-2000

R; Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.  
 1990 73 533-553

A:Reference number: 220484: MIRD-99103613: BMTD-9847350  
A:Title: The genome of *Melanoplus sanguinipes* entomopoxvirus.

A:Status: preliminary: translated from GB/EMBL/DBJ

A; Residues: 1-150 <AFO>

C:Genetics: MED:AF000000, NID:g404504/, FIDN:AA31/24.1; FID:g4045/04

**A;Note: MSV248**

Query Match	40.38; Score 119; DB 2; Length 150;
-------------	-------------------------------------

Matches 19; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

```
QY      3 QLASAGFYVGRNDVYKCFCCDDGLRCWESGDDPWEVHAKEIPRC 47
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      36 RLCEAGFFYTNIGDITVCFNCGLKIKNMLYYNDPWIEHKSWSIPNC 80
```

RESULT 14

orf13 protein - Autographa californica nuclear polyhedrosis virus

C:\Accession: D36828: C72853

K; Brauhage, S.C.; Daniel, K.D.; Kelly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D. *Virology* 191, 1003-1008, 1992

a, i.e., sequence, genomic organization or the EcoRI-A fragment of Autographa californica VP8 of rotavirus.

A;Accession: D36828

A;Molecule type: DNA

A;Cross-references: GB:552569

Virology 202, 586-605, 1994

A: Reference number: A72850; MUID:94303173; PMID:8030224

A;Status: preliminary

A;Residues: 1-199, 'L', 201-286 <AYR>

C:Genetics:  
A:Gene: Ac-TAP1

C; Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 40.0%; Score 118; DB 2; Length 200;  
Best Local Similarity 43.2%; Pred. No. 1.8e-06;  
Matches 19; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

**QY**      4    LASAGFYTVGRNDVXKCFCCDGGSLRCWESGDDPWEVEHAKWFPRC    47  
         : | | | | | | : | | | | | | : | | | | | |  
**Db**     153   IAEAGLFYTGRGDEIVCFPCDCCVRDWHHTNEDTWQRHAALNPQC    196

RESULT 15  
T31067

C:Species: Mus musculus (house mouse)  
BIR repeat containing ubiquitin-conjugating enzyme BRUCE - mouse

C:Accession: T31067  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000

J. Cell Biol. 141, 1415-1422, 1998

A;Reference number: Z20963; MUID:98292517; PMID:9628897

A; Status: preliminary; translated from GB/EMBL/DBJ

A;Residues: 1-4845 <HAU>

A; Note: localized to the Golgi compartment and the vesicular system

[illegible]

Query Match	39.8%;	Score 117.5;	DB 2;	Length 4845;
Best Local Similarity	42.0%;	Pred. No. 2.7e-05;		
Matches 21; Conservative	6;	Mismatches 20;	Indels 3;	Gaps 1;

```

QY      1  PEQLASAGFY--VGRNDYKCFCCDGLRCWESDDPWVEHAKWPRC 47
      1 : : : : : : : : : : : : : : : : : : : : : :
Db     281  PDPMAAGFYHQPASSGDDRAMCFCTCSVCLVCWEPTDEPWEHERHSPNC 330

```

Search completed: May 5, 2003, 16:08:13  
Job time : 7.25346 secs

Tue May 6 18:23:53 2003

us-08-569-749-9.rpr

Page 4

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:02:07 ; Search time 5.91705 Seconds

(without alignments)  
699,970 Million cell updates/sec

Title: US-08-569-749-9

Sequence: 1 PSQLASAGYVYGRNDVYKC.....CHESGDDPVYENAKFPKCE 48

Scoring table: BLOSUM62

Searched: 328255 seqs, 8628685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications: AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	295	100.0	438 1	US-08-464-588-2 Sequence 2, Appl1
2	283	95.9	68 9	US-09-201-936-27 Sequence 27, Appl1
3	283	95.9	618 9	US-09-201-936-8 Sequence 8, Appl1
4	283	95.9	618 10	US-09-974-592-8 Sequence 8, Appl1
5	282	95.6	68 9	US-09-201-936-26 Sequence 26, Appl1
6	282	95.6	604 9	US-09-201-936-6 Sequence 6, Appl1
7	282	95.6	604 10	US-09-974-592-6 Sequence 14, Appl1
8	282	95.6	612 10	US-09-974-592-14 Sequence 14, Appl1
9	276	93.6	591 9	US-09-201-936-42 Sequence 42, Appl1
10	268	90.8	600 10	US-09-974-592-12 Sequence 12, Appl1
11	262	88.8	602 9	US-09-201-936-40 Sequence 40, Appl1
12	198	67.1	68 9	US-09-201-936-28 Sequence 28, Appl1
13	198	67.1	68 9	US-10-041-859-18 Sequence 18, Appl1
14	198	67.1	172 9	US-10-041-859-12 Sequence 12, Appl1
15	192	65.1	68 9	US-10-041-859-14 Sequence 14, Appl1
16	192	65.1	172 9	US-10-041-859-8 Sequence 8, Appl1
17	192	65.1	346 9	US-10-041-859-2 Sequence 16, Appl1
18	189	64.1	68 9	US-10-041-859-16 Sequence 16, Appl1
19	189	64.1	172 9	US-10-041-859-10 Sequence 10, Appl1

#### ALIGNMENTS

US-08-464-588-2	Sequence 2, Appl1	US-10-041-859-15	Sequence 15, Appl1	
188	63.7	68 9	US-10-041-859-9	
21	188	63.7	68 9	US-09-201-936-29
22	182	61.7	68 9	US-10-041-859-17
23	182	61.7	172 9	US-10-041-859-11
24	182	61.7	172 9	US-09-201-936-12
25	182	61.7	275 9	US-08-913-322-22
26	178	60.3	1403 8	US-08-913-322-24
27	178	60.3	1403 8	US-09-201-936-25
28	174	59.0	66 9	US-09-201-936-20
29	174	59.0	107 9	US-09-965-967-30
30	174	59.0	278 9	US-09-964-899-39
31	174	59.0	497 9	US-09-201-936-4
32	174	59.0	497 10	US-09-974-592-4
33	160	54.2	66 9	US-09-201-936-24
34	160	54.2	68 9	US-10-041-859-19
35	160	54.2	109 9	US-09-965-967-30
36	160	54.2	172 9	US-10-041-859-13
37	160	54.2	496 9	US-09-201-936-10
38	160	54.2	496 10	US-09-974-592-10
39	159	53.9	68 9	US-09-201-936-20
40	156	52.9	68 9	US-09-201-936-21
41	156	52.9	68 9	US-09-201-936-30
42	156	52.9	110 9	US-09-965-967-21
43	156	52.9	498 9	US-09-201-936-13
44	144	48.8	67 9	US-09-201-936-14
45	142	48.1	67 9	US-09-201-936-23

RESULT 1  
US-08-464-588-2  
Sequence 2, Appl1  
Publication No. US20030073159A1

GENERAL INFORMATION:  
APPLICANT: HE. ET AL.  
TITLE OR INVENTION: Human Inhibitor of Apoptosis Gene 1  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARBILLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,588  
FILING DATE: June 5, 1995  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05922  
FILING DATE: 11 MAY 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1744  
TELEFAX: 201-994-1744

INFORMATION FOR SEQ. ID NO. 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 438 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN

US-08-464-588-2

Query Match 100.0%; Score 295; DB 1; Length 438;  
Best Local Similarity 100.0%; Pred. No. 1.2e-26;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVCKCFCGCGGLRCWESGDDPWEHAKWPPRCE 48  
DB 107 PEOLASAGFYVGRNDVCKCFCGCGGLRCWESGDDPWEHAKWPPRCE 154

RESULT 2

US-09-201-936-27  
Sequence 27, Application US/09201936  
Publication No. US20020187946A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
APPLICANT: Liston, Peter  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
CURRENT FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 27  
LENGTH: 68  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-201-936-27

Query Match 95.9%; Score 283; DB 9; Length 68;  
Best Local Similarity 97.9%; Pred. No. 4.8e-26;  
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVCKCFCGCGGLRCWESGDDPWEHAKWPPRCE 48  
DB 19 PEOLASAGFYVGRNDVCKCFCGCGGLRCWESGDDPWEHAKWPPRCE 66

RESULT 3

US-09-201-936-8  
Sequence 8, Application US/09201936  
Publication No. US20020187946A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
APPLICANT: Liston, Peter  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
CURRENT FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 8  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-201-936-8

Query Match 95.9%; Score 283; DB 9; Length 618;  
Best Local Similarity 97.9%; Pred. No. 4.1e-25;  
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVCKCFCGCGGLRCWESGDDPWEHAKWPPRCE 48  
DB 287 PEOLASAGFYVGRNDVCKCFCGCGGLRCWESGDDPWEHAKWPPRCE 334

RESULT 4

US-09-974-592-8  
Sequence 8, Application US/09974592  
Patent No. US20020120121A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratl, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 07891/009004  
CURRENT APPLICATION NUMBER: US/09/974,592  
CURRENT FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: US 09/617,053  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-974-592-8

Query Match 95.9%; Score 283; DB 10; Length 618;  
Best Local Similarity 97.9%; Pred. No. 4.1e-25;  
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVCKCFCGCGGLRCWESGDDPWEHAKWPPRCE 48  
DB 287 PEOLASAGFYVGRNDVCKCFCGCGGLRCWESGDDPWEHAKWPPRCE 334

RESULT 5

US-09-201-936-26  
Sequence 26, Application US/09201936  
Publication No. US20020187946A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
APPLICANT: Liston, Peter  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
CURRENT FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956

```

FILE REFERENCE: 07891/009004
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 604
TYPE: PRT
ORGANISM: Homo sapiens
US-09-974-592-6

Query Match          95.6%; Score 282; DB 10; Length 604;
Best Local Similarity 92.8%; Pred. No. 5.2e-25;
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1  PEOLASAGFYVGRNDVYKFCFCDDGLRCWESGDDPWVHAHAKPFRC 48
        |||.....:|||||.....:|||||.....:|||||.....:
Db      273  PEOLASAGFYVGRNDVYKFCFCDDGLRCWESGDDPWVHAHAKPFRC 320

RESULT 8
US-09-974-592-14
Sequence 14, Application US/09974592
Patent No. US20020120121A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009004
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 612
TYPE: PRT
ORGANISM: Mus musculus
US-09-974-592-14

Query Match          95.6%; Score 282; DB 10; Length 612;
Best Local Similarity 92.8%; Pred. No. 5.3e-25;
Matches 45; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  PEOLASAGFYVGRNDVYKFCFCDDGLRCWESGDDPWVHAHAKPFRC 48
        |||.....:|||||.....:|||||.....:|||||.....:
Db      280  PEOLASAGFYVGRNDVYKFCFCDDGLRCWESGDDPWVHAHAKPFRC 327

RESULT 9
US-09-201-936-42
Sequence 42, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS

```

```
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 42
LENGTH: 591
TYPE: PRT
ORGANISM: Mus musculus
US-09-201-936-42
```

```
Query Match          93.6%; Score 276; DB 9; Length 591;
Best Local Similarity 91.7%; Pred. No. 2.5e-21;
Matches 44; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 PQLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 48
Db 259 PQLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 306
```

```
RESULT 10
US-09-974-592-12
Sequence 12, Application US/09974592
Patent No. US20020120121A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009004
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 600
TYPE: PRT
ORGANISM: Mus musculus
US-09-974-592-12
```

```
Query Match          90.8%; Score 268; DB 10; Length 600;
Best Local Similarity 89.4%; Pred. No. 2.2e-23;
Matches 42; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 2 EQLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 48
Db 272 EQLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 318
```

```
RESULT 11
US-09-201-936-40
Sequence 40, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
```

```
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 40
LENGTH: 602
TYPE: PRT
ORGANISM: Mus musculus
US-09-201-936-40
```

```
Query Match          88.8%; Score 262; DB 9; Length 602;
Best Local Similarity 87.2%; Pred. No. 1.1e-22;
Matches 41; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 2 EQLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 48
Db 274 EQLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 320
```

```
RESULT 12
US-09-201-936-28
Sequence 28, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 68
TYPE: PRT
ORGANISM: Oryzias pseudotsugata
US-09-201-936-28
```

```
Query Match          67.1%; Score 198; DB 9; Length 68;
Best Local Similarity 60.4%; Pred. No. 3.6e-16;
Matches 29; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
```

```
Qy 1 PQLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 48
Db 19 PQLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 66
```

```
RESULT 13
US-10-041-859-18
```

```
; Sequence 18, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 68
; TYPE: PRN
; ORGANISM: Orgyia pseudotsugata
US-10-041-859-18
```

```
Query Match 67.1%; Score 198; DB 9; Length 68;
Best Local Similarity 60.4%; Pred. No. 3.6e-16;
Matches 29; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
```

```
OY 1 PEOLASAGFYVGRNDVYKCCDGLRCWESGDDPWVEHAKWPPRC 48
||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 19 PEELAEAGFYTGQDKTRCFCDDGLKDWESDVPWQHARWYDRCE 66
```

## RESULT 14

```
US-10-041-859-12
; Sequence 12, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRN
; ORGANISM: Orgyia pseudotsugata
US-10-041-859-12
```

```
Query Match 67.1%; Score 198; DB 9; Length 172;
Best Local Similarity 60.4%; Pred. No. 8.9e-16;
Matches 29; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
```

```
OY 1 PEOLASAGFYVGRNDVYKCCDGLRCWESGDDPWVEHAKWPPRC 48
||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 86 PEELAEAGFYTGQDKTRCFCDDGLKDWESDVPWQHARWYDRCE 133
```

## RESULT 15

```
US-10-041-859-14
; Sequence 14, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
```

```
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 68
; TYPE: PRN
; ORGANISM: Bombyx mori
US-10-041-859-14
```

```
Query Match 65.1%; Score 192; DB 9; Length 68;
Best Local Similarity 63.8%; Pred. No. 1.8e-15;
Matches 30; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
```

```
OY 1 PEOLASAGFYVGRNDVYKCCDGLRCWESGDDPWVEHAKWPPRC 47
||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 19 PEELAEAGFYTGQDKTRCFCDDGLKDWESDVPWQHARWYDRCE 65
```

Search completed: May 5, 2003, 16:11:07  
Job time : 6.91705 secs





```

CC -1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
CC -1- PROCESS.
CC -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
CC -1- SIMILARITY: MEMBER OF THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF
CC -1- APOPTOSIS PROTEIN REPEAT).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL: AF048592; AAB88044.1; -.
DR HSSP: Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; CARD; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS01043; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR Apoptosis: Zinc-finger; Repeat.
FT REPEAT 30 97 BIR_REPEAT 1.
FT REPEAT 176 242 BIR_REPEAT 2.
FT REPEAT 262 329 BIR_REPEAT 3.
FT ZN_FING 563 597 C3HC4-TYPE.
SQ SEQUENCE 610 AA; 68924 MW; ADF47619650B44A6 CRC64;

Query Match 98.3%; Score 290; DB 13; Length 610;
Best Local Similarity 95.8%; Pred. No. 3,4e-30;
Matches 46; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASGFYVGRNDVKCFCDGGLNCWESGDDPWVHAHAKWPPRCE 48
Db 280 PEQLADAGFYVGRNDVDKCFCDGGLNCWESGDDPWIEHAHAKWPPRCE 327
|||||
|||||

RESULT 4
ID Q8UWD2 PRELIMINARY; PRT; 628 AA.
AC Q8UWD2;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Iap1.
GN IAP1.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
CX NCBI_TaxID=7955;
[1]
RN R.
RP R.
RX MEDLINE=20373792; PubMed=10917738;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.".
RL Cell Death Differ. 7:509-510(2000).
[2]
RN R.
RP R.
RX Iochana N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AF442500; AAL3679.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; CARD; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN.2.

```



Db 273 PQLASAGFYVYTHGSHDDVKCFCCDGLRCWESGDDPWVEHAKWPRCE 320

## RESULT 8

09DDN2 PRELIMINARY; PRT; 324 AA.  
AC 09DDN2;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Apoptosis inhibitor ch-IAP1 (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pendleton C.N., Bargmann W.J., Varadarajan J., Bose H.R. Jr.;  
RT "The apoptosis inhibitor ch-IAP1 is a direct transcriptional target of  
v-Rel and c-Rel."  
RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AF311289; AAC42316.1; -  
DR HSSP: Q13490; 10BH.  
DR InterPro: IPR001370; BIR.  
DR Pfam: PF00653; BIR; 3.  
DR SMART: SM00238; BIR; 3.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.  
DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
FT NON\_TER 324  
SQ SEQUENCE 324 AA; 36567 MW; 5E2B89DEAE3733F3 CRC64;

Query Match 91.9%; Score 271; DB 13; Length 324;  
Best Local Similarity 95.6%; Pred. No. 5.8e-28;  
Matches 43; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PQLASAGFYVYGRNDVVKCFCCDGLRCWESGDDPWVEHAKWPR 45  
Db 280 PQLADAGFYVYGRNDVVKCFCCDGLRCWESGDDPWVEHAKWPR 324

## RESULT 9

0921NO PRELIMINARY; PRT; 374 AA.  
AC 0921NO;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Similar to baculoviral IAP repeat-containing 2.  
GN BIRC2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC011338; AAH11338.1; -  
DR MGD: MGI:1197007; Birc2.  
DR InterPro: IPR001370; BIR.  
DR Pfam: PF00653; BIR; 3.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; UNKNOWN\_3.  
DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
SQ SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7E46F3 CRC64;

Query Match 90.8%; Score 268; DB 11; Length 374;  
Best Local Similarity 89.4%; Pred. No. 1.7e-27;  
Matches 42; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 EQLASAGFYVYGRNDVVKCFCCDGLRCWESGDDPWVEHAKWPRCE 48  
Db 272 QELASAGFYVYTHGSHDDVKCFCCDGLRCWESGDDPWVEHAKWPRCE 318

## RESULT 10

088642 PRELIMINARY; PRT; 224 AA.  
AC 088642;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Inhibitor of apoptosis protein (Fragment).  
GN R1AP1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-WISTAR; TISSUE-OVARY;  
RA Bradley C.K., Lareu R.R., Dharmarajan A.M.;  
RT "Cloning and characterisation of an inhibitor of apoptosis protein  
(IAP) in the rat corpus luteum."  
RT Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AF081503; AAC32497.1; -  
DR HSSP: Q13490; 10BH.  
DR InterPro: IPR001370; BIR.  
DR Pfam: PF00653; BIR; 3.  
DR SMART: SM00238; BIR; 2.  
DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
FT NON\_TER 224  
SQ SEQUENCE 224 AA; 25209 MW; 213A52534D5EB56A CRC64;

Query Match 70.8%; Score 209; DB 11; Length 224;  
Best Local Similarity 91.9%; Pred. No. 6.8e-20;  
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PQLASAGFYVYGRNDVVKCFCCDGLRCWESGDDPW 37  
Db 188 PQLASAGFYVYGRNDVVKCFCCDGLRCWEPDDPW 224

## RESULT 11

09EN27 PRELIMINARY; PRT; 264 AA.  
AC 09EN27;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE AMV021.  
GN AMV021.  
OS Amsacta moorei entomopoxvirus (AmePV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;  
OC Entomopoxvirus B.  
OX NCBI\_TaxID=28321;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-20396580; PubMed-10936094;  
RA Bawden A.L., Glassberg K.J., Digians J., Shaw R., Farmerie W.,  
Moyer R.W.;  
RT "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:  
Analysis and Comparison with Other Poxviruses."  
RT Virology 274:120-139(2000).  
RL [2]  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Bawden A.L., Glassberg K.J., Digians J., Shaw R., Farmerie W.,  
Moyer R.W.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF250284; AAG02727.1; -  
DR HSSP: Q13490; 10BH.  
DR InterPro: IPR001370; BIR.  
DR Pfam: PF00653; BIR; 2.  
DR SMART: SM00238; BIR; 2.

QY 2 EQLASAGFYVYGRNDVVKCFCCDGLRCWESGDDPWVEHAKWPRCE 48  
Db 272 QELASAGFYVYTHGSHDDVKCFCCDGLRCWESGDDPWVEHAKWPRCE 318

```

DR SMART; SMO0184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
SO SEQUENCE 264 AA; 30547 MW; 2EB72DA4B5B0920A CRC64;

Query Match
Best Local Similarity 67.1%; Score 198; DB 13; Length 264;
Matches 29; Conservative 10; Mismatches 8; Indels 0; Gaps 0.

OY 2 POLASAGFYVGRNDVYKFCFCCDGLRCWESGDDPWVEHAKWPPRCE 48
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 126 EKLAEGFFYTGKSDVKVCKFYCDGLNKWETDDDPWIOHAKMFDCD 172

RESULT 12
O9HAP7 PRELIMINARY; PRT; 280 AA.
O9HAP7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Livin inhibitor of-apoptosis (inhibitor of apoptosis) (BA261N11.1.1)
DE (Baculoviral IAP repeat-containing protein 7 (Livin), isoform 1).
DE LYLVIN OR BIRC7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_taxid:9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Kasof G.M., Gomes B.C.;
RT "Livin, a novel inhibitor-of-apoptosis (IAP) family member.";
RL J. Biol. Chem. 0:0-0(2000).
LN (2)
LN SEQUENCE FROM N.A.
RP Asnash Y., Allan A., Pollack A., Panet A., Ben-Yehuda D.;
RT "Two splicing variants of a new inhibitor of apoptosis gene with
RT different biological properties and tissue distribution pattern.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
LN (3)
LN SEQUENCE FROM N.A.
RP Hall R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF311388; AAC333622.1; -
DR EMBL; AJ309298; CAC37337.1; -
DR EMBL; AL121827; CAC36112.1; -
DR HSSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SMO0238; BIR; 1.
DR SMART; SMO0184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; zf_RING_1; UNKNOWN_1.
KW Zinc-finger.
SQ SEQUENCE 280 AA; 30865 MW; 630BE9C0737F7952 CRC64;

Query Match
Best Local Similarity 66.1%; Score 195; DB 4; Length 280;
Matches 30; Conservative 7; Mismatches 11; Indels 0; Gaps 0.

OY 1 POLASAGFYVGRNDVYKFCFCCDGLRCWESGDDPWVEHAKWPPRCE 48
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 105 PELLAAAGFFHTGHODKYKCFYCYGGLGWSKNGDDPWIEHAKWPPSCQ 152

RESULT 13
O9H2A8 PRELIMINARY; PRT; 298 AA.
O9H2A8;
AC Q9H2A8;

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GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=KIDNEY;
RA Lin J.-H., Dang G., Huang Q., Morser J.;
RT "A Novel member of the inhibitor of apoptosis protein family.";
RL Blochem. Biophys. Res. Commun. 0.0-0(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Ashbab Y., Allan A., Pollack A., Panet A., Ben-Yehuda D.;
RT "Two splicing variants of a new inhibitor of apoptosis gene with
different biological properties and tissue distribution pattern.";
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Hall R.;
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF301009; AAC37878.1; -
DR EMBL; AJ309298; CAC37338.1; -
DR EMBL; AL121827; CAC36111.1; -
DR HSSP; O13490; 10BH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; ZnF_fing.
DR Pfam; PF00653; BIR_1.
DR Pfam; PF00097; Zf-C3HC4; 1.
DR SMART; SMO0238; BIR_1.
DR SMART; SMO0184; RING_1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; UNKNOWN_1.
KW Zinc-finger.
SQ SEQUENCE 298 AA; 32798 MW; B2EAAEE531BEC101 CRC64;

Query Match 66.1%; Score 195; DB 4; Length 298;
Best Local Similarity 62.5%; Pred. No. 6.7e-18;
Matches 30; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 PEOLASGEFYVGRNDVKCFCCDGLRCWESGDDPNVEHAKWPFRCE 48
   |||::|||::| | | :||| ||| :: |||| ||||||| :
DB 105 PELLAAAGFFHHGHODKYRCFCYCGLGSWMKRGGDPWEHAKWPFSCQ 152

RESULT 14
O96CA5 PRELIMINARY; PRT; 298 AA.
AC O96CA5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to baculoviral IAP repeat-containing 7 (Iivln) .
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; BC014475; AAAH4475.1; -
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; ZnF_fing.
```



GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:51:32 ; Search time 1.99078 Seconds

(without alignments)  
1000.040 Million cell updates/sec

Title: US-08-569-749-9

Perfect score: 295  
Sequence: 1 PEQLASAGFYVGRNDVYC.....CWESGDPEVWEHAKWPRCE 48

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 45 summaries

Database : SwissProt\_40:\*

Prod. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	295	100.0	618	1	BIR3_HUMAN
2	290	98.3	611	1	BIR1_CHICK
3	282	95.6	358	1	PIAP_PIG
4	282	95.6	604	1	BIR2_HUMAN
5	282	95.6	612	1	BIR2_MOUSE
6	268	90.8	600	1	BIR2_MOUSE
7	198	67.1	298	1	IAP3_NPVOP
8	195	66.1	268	1	BIR7_HUMAN
9	187	63.4	1403	1	BIRF_MOUSE
10	186	63.1	1402	1	BIRG_MOUSE
11	186	63.1	1403	1	BIRA_MOUSE
12	186	63.1	1403	1	BIRE_MOUSE
13	183	62.0	1447	1	BIRB_MOUSE
14	182	61.7	275	1	IAP_GVCP
15	178	60.3	1403	1	BIRL_HUMAN
16	174	59.0	496	1	BIR4_MOUSE
17	174	59.0	496	1	BIR4_RAT
18	174	59.0	497	1	BIR4_HUMAN
19	171	58.0	236	1	BIR8_HUMAN
20	171	58.0	236	1	BIR8_PANTR
21	170	57.6	236	1	BIR8_MOUSE
22	160	54.2	438	1	IAP1_DROME
23	156	52.9	498	1	IAP2_DROME
24	118	40.0	286	1	IAP1_NPVAC
25	117.5	39.8	4829	1	BIR6_HUMAN
26	111	37.6	275	1	IAP1_NPVOP
27	110	37.3	239	1	ZEP_IRV6
28	104	35.3	997	1	BIRL_SCHPO
29	90.5	30.7	140	1	BIR5_MOUSE
30	90.5	30.7	142	1	BIR5_RAT
31	87.5	29.7	142	1	BIR5_HUMAN
32	67.5	22.9	224	1	IAPL_ASFB7
33	65.5	22.2	224	1	IAPL_ASFMI

34	61.5	20.8	224	1	IAPL_ASFC3	011451 african swi
35	61.5	20.8	224	1	IAPL_ASFCH	012407 african swi
36	61.5	20.8	238	1	IAPL_ASFM2	011452 african swi
37	58.5	19.8	1173	1	TSP1_XENLA	P35448 xenopus lae
38	58	19.7	68	1	MT_LYMP1	002033 lytechinus
39	58	19.7	556	1	NUMB_DROME	P16554 drosophila
40	57.5	19.5	556	1	80DP_HUMAN	P36539 homo sapien
41	57.5	19.5	555	1	HYDL_STRHA	Q05355 streptomyce
42	57	19.3	1004	1	PO1L_SCICO	Q03377 sclara copr
43	56	19.0	65	1	MTB_STRPU	Q27287 strongyloce
44	55.5	18.8	1202	1	JAG2_RAT	P97607 rattus norv
45	55.5	18.8	1247	1	JAG2_MOUSE	Q9qye5 mus musculu

## ALIGNMENTS

RESULT 1  
BIR3\_HUMAN STANDARD; PRT; 618 AA.  
ID BIR3\_HUMAN  
AC Q13490; Q16516;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis protein 2) (HIAP2) (HIAP-2) (C-IAP1) (TNFR2-TRAF signaling complex protein 2) (BIR3 OR API2 OR IAP2 OR MIH3).  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-96128127; PubMed-8548810;  
RT Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;  
RT "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral-inhibitor of apoptosis proteins.";  
RT Cell 83:1243-1252(1995);  
RN [2]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-96149249; PubMed-8552191;  
RT Liston P., Roy N., Ramal K., Lefebvre C., Baird S., Cherton-Horvat G., Farhant R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";  
RT Nature 379:349-353(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA TISSUE-Petal liver;  
RC MEDLINE-96209843; PubMed-8643514;  
RT Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";  
RT Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA TISSUE-Uterus;  
RC Strausberg R.;  
RT Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP STRUCTURE BY NMR OF 266-363.  
RA MEDLINE-99332054; PubMed-10404221;  
RT Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;  
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP) repeat.";  
RL Nat. Struct. Biol. 6:648-651(1999).  
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

```
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
CC LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/BIRC3IPD239.html".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L49431; AAC41942.1; -
DR EMBL: U45879; AAC50372.1; -
DR EMBL: U37547; AAC50508.1; -
DR EMBL: BC016174; AAH16174.1; -
DR PDB: 1OBI; 20-OCT-99.
DR Gene: HGNC:590; BIRC2.
DR MIM: 601721; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger; Repeat; 3D-structure.
DR REPEAT 46 113 BIR 1.
DR REPEAT 184 250 BIR 2.
DR REPEAT 269 336 BIR 3.
DR DOMAIN 453 543 CARD.
DR ZN_FING 571 606 CARD.
DR CONFLICT 157 157 S -> P (IN REF. 2).
DR CONFLICT 308 308 C -> G (IN REF. 2).
DR CONFLICT 414 414 Q -> L (IN REF. 2).
DR CONFLICT 514 514 L -> W (IN REF. 2).
DR SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

Query Match 100.0%; Score 295; DB 1; Length 618;
Best local Similarity 100.0%; Pred. No. 5,6e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEOLASGFYVGRNDVKFCFCCDGLRCWESGDDPWVEHAKWFPFCE 48
DB 287 PEOLASGFYVGRNDVKFCFCCDGLRCWESGDDPWVEHAKWFPFCE 334

RESULT 2
ID BIR_CHICK STANDARD; PRT; 611 AA.
AC 090660;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis
DE protein).
```

```
GN IYA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Spleen;
RX MEDLINE=97101112; PubMed=8945639;
RA Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT "IYA, a vertebrate homologue of IAP that is expressed in T
RT lymphocytes.";
RL DNA Cell Biol. 15:981-988(1996).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.
CC -1- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN
CC BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.
CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF
CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U37466; AAB48118.1; -
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger; Repeat; Nuclear protein.
DR REPEAT 30 97 BIR 1.
DR REPEAT 176 242 BIR 2.
DR REPEAT 262 329 BIR 3.
DR DOMAIN 446 536 CARD.
DR ZN_FING 564 599 RING-TYPE.
DR SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;

Query Match 98.3%; Score 290; DB 1; Length 611;
Best local Similarity 95.8%; Pred. No. 2,3e-28;
Matches 46; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASGFYVGRNDVKFCFCCDGLRCWESGDDPWVEHAKWFPFCE 48
DB 280 PEOLASGFYVGRNDVKFCFCCDGLRCWESGDDPWVEHAKWFPFCE 327

RESULT 3
ID PIAP_PIG STANDARD; PRT; 358 AA.
AC 062640;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
```



DE Putative inhibitor of apoptosis.  
 GN PIAP.  
 OS Sus scrofa (pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Aorta.  
 RX MEDLINE=96162622; PubMed=9501011;  
 RA Stehlik C., de Martin R., Binder B.R., Lipp J.;  
 RT "Cytokine induced expression of porcine inhibitor of apoptosis  
 protein (Iap) family member is regulated by NF-kappa B.";  
 RL Blochem. Biophys. Res. Commun. 243:827-832(1998).  
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -----  
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 CC -----  
 DR EMBL: U79142; AAC39171.1; -  
 DR HSSP: Q13490; IOBH.  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR001841; Znf\_ring.  
 DR Pfam: PF00097; zf\_C3HC4; 1.  
 DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00653; BIR; 2.  
 DR SMART: SM00238; BIR; 2.  
 DR SMART: SM00184; CARD; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 2.  
 DR PROSITE: PS50209; CARD; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 DR Apoptosis; zinc-finger; Repeat.  
 FT REPEAT 4 70 BIR 1.  
 FT REPEAT 90 157 BIR 2.  
 FT DOMAIN 193 283 CARD.  
 FT ZN\_FING 311 346 RING-TYPE.  
 SQ SEQUENCE 358 AA; 40977 MM; EB2268FA9A6190A4 CRC64;  
 Query March 95.6%; Score 282; DB 1; Length 358;  
 Best Local Similarity 93.8%; Pred. No. 1.3e-27;  
 Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 PEOLASAGFYVGRNDYKCCDGLRCWESGDDPWYEHAKVPRCE 48  
 Db 108 PEOLASAGFYVGRNDYKCCDGLRCWESGDDPWYEHAKVPRCE 155  
 RESULT 4  
 BIR2\_HUMAN STANDARD: PRT; 604 AA.  
 AC Q13489; O16628; Q9DP46; Q9HC2;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Baculoviral IAP repeat-containing protein 1 (inhibitor of apoptosis  
 DE protein 1) (HIA1) (HRA1) (C-IAP2) (TNFR2-TRAF signaling complex  
 DE protein 1) (IAP homolog C)  
 GN BIRC2 OR API1 OR IAP1 OR MHC.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96128127; PubMed=8548810;  
 RA Roche M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;  
 RT "The TNFR2-TRAF signaling complex contains two novel proteins related  
 RT to baculoviral inhibitor of apoptosis proteins.";  
 RL Cell 83:1243-1252(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Liver;  
 RX MEDLINE=96149249; PubMed=8552191;  
 RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertov-Horvat G.,  
 RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
 RT "Suppression of apoptosis in mammalian cells by NAIP and a related  
 RT family of IAP genes.";  
 RL Nature 379:349-353(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Fetal liver;  
 RX MEDLINE=96209843; PubMed=8643514;  
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls R.L., Vaux D.L.;  
 RA Horroverts A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,  
 RA ten Cate J.W., Pannekoek H.;  
 RT "Vascular endothelial genes that are responsive to tumor necrosis  
 RT factor-alpha in vitro are expressed in atherosclerotic lesions,  
 RT including inhibitor of apoptosis protein-1, stannin, and two novel  
 RT genes.";  
 RL Blood 93:3418-3431(1999).  
 RN [5]  
 RP SEQUENCE OF 362-441 FROM N.A.  
 RX MEDLINE=20519161; PubMed=11066071;  
 RA Baens M., Steyis A., Dierlamm J., De Wolf-Peters C., Marynen P.;  
 RT "Structure of the MALT gene and molecular characterization of the  
 RT B-cell lymphomas of MALT type.";  
 RL Genes Chromosomes Cancer 29:281-291(2000).  
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
 CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
 CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
 CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
 CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions  
 CC inhibit apoptotic suppressor activity.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN  
 CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,  
 CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.  
 CC -1- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation  
 CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid  
 CC tissue). This translocation is found in approximately 50% of  
 CC cytogenetically abnormal low-grade MALT lymphoma and involves  
 CC MALT1 and BIRC2.  
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: L49432; AAC1943.1; -

Query	1	PEOLASAGFYGRNDVKKFCDDGLRCWESGDDPWVYHNAWPRCE	48
Db	273	PEOLASAGFYGVNSDDVKFCDDGLRCWESGDDPWVQHAHWPRCE	320

Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0

Query Match  
Best Local Similarity 95.6%; Score 282; DB 1; Length 604;  
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0

Result 5

ID	BIR3_MOUSE	STANDARD	PRT	612 AA
AC	Q62210; 008864;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis protein 2) (MIAP) (MIAP-2).			
GN	BIRC3 OR API2 OR IAP2.			
OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RA	MEDLINE=96128127; PubMed=8548810;			
RA	Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;			
RT	"The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";			
RL	Cell 83:1243-1252(1995).			
RV	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skeletal muscle;			
RC	MEDLINE=96110590; PubMed=9441758;			
RC				

```

RA  Lliston P, Lefebvre C., Fong W.G., Xian J.Y., Korneluk R.G.:
RB  "Genomic characterization of the mouse inhibitor of apoptosis protein
RT  1 and 2 genes".
RL  Genomics 46:495-503(1997).
CC  -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC  WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC  FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC  NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC  -1- SUBUNIT: Interacts with SNAC and with PRS55; these interactions
CC  inhibit apoptotic suppressor activity (by similarity).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC  -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC  LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC  -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC  -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC  -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC  -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC  -----
CC  CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (see http://www.isb-slb.ch/announce/slb.ch).
CC  or send an email to license@slb-slb.ch).
CC  -----
DR  EMBL: L49433: AAC42078.1; -.
DR  EMBL: U088909: AAC53532.1; -.
DR  HSSP: Q13490.10BH.
DR  MGD: MGI:1197009; Birc3.
DR  InterPro: IPR001370; BIR.
DR  InterPro: IPR001315; CARD.
DR  InterPro: IPR001841; Znf-fing.
DR  Pfam: PF000097; zf-C3HC4; 1.
DR  Pfam: PF00619; CARD; 1.
DR  Pfam: PF00653; BIR; 3.
DR  SMART: SM00238; BIR; 3.
DR  SMART: SM00114; CARD; 1.
DR  SMART: SM00184; RING; 1.
DR  PROSITE: PS01282; BIR_REPEAT_1; 3.
DR  PROSITE: PS0143; BIR_REPEAT_2; 3.
DR  PROSITE: PS50209; CARD; 1.
DR  PROSITE: PS00518; zf_RING_1; FALSE_NEG.
DR  PROSITE: PS50089; zf_RING_2; 1.
DR  PROSITE: PS50089; zinc-finger; Repeat.
KW  Apoptosis; zinc-finger; Repeat.
FT  REPEAT 46 113 BIR 1.
FT  REPEAT 177 243 BIR 2.
FT  REPEAT 262 329 BIR 3.
FT  DOMAIN 447 537 CARD.
FT  ZN_FING 565 600 RING-TYPE.
FT  CONFLICT 380 380 E -> K (IN REF. 2).
SQ  SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match 95.6%; Score 282; DB 1; Length 612;
Best Local Similarity 93.8%; Pred. No. 2, 2e-27;
Matches 45; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PEQLASAGFYVGRNDVKKFCDCDGLRCWESGDDPWVHAKWAPRCE 48
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DB 280 PEQLASAGFYVGRNDVKKFCDCDGLRCWEGDDPDPIHAKWAPRCE 327

RESULT 6
BIR2_MOUSE STANDARD: PRT; 600 AA.
ID BIR2_MOUSE
AC 008863;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (inhibitor of apoptosis
   protein 1) (MIAP1) (MIAP-1).
EN BIRC2 OR APL1 OR IAP1.
OS Mus musculus (Mouse).

```



CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Fetal kidney;  
 RX PubMed=11162435;  
 RA Lin J.-H., Deng G., Huang O., Morser J.;  
 RT "KIP, a novel member of the inhibitor of apoptosis protein family,";  
 RL Biochem. Biophys. Res. Commun. 279:820-831(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Melanoma;  
 RX PubMed=11322947;  
 RA Ashbash Y., Allian A., Pollack A., Panet A., Yehuda D.B.;  
 RT "Two splicing variants of a new inhibitor of apoptosis gene with  
 different biological properties and tissue distribution pattern,";  
 RL FEBS Lett. 495:56-60(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Kidney;  
 RX PubMed=11024045;  
 RA Kasof G.M., Gomes B.C.;  
 RT "Livin, a novel inhibitor of apoptosis protein family member,";  
 RL J. Biol. Chem. 276:3238-3246(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,  
 Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 Buck D., Burrill W.D., Butler A.P., Gardner C., Carter N.P.,  
 Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 Clegg S., Cobley V.E., Collier R.E., Connor F.E., Corby N.R.,  
 Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 Levanthalpo M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 Marsh V.L., Martin S.L., McCannachie L.J., McEay K., McMorris A.A.,  
 Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 Oliver K., Palmer A., Patel R., Pearce T.A.V., Peck A.I.,  
 Phillimore B.J.C.T., Prithaltingam S.R., Plumb R.W., Ramsay H.,  
 Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,  
 Skuse C.D., Smith M.L., Soderlund C., Steward C.A., Sultston J.E.,  
 Swann R.M., Symeon N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams  
 Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
 Wilmink L., Wray P.W., Hubbard T., Durbill R.M., Bentley D.R., Beck S.,  
 Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20,";  
 RL Nature 414:865-871(2001).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Skin;  
 RA Strausberg R.;  
 RN Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP FUNCTION, AND MUTAGENESIS OF GLU-87; GLU-88; CYS-124; ASP-120 AND  
 RX ASP-118.  
 RA PubMed=11084335;  
 RA Vucic D., Stenacke H.R., Pisabarro M.T., Salvassen G.S., Dixit V.M.;  
 RT "ML-1AP, a novel inhibitor of apoptosis that is preferentially  
 expressed in human melanomas,";  
 RL Curr. Biol. 10:1359-1366(2000).  
 RN [7]  
 RP INTERACTION WITH SMAC.  
 RX PubMed=11801603;  
 RA Vucic D., Deshayes K., Akerly H., Pisabarro M.T., Kadkhodayan S.,  
 Fairbrother W.J., Dixit V.M.;

RT	"SMAC negatively regulates the anti-apoptotic activity of melanoma inhibitor of apoptosis (ML-IAP)."
RL	J. Biol. Chem. 277:12275-12279(2002).
RN	[8]
RP	ACTIVATION OF MAP KINASES.
RX	Pubmed-11865055;
RA	Sanna M.G., da Silva Correia J., Ducrey O., Lee J., Nomoto K., Schrantz N., Deneaux O.L., Ulevitch R.J.;
RT	"IAP suppression of apoptosis involves distinct mechanisms: the TNF1/JNK1 signaling cascade and caspase inhibition.";
RL	Mol. Cell. Biol. 22:11794-11796(2002).
CC	-1- FUNCTION: Protects against apoptosis induced by TNF or by chemical agents such as adriamycin, etoposide or staurosporine. Suppression of apoptosis is mediated by activation of MAPK9/JNK1, and possibly also of MAP9/JMK2. This activation depends on TRAF1 and NF2C2/TAFL1. In vitro, inhibits caspase-3 and proteolytic activation of pro-caspase-9. Isoform 1 blocks staurosporine-induced apoptosis and isoform 2 blocks etoposide-induced apoptosis.
CC	-1- SUBUNIT: Binds to caspase-9. Interaction with SMC via the BIR domain disrupts binding to caspase-9 and apoptotic suppressor activity. Interacts with TRAF1. In vitro, interacts with caspase-3 and caspase-7 via its BIR domain.
CC	-1- SUBCELLULAR LOCATION: Nuclear, and in a filamentous pattern throughout the cytoplasm.
CC	-1- ALTERNATIVE PRODUCTS: 3 isoforms; 1/Llyin beta, 2/Llyin alpha (shown here) and 3: are produced by alternative splicing.
CC	-1- TISSUE SPECIFICITY: Very low levels or not detectable in most adult tissues. Detected in adult heart, placenta, lung, lymph node, spleen and ovary, and in several carcinoma cell lines (isoforms 1 and 2). Isoform 2 (but not isoform 1) is detected in fetal kidney, heart and spleen, and at lower levels in adult brain, skeletal muscle and peripheral blood leukocytes.
CC	-1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC	-1- SIMILARITY: CONTAINS 1 BIR REPEAT.
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC	-----
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CC	-----
DR	EMBL; AF301009; AAG37878.1; -
DR	EMBL; AJ309298; CAC37337.1; -
DR	EMBL; AJ309298; CAC37338.1; -
DR	EMBL; AF311388; AAG33622.1; -
DR	EMBL; AL121827; CAC36111.1; -
DR	EMBL; AL121827; CAC36112.1; -
DR	EMBL; AL121827; CAC36113.1; ALT_INIT.
DR	EMBL; BC014475; AAH14475.1; -
DR	HSSP; Q13490; 10BH.
DR	Gnew; HGNC:13702; BIRC7.
DR	MIM; 605737; -
DR	InterPro; IPRO01370; BIR.
DR	InterPro; IPRO01841; Znf_fing.
DR	Pfam; PF00653; BIR; 1.
DR	Pfam; PF00097; zf-C3HC4; 1.
DR	PROSITE; PS01282; BIR_REPEAT_1; 1.
DR	PROSITE; PS0143; BIR_REPEAT_2; 1.
DR	PROSITE; PS00518; ZF_RING_1; 1.
DR	PROSITE; PS50083; ZF_RING_2; 1.
DR	Apoptosis; zinc-finger; Alternative splicing.
KW	REPEAT 90 155
FT	FT ZN_FING 252 286
FT	FT DOMAIN 64 69
FT	VASNPIC 1 149
FT	MGPSDKACLRGPGOPSHWAGDGPTQERGPRSLGSPLYG
FT	LDTQRANDHYDQGLIGCLRPLRTEEBEBSGAGATLSRPAP
FT	GMGESEELRLASFDPPLAEVPEPLLAAGFFTHGHODKVR
FT	CFCFYGIQSRRGDDEPWTEIAKWPF -> WPLPDWDYEAAL
FT	WRRLHSPPRCPCPALGGCGRGGRGNPDPRSGIKGVYGAL

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FT FT VARSPLIC 216 233 MISSING (IN ISOFORM 3).
FT FT MUTAGEN 87 88 EE->AA: NO CHANGE IN SMAC INTERACTION AND
FT FT MUTAGEN 120 120 ANTI-APOPTOTIC ACTIVITY.
FT FT MUTAGEN 120 120 D->A: ABOLISHES INHIBITION OF CASPASES,
FT FT MUTAGEN 124 124 SMAC BINDING AND ANTI-APOPTOTIC ACTIVITY.
FT FT MUTAGEN 138 138 C->A: ABOLISHES INHIBITION OF CASPASES +
FT FT MUTAGEN 138 138 AND ANTI-APOPTOTIC ACTIVITY.
FT FT CONFLICT 223 223 D->A: ABOLISHES INHIBITION OF CASPASES,
SO SEQUENCE 298 AA: 32798 MW: B2EAAEE531BEC101 CRC64: SMAC BINDING AND ANTI-APOPTOTIC ACTIVITY.
Query Match Best Local Similarity 66.1%; Score 195; DB 1 Length 298;
Matches 30; Conservative 7; Mismatches 11; Indels 0; Gaps 0.
OY 1 PQLAASAGFYVGRNDVKCFCCDGLRCWESGDDPWVEHAAMPFCE 48
DB 105 PELLAAGPFHTGHODKVRCEFYGSLQSKRWGDDPWVEHAAMPFSCQ 152
RESULT 9
BIRF_MOUSE STANDARD: PRT: 1403 AA.
ID BIRF_MOUSE 09JIB6; P81704; 009122; 009121;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1f (neuronal apoptosis
DE inhibitor protein 6).
GN BIRC1F OR NAIP6 OR NAIP-RS4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN NM_011111
RP SEQUENCE FROM N.A.
RC MEDLINE=20414747; PubMed=10958627;
RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
RL "Genomic sequence analysis of the mouse Naip gene array.";
RN [2]
RP SEQUENCE OF 82-168 FROM N.A.
RC STRAIN=129/SVJ;
RC MEDLINE=97131520; PubMed=89375718;
RA Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
RT within the Lgl1 critical interval and contains multiple copies of Naip
RT exon 5.";
RL Genomics 38:405-417(1996).
CC -! FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -! SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -! SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC -----
DR EMBL; AF242431; AAF82751.1; -
DR EMBL; U66327; AAC52975.1; -
DR HSSP; O13490; IOBH.
DR MGD; MG1:1298222; Birc1f.
DR InterPro: IPRO01370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00236; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2

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DR PROSITE, PS50143; BIR_REPEAT_2; 3.
KW PROSITE; PS50837; NACHT; 1.
FT Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SO SEQUENCE 1403 AA; 159823 MW; 9DA91250358CAE9 CRC64;

Query Match 63.4%; Score 187; DB 1; Length 1403;
Best Local Similarity 60.4%; Pred. No. 2,4e-15;
Matches 29; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Oy 1 PEOASAGFYVGRNDVKCFCCDGGELRCWESGDDPWVHAHAKWPPRCE 48
178 PRLASAGFVETGKRDYQCFSGCSGLANWEGDDPWVHAHAKWPPKCE 225

RESULT 10
BIRG_MOUSE STANDARD; PRT; 1402 AA.
ID BIRG_MOUSE AC- Q9JIB3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis
DE inhibitory protein 7).
DE BIRCig OR NAlp).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20416747; PubMed-1095862;
RA Engrilzi M.G., Hadinoto V., Growley J.D., Miller W., Dietrich W.F.;
"Genomic sequence analysis of the mouse Nalp gene array.";
RL Genome Res. 10:1095-1102(2000).
-1 FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
SIGNALS.
-1 SIMILARITY: CONTAINS 3 BIR REPEATS.
-1 SIMILARITY: CONTAINS 1 NACHT DOMAIN.
-----
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CC -----
DR EMBL; AF242433; AAF82749.1; -
DR HSSP; Q13490; IOBH.
DR MGD; MGI:1858256; Bircig.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SO SEQUENCE 1402 AA; 159662 MW; C1DFFBA359893E0D CRC64;

Query Match 63.1%; Score 186; DB 1; Length 1402;
Best Local Similarity 60.4%; Pred. No. 3,2e-15;
Matches 29; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Oy 1 PEOASAGFYVGRNDVKCFCCDGGELRCWESGDDPWVHAHAKWPPRCE 48
178 PRLASAGFVETGKRDYQCFSGCSGLANWEGDDPWVHAHAKWPPKCE 225

```

DB 178 PRLSAGFVFTGKRDYVOCFCSCGSLGNWEDDPWEKHAKEPCKE 225

RESULT 11

BIRLA\_MOUSE

ID BIRLA\_MOUSE STANDARD: PRT: 1403 AA.

AC 090W5: 09R017: 09T15:

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Baculoviral IAP repeat-containing protein 1a (Neuronal apoptosis inhibitory protein 1).

GN BIRCI1 OR NAIP1 OR NAIP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Yaregchi Z., Korneluk R.G., Mackenzie A.E.:

RT "Cloning and characterization of the multiple copies of the murine homologue of NAIP (neuronal apoptosis inhibitory protein).";

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE-99431676; PubMed-10501978;

RT "Huang S., Scharf J.M., Gromney J.D., Endrizzi M.G., Dietrich W.F.;

RT functional transcript.

RL Mamm. Genome 10:1032-1035(1999).

RN [3]

RP SEQUENCE FROM N.A.

RA MEDLINE-20414747; PubMed-10958627;

RT Endrizzi M.G., Hadinoto V., Gromney J.D., Miller W., Dietrich W.F.;

RT "Genomic sequence analysis of the mouse Naip gene array.";

RL "Genomic Res. 10:1095-1102(2000)."

CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF SIGNALS.

CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.

CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.

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CC EMBL: AF007769; AAB69223.1; -

DR EMBL: AF135491; AAD56763.1; -

DR EMBL: AF242432; AAF82752.1; -

DR HSSP: Q13490; 10BH.

DR MGD: MGI:1298223; Birc1a.

DR InterPro: IPR001370; BIR.

DR Pfam: PF00653; BIR: 3.

DR SMART: SM00238; BIR: 3.

DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.

DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.

DR PROSITE: PS50837; NACHT; 1.

KW Apoptosis; Repeat; Multigene family.

FT REPEAT 60 127 BIR 1.

FT REPEAT 159 227 BIR 2.

FT REPEAT 278 345 BIR 3.

FT DOMAIN 464 758 NACHT.

FT CONFLICT 343 343 I -> V (IN REF. 2).

FT CONFLICT 359 359 L -> Q (IN REF. 2).

FT CONFLICT 624 624 E -> K (IN REF. 2).

FT CONFLICT 1092 1092 D -> E (IN REF. 3).

FT CONFLICT 1116 1116 D -> N (IN REF. 3).

FT CONFLICT 1123 1123 G -> R (IN REF. 3).

FT CONFLICT 1129 1129 L -> H (IN REF. 1).

FT CONFLICT 1140 1140 T -> M (IN REF. 2).

FT CONFLICT 1269 1269 A -> V (IN REF. 3).

SO SEQUENCE 1403 AA; 158692 MW; B31630259595EB67 CRC64;

Query Match

Best local Similarity 60.4%; Score 186; DB 1; Length 1403;

Matches 29; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 PRLSAGFVFTGKRDYVOCFCSCGSLGNWEDDPWEKHAKEPCKE 48

DB 178 PRLSAGFVFTGKRDYVOCFCSCGSLGNWEDDPWEKHAKEPCKE 225

RESULT 12

BIRLA\_MOUSE

ID BIRLA\_MOUSE STANDARD: PRT: 1403 AA.

AC 09R016: 09R029; P81703; 009122; 009121;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Baculoviral IAP repeat-containing protein 1e (Neuronal apoptosis inhibitory protein 1).

GN BIRCI1 OR NAIP1 OR NAIP-RS3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-99431676; PubMed-10501978;

RT Huang S., Scharf J.M., Gromney J.D., Endrizzi M.G., Dietrich W.F.;

RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct functional transcripts.";

RL Mamm. Genome 10:1032-1035(1999).

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE-99417674; PubMed-10486205;

RT Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,

RT Kunkel L.M., Miller W., Dietrich W.F.;

RT "Comparative sequence analysis of the mouse and human Lgn1/SMA interval.";

RL Genomics 60:137-151(1999).

RN [3]

RP SEQUENCE OF 82-168 FROM N.A.

RC STRAIN=129/SvJ.

RX MEDLINE-97131520; PubMed-8975718;

RA Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,

RA Kunkel L.M., Dietrich W.F.;

RT "The mouse region syntenic for human spinal muscular atrophy lies within the Lgn1 critical interval and contains multiple copies of Naip exon 5.";

RT Genomics 38:405-417(1996).

RL Genomics 38:405-417(1996).

CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF SIGNALS.

CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.

CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.

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CC EMBL: AF135492; AAD56764.1; -

DR EMBL: AF131205; AAD56760.1; -

DR EMBL: U66326; AAC52974.1; -

DR HSSP: Q13490; 10BH.

DR MGD: MGI:1298220; Birc1e.

DR InterPro: IPR001370; BIR.

DR Pfam: PF00653; BIR: 3.

DR SMART: SM00238; BIR: 3.

DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
 DR PROSITE: PS0837; NACHT; 1.  
 KW Apoptosis; Repeat; Multigene family.  
 FT REPEAT 60 127 BIR 1.  
 FT REPEAT 159 227 BIR 2.  
 FT REPEAT 278 345 BIR 3.  
 FT DOMAIN 464 759 NACHT.  
 FT CONFLICT 92 92 K -> R (IN REF. 1).  
 FT CONFLICT 144 144 S -> R (IN REF. 1).  
 FT CONFLICT 242 242 T -> A (IN REF. 2).  
 FT CONFLICT 472 472 T -> A (IN REF. 2).  
 FT CONFLICT 516 516 A -> D (IN REF. 2).  
 FT CONFLICT 521 521 A -> T (IN REF. 2).  
 FT CONFLICT 533 533 V -> A (IN REF. 2).  
 FT CONFLICT 538 538 S -> I (IN REF. 2).  
 FT CONFLICT 1092 1092 E -> I (IN REF. 2).  
 FT CONFLICT 1129 1129 H -> L (IN REF. 2).  
 FT CONFLICT 1137 1137 R -> Q (IN REF. 2).  
 FT CONFLICT 1242 1242 V -> I (IN REF. 2).  
 FT CONFLICT 1276 1276 D -> N (IN REF. 2).  
 SQ SEQUENCE 1403 AA; 159695 MW; B27F645043BCEC42 CRC64;

Query Match 63.1%; Score 186; DB 1; Length 1403;  
 Best Local Similarity 60.4%; Pred. No. 3.2e-15;  
 Matches 29; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

OY 1 PEOLASGFTYVGRNDYKFCDCGRLCWESGDDPWEHAKWPRCE 48  
 178 PVLASAGFVETGKRDYVOCFCGSLGNWEGDDPWKEHAKWPRCE 225

RESULT 13  
 BIR\_MOUSE  
 ID BIR\_MOUSE STANDARD; PRT; 1447 AA.  
 AC Q90UR4; Q90R30; Q09124;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Baculoviral IAP repeat-containing protein 1b (Neuronal apoptosis  
 inhibitory protein 2).  
 GN BIRC1B OR NAIP2 OR NAIP-RS6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99431676; PubMed-10501978;  
 RA Huang S., Scharf J.M., Gromney J.D., Endrizzi M.G., Dietrich W.F.;  
 RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct  
 functional transcripts."  
 RL Mamm. Genome 10:1032-1035(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99315342; PubMed-10384056;  
 RA Varachi Z., Diez E., Gros P., Mackenzle A.;  
 RT "cDNA cloning and the 5' genomic organization of Naip2, a candidate  
 gene for murine Legionella resistance."  
 RL Mamm. Genome 10:761-763(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-129/SV;  
 RX MEDLINE-99417674; PubMed-10486205;  
 RA Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,  
 RA Kunzel L.M., Miller W., Dietrich W.F.;  
 RT "Comparative sequence analysis of the mouse and human Lgn1/SMa  
 interval."  
 RL Genomics 60:137-151(1999).  
 RN [4]  
 RP SEQUENCE OF 82-168 FROM N.A.  
 RC STRAIN-129/SV;  
 RX MEDLINE-97131520; PubMed-8975718;

RA Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,  
 RA Kunzel L.M., Dietrich W.F.;  
 RT "The mouse region syntenic for human spinal muscular atrophy lies  
 within the Lgn1 critical interval and contains multiple copies of Naip  
 exon 5."  
 RL Genomics 38:405-417(1996).  
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
 CC SIGNALS.  
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL; AF135489; AAD56761.1; -;  
 CC EMBL; AF135490; AAD56762.1; -;  
 CC EMBL; AF102871; AAC73002.1; -;  
 CC EMBL; AF131205; AAD56759.1; -;  
 CC EMBL; U66329; AAC52977.1; -;  
 CC HSSP; Q13490; 10BH.  
 CC MCD; MG11298226; Birc1b.  
 CC InterPro; IPR001370; BIR.  
 CC Pfam; PF00653; BIR; 3.  
 DR SMART; SM00238; BIR; 3.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS0837; NACHT; 1.  
 KW Apoptosis; Repeat; Multigene family.  
 FT REPEAT 60 127 BIR 1.  
 FT REPEAT 159 227 BIR 2.  
 FT REPEAT 278 345 BIR 3.  
 FT DOMAIN 464 759 NACHT.  
 FT CONFLICT 377 377 D -> G (IN REF. 3).  
 FT CONFLICT 403 403 L -> F (IN REF. 3).  
 FT CONFLICT 478 478 L -> Y (IN REF. 3).  
 FT CONFLICT 540 540 N -> Y (IN REF. 3).  
 FT CONFLICT 862 862 K -> N (IN REF. 3).  
 FT CONFLICT 1079 1080 SD -> FN (IN REF. 3).  
 FT CONFLICT 1089 1089 R -> C (IN REF. 3).  
 FT CONFLICT 1115 1115 K -> E (IN REF. 3).  
 FT CONFLICT 1122 1122 T -> A (IN REF. 3).  
 FT CONFLICT 1136 1136 D -> E (IN REF. 3).  
 FT CONFLICT 1157 1157 S -> G (IN REF. 3).  
 FT CONFLICT 1167 1167 G -> R (IN REF. 3).  
 FT CONFLICT 1271 1271 F -> C (IN REF. 3).  
 SQ SEQUENCE 1447 AA; 164033 MW; 9EF6CA73BA60A2 CRC64;

Query Match 62.0%; Score 183; DB 1; Length 1447;  
 Best Local Similarity 60.4%; Pred. No. 7.8e-15;  
 Matches 29; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

OY 1 PEOLASGFTYVGRNDYKFCDCGRLCWESGDDPWEHAKWPRCE 48  
 178 PVLASAGFVETGKRDYVOCFCGSLGNWEGDDPWKEHAKWPRCE 225

RESULT 14  
 IAP\_GVCP  
 ID IAP\_GVCP STANDARD; PRT; 275 AA.  
 AC P41436;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis inhibitor IAP.  
 GN IAP.  
 OS Cydia pomonella granulosis virus (CpGV) (Cydia pomonella  
 OS granulovirus).  
 OS dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.

OX NCBI\_TaxID=28289;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=M1.  
RX MEDLINE=93188168; PubMed=8445726;  
RA Crook N.E., Clem R.J., Miller L.R.;  
RT "An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif";  
RL J. Virol. 67:2168-2174(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Mexican;  
RX Kang W.K., Crook N.E., Minstaneley D., O'Reilly D.R.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY  
CC PREVENTING VIRAL STIMULATION OF APOPTOSIS.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC -----  
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CC -----  
DR EMBL; U53466; AAB39098.1; -;  
DR HSSP; Q13490; IOBH.  
DR InterPro; IPR001370; BIR.  
DR InterPro; IPR001841; Znf\_fing.  
DR Pfam; PF00653; BIR\_2.  
DR SMART; SM00238; BIR\_2.  
DR SMART; SM00184; RING\_1.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.  
DR PROSITE; PS50143; BIR\_REPEAT\_2; 2.  
DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE; PS50089; ZF\_RING\_2; 1.  
KW Apoptosis; zinc-finger; Repeat.  
FT REPEAT 7 73 BIR 1.  
FT REPEAT 108 175 BIR 2.  
FT ZN\_FING 228 263 RING-TYPE.  
SQ SEQUENCE 275 AA; 31290 MW; 84605448869CAD60 CRC64;  
Query Match 61.7%; Score 182; DB 1; Length 275;  
Best Local Similarity 59.6%; Pred. NO. 2.2e-15;  
Matches 28; Conservative 6; Mismatches 13; Indels 0; Gaps 0;  
QY 1 PEQLASAGFYVGRNDYKCFCCDGLRCWESGDDPWVTEHAKVPRC 47  
Db 126 PEQMDAGFEYTGVDNTRKCFYCDGLDWEDEVPMQHNRMKPRC 172  
RESULT 15  
BIR1\_HUMAN STANDARD; PRT; 1403 AA.  
AC Q13075; Q13730; Q99796; Q75857;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis  
DE Inhibitory protein).  
GN BIR1 OR NAIP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=fetal brain;  
RX MEDLINE=95112344; PubMed=7813013;  
RA Roy N., Mahadevan M.S., McLean M., Shuttler G., Yaraqhi Z.,  
RA Farahani R., Baird S., Besner-Johnston A., Lefebvre C., Kang X.,

RA Salih M., Aubry H., Tamai K., Guan X., Ioannou P., Crawford T.O.,  
RA de Jong P.J., Suth L., Ikeda J., Korneluk R.G., Mackenzie A.;  
RT "The gene for neuronal apoptosis inhibitory protein is partially  
RT deleted in individuals with spinal muscular atrophy";  
RL Cell 80:167-178(1995).  
RN [2]  
RP SEQUENCE FROM N.A., AND REVISIONS.  
RC TISSUE=Brain;  
RX MEDLINE=98163755; PubMed=9503025;  
RA Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farahani R.,  
RA Xuan J.-Y., Kang X., Lefebvre C., Ikeda J.-E., Korneluk R.G.,  
RA Mackenzie A.E.;  
RT "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular  
RT atrophy candidate genes SMN and NAIP";  
RL Genomics 48:121-127(1998).  
RN [3]  
RP SEQUENCE OF 386-623 FROM N.A.  
RA der Steege G., Draalijers T.G., Grootscholten P.M., Osinga J.,  
RA Arzeveno R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,  
RA Buys C.H.C.M.;  
RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 222-1403 FROM N.A.  
RA Jones K., Graves T., McPherson J.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP FUNCTION.  
RC TISSUE=Liver;  
RX MEDLINE=96149249; PubMed=8552191;  
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,  
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RT "Suppression of apoptosis in mammalian cells by NAIP and a related  
RT family of IAP genes";  
RL Nature 379:349-353(1996).  
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
CC SIGNALS.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY  
CC NEURONS. FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN  
CC SPINAL CORD.  
CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN  
CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE 1). SMAS  
CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE I  
CC (WERNIG-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE  
CC III (WOLFF-BART-KUGELBERG-WELANDER DISEASE) BASED UPON THE AGE OF  
CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE  
CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO  
CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000  
CC NEWBORNS.  
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.  
CC -----  
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CC -----  
DR EMBL; U19251; AAC52045.1; -;  
DR EMBL; U80017; AAC52047.1; -;  
DR EMBL; U21913; AAA64504.1; -;  
DR EMBL; AC005031; AAC62261.1; -;  
DR HSSP; Q13490; IOBH.  
DR Genew; HGNC:7634; BIR1.  
DR MIM; 600355; -;  
DR InterPro; IPR001370; BIR.  
DR Pfam; PF00653; BIR\_3.  
DR SMART; SM00238; BIR\_3.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
DR PROSITE; PS50837; NACHT; 1.  
KW Apoptosis; Repeat.



FT	REPEAT	60	127	BR 1.
FT	REPEAT	159	227	BR 2.
FT	REPEAT	278	345	BR 3.
FT	DOMAIN	464	758	NACHT.
FT	CONFLICT	222	223	PK -> YR (IN REF. 4).
FT	CONFLICT	386	387	VP -> ST (IN REF. 3).
FT	CONFLICT	535	535	M -> V (IN REF. 3).
FT	CONFLICT	553	553	Y -> H (IN REF. 3).
FT	CONFLICT	1228	1231	MISSING (IN REF. 4).
SO	SEQUENCE	1403 AA;	159613 MW;	566304C154AD55E64 CMC66;

Query Match	60.3%;	Score 178;	DB 1;	Length 1403;
Best Local Similarity	60.4%;	Pred. No. 3.1e-14;		
Matches 29; Conservative	5;	Mismatches 14;	Indels 0;	Gaps 0;

**QY** 1 PEGLASAGFYVGRNDVKCCPCDDGGLRCWESGDPPVEHAKWFPRCE 48  
| : | | : | : | | | | | | | | | |  
**Db** 178 PCVLSEAGFVFTGKQDTVQCSCGGCLGNWEEGDPPWEHAKWFKPCE 225

Search completed: May 5, 2003, 16:02:48  
Job time : 3.99078 secs

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:59:02 ; Search time 3.73848 Seconds

(without alignments)  
432.866 Million cell updates/sec

Title: US-08-569-749-6

Perfect score: 308  
Sequence: 1 CELYRMSTYSTFPAGVPVSE.....KVCFCGGLMDWKRGDSP 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	308	100.0	55	4	US-08-569-749-6
2	308	100.0	55	5	PCT-US96-12860-6
3	308	100.0	604	2	US-08-511-485-6
4	308	100.0	604	3	US-08-511-485-6
5	308	100.0	604	4	US-08-511-485-6
6	308	100.0	604	4	US-08-511-485-6
7	308	100.0	604	4	US-08-511-485-6
8	308	100.0	604	4	US-08-511-485-6
9	301	97.7	55	5	PCT-US96-12860-4
10	301	97.7	55	5	PCT-US96-12860-5
11	301	97.7	618	2	US-08-511-485-8
12	301	97.7	618	2	US-08-511-485-8
13	301	97.7	618	4	US-08-800-929A-8
14	301	97.7	618	4	US-08-800-929A-8
15	301	97.7	618	4	US-08-800-929A-8
16	301	97.7	618	4	US-08-800-929A-8
17	301	97.7	618	4	US-08-800-929A-8
18	299	97.1	68	2	US-08-511-485-18
19	294	95.5	612	2	US-08-511-485-18
20	294	95.5	612	4	US-08-800-929A-14
21	294	95.5	612	4	US-08-800-929A-14
22	294	95.5	612	4	US-08-800-929A-14
23	294	95.5	612	4	US-08-800-929A-14
24	292	94.8	68	2	US-08-511-485-19
25	287	93.2	600	4	US-08-800-929A-12
26	287	93.2	600	4	US-08-800-929A-12
27	287	93.2	600	4	US-08-800-929A-12

28	158	51.3	68	2	US-08-511-485-17	Sequence 17, Appl
29	158	51.3	497	2	US-08-511-485-4	Sequence 4, Appl
30	158	51.3	497	3	US-09-212-971-4	Sequence 4, Appl
31	158	51.3	497	4	US-08-800-929A-4	Sequence 4, Appl
32	158	51.3	497	4	US-08-800-929A-4	Sequence 4, Appl
33	152	49.4	68	2	US-08-511-485-16	Sequence 16, Appl
34	152	49.4	496	3	US-08-511-485-10	Sequence 10, Appl
35	152	49.4	496	3	US-08-511-485-10	Sequence 10, Appl
36	152	49.4	496	4	US-08-800-929A-10	Sequence 10, Appl
37	152	49.4	496	4	US-08-800-929A-10	Sequence 10, Appl
38	151	49.0	438	5	PCT-US95-0522A-2	Sequence 2, Appl
39	139	45.1	68	2	US-08-511-485-27	Sequence 27, Appl
40	134	43.5	68	2	US-08-511-485-26	Sequence 26, Appl
41	133	43.2	68	2	US-08-511-485-28	Sequence 28, Appl
42	133	43.2	268	4	US-08-836-134-22	Sequence 22, Appl
43	133	43.2	268	4	US-09-493-784-22	Sequence 22, Appl
44	131	42.5	68	2	US-08-511-485-21	Sequence 21, Appl
45	129	41.9	68	2	US-08-511-485-20	Sequence 20, Appl

#### ALIGNMENTS

RESULT 1  
US-08-569-749-6  
Sequence 6, Application US/08569749  
Patent No. 6187557  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Goeddel, David V  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 55 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-6

Query Match 100.0%; Score 308; DB 4; Length 55;  
Best Local Similarity 100.0%; Pred. No. 6, 9e-37;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CELYRMSTYSTFPAGVPVSESLRAGFYTGVDKVCFCGGLMDWKRGDSP 55  
DB 1 CELYRMSTYSTFPAGVPVSESLRAGFYTGVDKVCFCGGLMDWKRGDSP 55

RESULT 2  
PCT-US96-12860-6  
Sequence 6, Application PC/TUS9612860  
GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 55 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-6  
Query Match 100.0%; Score 308; DB 5; Length 55;  
Best Local Similarity 100.0%; Pred. No. 6,9e-37;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CELYRMSTYSTPAGVPVSESLARAGFYTGVDKVCFCGGLMDWKKRGDSP 55  
DB 1 CELYRMSTYSTPAGVPVSESLARAGFYTGVDKVCFCGGLMDWKKRGDSP 55  
RESULT 3  
US-08-511-485-6  
Sequence 6, Application US/08511485  
Patent No. 5919912  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
NUMBER OF SEQUENCES: 38  
NUMBER OF INVENTION: PROBES, AND DETECTION METHODS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200134  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 604 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-511-485-6  
Query Match 100.0%; Score 308; DB 2; Length 604;  
Best Local Similarity 100.0%; Pred. No. 1,2e-35;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYSTPAGVPVSESLARAGFYTGVDKVCFCGGLMDWKKRGDSP 55  
DB 28 CELYRMSTYSTPAGVPVSESLARAGFYTGVDKVCFCGGLMDWKKRGDSP 82

RESULT 4  
US-09-212-971-6  
Sequence 6, Application US/09212971B  
Patent No. 6107041  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
DISEASE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212,971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017,354  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 604  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-212-971-6  
Query Match 100.0%; Score 308; DB 3; Length 604;  
Best Local Similarity 100.0%; Pred. No. 1,2e-35;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYSTPAGVPVSESLARAGFYTGVDKVCFCGGLMDWKKRGDSP 55  
DB 28 CELYRMSTYSTPAGVPVSESLARAGFYTGVDKVCFCGGLMDWKKRGDSP 82

RESULT 5  
US-08-800-929A-6

Sequence 6, Application US/08800929A  
Patent No. 6133437  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF  
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996  
APPLICATION NUMBER: 60/017,354  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bleker-Brady, Kristina  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 604 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-800-929A-6  
Query Match 100.0%; Score 308; DB 4; Length 604;  
Best Local Similarity 100.0%; Pred. No. 1.2e-35;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CELYRMSTYTFPAGVVSERSLARAGFYTGVDKVKCFCCGIMLDNWKRGDSP 55  
DB 28 CELYRMSTYTFPAGVVSERSLARAGFYTGVDKVKCFCCGIMLDNWKRGDSP 82  
RESULT 6  
US-08-569-749-4  
Sequence 4, Application US/08569749  
Patent No. 6187557  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V  
APPLICANT: Roedel, Mike  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBAUGH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco

STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 604 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-4  
Query Match 100.0%; Score 308; DB 4; Length 604;  
Best Local Similarity 100.0%; Pred. No. 1.2e-35;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CELYRMSTYTFPAGVVSERSLARAGFYTGVDKVKCFCCGIMLDNWKRGDSP 55  
DB 28 CELYRMSTYTFPAGVVSERSLARAGFYTGVDKVKCFCCGIMLDNWKRGDSP 82  
RESULT 7  
US-09-617-053A-6  
Sequence 6, Application US/09617053A  
Patent No. 6300492  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 07891/009003  
CURRENT APPLICATION NUMBER: US/09/617,053A  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 604  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-617-053A-6  
Query Match 100.0%; Score 308; DB 4; Length 604;  
Best Local Similarity 100.0%; Pred. No. 1.2e-35;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CELYRMSTYTFPAGVVSERSLARAGFYTGVDKVKCFCCGIMLDNWKRGDSP 55  
DB 28 CELYRMSTYTFPAGVVSERSLARAGFYTGVDKVKCFCCGIMLDNWKRGDSP 82

RESULT 8  
PCT-US96-12860-4  
Sequence 4, Application PC/TUS9612860  
GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 604 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-4  
Query Match 100.0%; Score 308; DB 5; Length 604;  
Best Local Similarity 100.0%; Pred. No. 1,2e-35;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CELYRSTSTFPAGVPVSRSLARAGFYTGNDVKKCFCCGLMDNMRGDS 55  
DB 28 CELYRSTSTFPAGVPVSRSLARAGFYTGNDVKKCFCCGLMDNMRGDS 82  
RESULT 9  
US-08-569-749-5  
Sequence 5, Application US/08569749  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,749  
FILING DATE: 514  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 55 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-5  
Query Match 97.7%; Score 301; DB 4; Length 55;  
Best Local Similarity 98.2%; Pred. No. 6.9e-36;  
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CELYRSTSTFPAGVPVSRSLARAGFYTGNDVKKCFCCGLMDNMRGDS 55  
DB 1 CELYRSTSTFPAGVPVSRSLARAGFYTGNDVKKCFCCGLMDNMRGDS 55  
RESULT 10  
PCT-US96-12860-5  
Sequence 5, Application PC/TUS9612860  
GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 55 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-5  
Query Match 97.7%; Score 301; DB 5; Length 55;  
Best Local Similarity 98.2%; Pred. No. 6.9e-36;  
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRSTSTPAGVPSERSLARAGFYTGVDKVKCCGMLDNKRGDSP 55  
DB 1 CELYRSTSTPAGVPSERSLARAGFYTGVDKVKCCGMLDNKRGDSP 55

## RESULT 11

US-08-511-485-8  
Sequence 8, Application US/08511485  
Patent No. 5919912  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-511-485-8

Query Match 97.7%; Score 301; DB 2; Length 618;  
Best Local Similarity 98.2%; Pred. No. 1.2e-34;  
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRSTSTPAGVPSERSLARAGFYTGVDKVKCCGMLDNKRGDSP 55  
DB 45 CELYRSTSTPAGVPSERSLARAGFYTGVDKVKCCGMLDNKRGDSP 99

## RESULT 12

US-09-212-971-8  
Sequence 8, Application US/09212971B  
Patent No. 6107041  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE

FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212,971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017,354  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 8  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-212-971-8

Query Match 97.7%; Score 301; DB 3; Length 618;  
Best Local Similarity 98.2%; Pred. No. 1.2e-34;  
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRSTSTPAGVPSERSLARAGFYTGVDKVKCCGMLDNKRGDSP 55  
DB 45 CELYRSTSTPAGVPSERSLARAGFYTGVDKVKCCGMLDNKRGDSP 99

## RESULT 13

US-08-800-929A-8  
Sequence 8, Application US/08800929A  
Patent No. 6133437  
GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF  
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elding LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424

Prior Application: 424  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996  
APPLICATION NUMBER: 60/017,354  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bleker-Brady, Kristina  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-800-929A-8

Query Match  
Best Local Similarity 97.7%; Score 301; DB 4; Length 618;  
Matches 54; Conservativity 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTYTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMRKGDSP 55  
DB 45 CELYRMSTYTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMRKLGDS 99

RESULT 14  
US-08-569-749-2  
Sequence 2, Application US/08569749

GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-2

Query Match  
Best Local Similarity 97.7%; Score 301; DB 4; Length 618;  
Matches 54; Conservativity 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTYTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMRKGDSP 55  
DB 45 CELYRMSTYTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMRKLGDS 99

RESULT 15  
US-09-617-053A-8  
Sequence 8, Application US/09617053A

GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Iliston, Peter

APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 07891/009003  
CURRENT APPLICATION NUMBER: US/09/617,053A  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/800,929  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-617-053A-8

Query Match  
Best Local Similarity 97.7%; Score 301; DB 4; Length 618;  
Matches 54; Conservativity 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTYTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMRKGDSP 55  
DB 45 CELYRMSTYTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMRKLGDS 99

Search completed: May 5, 2003, 16:09:10  
Job time: 4.73848 secs

GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:02:07 ; Search time 6.77995 Seconds

(without alignments)  
699.970 Million cell updates/sec

Title: US-08-569-749-6

Perfect score: 308

Sequence: 1 CELYRMSYTFPPAGVPVSE.....KVKFCGGLMDMKRGDSP 55

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEM\_PUB pep: \*  
2: /cgn2\_6/ptodata/2/pubppaa/PCF\_NEM\_PUB pep: \*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEM\_PUB pep: \*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_FUBCOMB pep: \*  
5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEM\_PUB pep: \*  
6: /cgn2\_6/ptodata/2/pubppaa/US07\_FUBCOMB pep: \*  
7: /cgn2\_6/ptodata/2/pubppaa/PCFUS\_FUBCOMB pep: \*  
8: /cgn2\_6/ptodata/2/pubppaa/US08\_FUBCOMB pep: \*  
9: /cgn2\_6/ptodata/2/pubppaa/US09\_NEM\_PUB pep: \*  
10: /cgn2\_6/ptodata/2/pubppaa/US09\_FUBCOMB pep: \*  
11: /cgn2\_6/ptodata/2/pubppaa/US10\_NEM\_PUB pep: \*  
12: /cgn2\_6/ptodata/2/pubppaa/US10\_FUBCOMB pep: \*  
13: /cgn2\_6/ptodata/2/pubppaa/US60\_NEM\_PUB pep: \*  
14: /cgn2\_6/ptodata/2/pubppaa/US60\_FUBCOMB pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	308	100.0	604	9 US-09-201-936-6	Sequence 6, Appli
2	308	100.0	604	10 US-09-974-592-6	Sequence 6, Appli
3	301	97.7	306	10 US-09-778-927A-62	Sequence 62, Appli
4	301	97.7	618	9 US-09-201-936-8	Sequence 8, Appli
5	301	97.7	618	10 US-09-974-592-8	Sequence 8, Appli
6	299	97.1	68	9 US-09-201-936-18	Sequence 18, Appli
7	294	95.5	591	9 US-09-201-936-42	Sequence 42, Appli
8	294	95.5	612	10 US-09-974-592-14	Sequence 14, Appli
9	292	94.8	68	9 US-09-201-936-19	Sequence 19, Appli
10	287	93.2	600	10 US-09-974-592-12	Sequence 12, Appli
11	287	93.2	602	9 US-09-201-936-10	Sequence 40, Appli
12	158	51.3	68	9 US-09-201-936-17	Sequence 17, Appli
13	158	51.3	110	9 US-09-965-967-22	Sequence 22, Appli
14	158	51.3	497	9 US-09-201-936-4	Sequence 4, Appli
15	158	51.3	497	10 US-09-974-592-4	Sequence 4, Appli
16	152	49.4	68	9 US-09-201-936-16	Sequence 16, Appli
17	152	49.4	496	9 US-09-201-936-10	Sequence 10, Appli
18	152	49.4	496	10 US-09-974-592-10	Sequence 10, Appli
19	151	49.0	438	1 US-08-464-588-2	Sequence 2, Appli

20	140	45.5	110	9 US-09-965-967-21	Sequence 21, Appli
21	139	45.1	68	9 US-09-201-936-27	Sequence 27, Appli
22	134	43.5	68	9 US-09-201-936-26	Sequence 26, Appli
23	133	43.2	68	9 US-09-201-936-28	Sequence 28, Appli
24	133	43.2	68	9 US-10-041-859-18	Sequence 18, Appli
25	133	43.2	172	9 US-10-041-859-12	Sequence 12, Appli
26	131	42.5	68	9 US-09-201-936-21	Sequence 21, Appli
27	129	41.9	68	9 US-09-201-936-20	Sequence 20, Appli
28	129	41.9	68	9 US-10-041-859-19	Sequence 19, Appli
29	129	41.9	109	9 US-09-965-967-30	Sequence 30, Appli
30	128	41.6	172	9 US-10-041-859-13	Sequence 13, Appli
31	128	41.6	1403	8 US-08-913-322-22	Sequence 22, Appli
32	128	41.6	1403	8 US-08-913-322-24	Sequence 24, Appli
33	121.5	39.4	67	9 US-09-201-936-22	Sequence 22, Appli
34	116	37.7	68	9 US-10-041-859-14	Sequence 14, Appli
35	116	37.7	172	9 US-10-041-859-8	Sequence 8, Appli
36	116	37.7	346	9 US-10-041-859-2	Sequence 2, Appli
37	115.5	37.5	67	9 US-09-201-936-23	Sequence 23, Appli
38	112	36.4	66	9 US-09-201-936-24	Sequence 24, Appli
39	112	36.4	66	9 US-09-201-936-25	Sequence 25, Appli
40	112	36.4	107	9 US-09-965-967-20	Sequence 20, Appli
41	112	36.4	278	9 US-09-964-899-39	Sequence 39, Appli
42	111.5	36.2	67	9 US-09-201-936-11	Sequence 11, Appli
43	111.5	36.2	109	9 US-09-965-967-19	Sequence 19, Appli
44	110	35.7	68	9 US-10-041-859-16	Sequence 16, Appli
45	110	35.7	172	9 US-10-041-859-10	Sequence 10, Appli

## ALIGNMENTS

RESULT 1  
US-09-201-936-6  
Sequence 6, Application US/09201936  
Publication No. US20020187946A1  
GENERAL INFORMATION:  
APPLICANT: Mackenzie, Robert G.  
APPLICANT: Korneluk, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
FILE OF INVENTION: PROBES, AND DETECTION METHODS  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
CURRENT FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCF/1B96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 604  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-201-936-6  
Query Match 100.0%; Score 308; DB 9; Length 604;  
Best Local Similarity 100.0%; Pred. No. 9.7e-33;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CELYRMSYTFPPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDMKRGDSP 55  
|||||  
Db 28 CELYRMSYTFPPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDMKRGDSP 82  
|||||  
RESULT 2  
US-09-974-592-6  
Sequence 6, Application US/09974592



```
Patent No. US20020120121A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 07891/009004
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 604
TYPE: PRT
ORGANISM: Homo sapiens
US-09-974-592-6

Query Match
Best Local Similarity 100.0%; Score 308; DB 10; Length 604;
Best Local Similarity 100.0%; Pred. No. 9.7e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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RESULT 3
US-09-978-927A-62
Sequence 62, Application US/09778927A
Patent No. US20020068342A1
GENERAL INFORMATION:
APPLICANT: KHOSRAVI, Rami et al.
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
FILE REFERENCE: 2786-0160P
CURRENT APPLICATION NUMBER: US/09/778,927A
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: IL 134453
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: IL135341
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 62
LENGTH: 306
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc-feature
LOCATION: (1)...(306)
OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-927A-62
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Query Match
Best Local Similarity 97.7%; Score 301; DB 10; Length 306;
Best Local Similarity 98.2%; Pred. No. 3.9e-32;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVKFCGCGMLMDNKRKRDSP 55
DB 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVKFCGCGMLMDNKRKRDSP 99
```

RESULT 4  
US-09-201-936-8

```
Sequence 8, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-8
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Query Match
Best Local Similarity 97.7%; Score 301; DB 9; Length 618;
Best Local Similarity 98.2%; Pred. No. 8.5e-32;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVKFCGCGMLMDNKRKRDSP 55
DB 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVKFCGCGMLMDNKRKRDSP 99
```

```
RESULT 5
US-09-974-592-8
Sequence 8, Application US/09974592
Patent No. US20020120121A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 07891/009004
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-974-592-8
```

```
Query Match
Best Local Similarity 97.7%; Score 301; DB 10; Length 618;
Best Local Similarity 98.2%; Pred. No. 8.5e-32;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVKFCGCGMLMDNKRKRDSP 55
DB 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVKFCGCGMLMDNKRKRDSP 99
```

```
RESULT 6
US-09-201-936-18
; Sequence 18, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201, 936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-18
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Query Match          97.1%; Score 299; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.3e-32;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 2 ELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNMRGDS 55
Db 1 ELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNMRGDS 54
RESULT 7
US-09-201-936-42
; Sequence 42, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201, 936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-42
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Query Match          95.5%; Score 294; DB 9; Length 591;
Best Local Similarity 94.5%; Pred. No. 6.9e-31;
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Matches 52; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Oy 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNMRGDS 55
Db 24 CELYRMSTYSAFPRGVPSERSLARAGFYTGVDKVCFCGGLMDNMRGDS 78
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RESULT 8
US-09-974-592-14
; Sequence 14, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; EARLIER FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-974-592-14
```

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Query Match          95.5%; Score 294; DB 10; Length 612;
Best Local Similarity 94.5%; Pred. No. 7.2e-31;
Matches 52; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
Oy 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNMRGDS 55
Db 45 CELYRMSTYSAFPRGVPSERSLARAGFYTGVDKVCFCGGLMDNMRGDS 99
RESULT 9
US-09-201-936-19
; Sequence 19, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201, 936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-19
```

US-09-201-936-19

Query Match 94.8%; Score 292; DB 9; Length 68;  
Best Local Similarity 98.1%; Pred. No. 1,1e-31;  
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 ELXRMSTYTFPPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMKRGDSP 55  
1 ELXRMSTYTFPPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMKRGDSP 54

RESULT 10  
US-09-974-592-12  
Sequence 12, Application US/09974592  
Patent No. US20020120121A1

GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K.  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
DISEASE  
FILE REFERENCE: 07891/009004  
CURRENT APPLICATION NUMBER: US/09/974,592  
CURRENT FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: US 09/617,053  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 600  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-974-592-12

Query Match 93.2%; Score 287; DB 10; Length 600;  
Best Local Similarity 90.9%; Pred. No. 6e-30;  
Matches 50; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 CELYRMSTYTFPPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMKRGDSP 55  
26 CELYRMSTYTFPPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMKRGDSP 80

RESULT 11

US-09-201-936-40  
Sequence 40, Application US/09201936  
Publication No. US20020187946A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
APPLICANT: Liston, Peter  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
CURRENT FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 40  
LENGTH: 602  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-201-936-40

Query Match 93.2%; Score 287; DB 9; Length 602;  
Best Local Similarity 90.9%; Pred. No. 6e-30;  
Matches 50; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

2 ELXRMSTYTFPPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMKRGDSP 55  
28 CELYRMSTYTFPPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMKRGDSP 82

RESULT 12

US-09-201-936-17  
Sequence 17, Application US/09201936  
Publication No. US20020187946A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
CURRENT FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 17  
LENGTH: 68  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-201-936-17

Query Match 51.3%; Score 158; DB 9; Length 68;  
Best Local Similarity 52.8%; Pred. No. 7.6e-14;  
Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

2 ELXRMSTYTFPPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMKRGDSP 54  
1 EFNRLKTFANFPSPGSPVASTLARAGFYTGEDYVRCFCHAAVDRMVGDS 53

RESULT 13

US-09-965-967-22  
Sequence 22, Application US/09965967  
Patent No. US20020177557A1  
GENERAL INFORMATION:  
APPLICANT: Shi, Yigong  
TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis  
FILE REFERENCE: PU-0031 (01-1739-1)  
CURRENT APPLICATION NUMBER: US/09/965,967  
CURRENT FILING DATE: 2001-09-28  
PRIOR APPLICATION NUMBER: 60/236,574  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/256,830  
PRIOR FILING DATE: 2000-12-20  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 110  
TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-965-967-22

Query Match
Best Local Similarity 51.3%; Score 158; DB 5; Length 110;
Pred. No. 1.3e-13;
Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

OY 2 ELYRSTYSTFPAGVPSERSIARAGFYTTGVNDVKCECCGLMDNKRKGS 54
DB 16 EFNRLKTFANFPSSGSPVASSTIARAGFLYTGEGDTRCFSCAAVDRMOYGDS 68

RESULT 14
US-09-201-936-4
; Sequence 4, Application US/09201936
; Publication No. US20020187946b1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT FILING DATE: US/09/201,936
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-4

Query Match
Best Local Similarity 51.3%; Score 158; DB 9; Length 497;
Pred. No. 7.2e-13;
Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

OY 2 ELYRSTYSTFPAGVPSERSIARAGFYTTGVNDVKCECCGLMDNKRKGS 54
DB 26 EFNRLKTFANFPSSGSPVASSTIARAGFLYTGEGDTRCFSCAAVDRMOYGDS 78

RESULT 15
US-09-974-592-4
; Sequence 4, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K.
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
```

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-4.

Query Match
Best Local Similarity 51.3%; Score 158; DB 10; Length 497;
Pred. No. 7.2e-13;
Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

OY 2 ELYRSTYSTFPAGVPSERSIARAGFYTTGVNDVKCECCGLMDNKRKGS 54
DB 26 EFNRLKTFANFPSSGSPVASSTIARAGFLYTGEGDTRCFSCAAVDRMOYGDS 78

Search completed: May 5, 2003, 16:11:05
Job time : 7.77995 secs
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GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model.

Run on: May 5, 2003, 15:58:42 ; Search time 6.01959 Seconds

(without alignments)  
878.365 Million cell updates/sec

Title: US-08-569-749-6

Perfect score: 308

Sequence: 1 CELYRMSTYSTFPAGVPVSE.....RVKRCGGLMDNMKRGDSP 55

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308	100.0	604	2	S68449 apoptotic inhibitor
2	301	97.7	618	2	S68450 apoptotic inhibitor
3	158	51.3	497	2	S68544 apoptotic inhibitor
4	141	45.8	358	2	JC5964 apoptotic inhibitor
5	133	43.2	268	2	T10304 inhibitor of apopt
6	133	43.2	268	2	A53989 apoptosis-inhibi
7	128	41.6	1232	2	A55478 neuronal apoptosi
8	126	40.9	208	2	T03183 neuronal apoptosi
9	125	40.6	1447	2	T42628 neuronal apoptosi
10	124	40.3	298	2	JC7568 kidney inhibitor o
11	106.5	34.6	275	2	A45679 neuronal apoptosi
12	106	34.4	496	2	S68452 apoptosis inhibito
13	106	34.4	497	2	S69545 apoptosis inhibito
14	102	33.1	150	2	T28409 ORF MSY248 probabl
15	94	30.5	275	2	T10310 apoptosis-inhibiti
16	83.5	27.1	286	2	D36828 orf13 protein - Au
17	83.5	27.1	292	2	T41772 IAP1 orf127 - Bomby
18	77	25.0	155	2	T30489 apoptosis inhibito
19	74.5	24.2	997	2	T43523 cull7 protein - fi
20	72.5	23.5	234	2	T30427 probable apoptosi
21	72.5	23.5	4845	2	T31067 BIR repeat contain
22	65	21.1	329	2	T28403 ORF MSY242 probabl
23	60	19.5	932	2	H86325 hypothetical prote
24	59	19.2	733	2	T04070 hypothetical prote
25	58	18.8	288	2	B72272 thrombin (EC 3.4.2
26	57.5	18.7	236	2	C42896 hypothetical prote
27	57.5	18.7	337	2	T27615 ecarin precursor -
28	57.5	18.7	616	2	A55796 3-methyl-adenine D
29	57	18.5	187	2	B98183

30	57	18.5	187	2	F86029 3-methyladenine DN
31	57	18.5	707	2	T40070 origin recognition
32	57	18.5	1401	2	T17452 Werner syndrome pr
33	57	18.5	1401	2	T30247 Werner syndrome pr
34	57	18.5	1930	2	F86200 protein F12K1.17
35	56.5	18.3	1192	2	G70513 5-methyltetrahydro
36	55.5	18.0	617	2	S10511 thrombin (EC 3.4.2
37	55.5	18.0	219	2	A35827 thrombin (EC 3.4.2
38	55	17.9	428	2	H72858 apoptosis inhibito
39	55	17.9	422	2	G90259 hypothetical prote
40	55	17.9	422	2	H90271 hypothetical prote
41	55	17.9	422	2	H90275 hypothetical prote
42	55	17.9	422	2	H90501 hypothetical prote
43	55	17.9	422	2	B90327 hypothetical prote
44	55	17.9	1156	2	T14899 aminophospholipid
45	54.5	17.7	155	2	T37471 apoptosis inhibito

#### ALIGNMENTS

```

RESULT 1
S68449
apoptosis inhibitor hlap-1 - human
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68449
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha
Nature 379, 349-353, 1996
A>Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68449
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-604 <LIS>
A:Cross-references: EMBL:U45878; NID:g1184315; PIDN:AAC50371.1; PID:g1184316
C:Function:
A:Description: apoptotic suppressor
C:Keywords: apoptosis; zinc finger
C:Superfamily: RING finger homology
F:553-597/Domain: RING finger homology <RNG>

Query Match 100.0%; Score 308; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 2.4e-31;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGNDKVCFCGGLMDNMKRGDSP 55
DB 28 CELYRMSTYSTFPAGVPVSESLARAGFYTGNDKVCFCGGLMDNMKRGDSP 82

RESULT 2
S68450
apoptosis inhibitor hlap-2 - human
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68450
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha
Nature 379, 349-353, 1996
A>Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68450
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-618 <LIS>
A:Cross-references: EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g1184318
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptosis; zinc finger
F:567-611/Domain: RING finger homology <RNG>

Query Match 97.7%; Score 301; DB 2; Length 618;

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07 5 RMSTSTSEEPAGVPSERSLARGFYTGVDNKVKCFCCGLMDNWKRGDSP 55  
1 1 : : 11 11111 1 : 11111 1 : 11 1

A:Reference number: A55478; MUID:95112344; PMID:7813013  
A:Accession: A55478

```
A;Molecule type: mRNA
A;Residues: 1-1232 <ROY>
```

```

A:Cross-references: GB:019251
C:Genetics:
A:Gene: GDB:SMAe, SMA
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A:Map position: 5q12.2-5q13
C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
F:94-110/Domain: transmembrane #status predicted <TM1>
F:470-477/Region: nucleotide-binding motif A (P-loop)
F:479-496/Domain: transmembrane #status predicted <TM2>
F:476/Binding site: ATP (Lys) #status predicted
F:618,632,823,923,1035/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 41.6%; Score 128; DB 2; Length 1252;
Best Local Similarity 40.7%; Pred. No. 4.6e-08;
Matches 22; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 2 ELRYMSTYSPAGVPYSESLARAGFYTGVDVKKCCGGLMDNMKRGDSP 55
| | : : : | : : : | : : : | : : : | : : : | : : : |
DB 278 EELRLDSFKMPRNSANGVALARAGLFTYTGKIDVCGSCGGLKMGEDDP 331

RESULT 8
T03183
probable apoptosis inhibitor - Chilo iridescent virus
C:Species: Chilo iridescent virus
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Sep-2000
C:Accession: T03183
R:Barh, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A:Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.10183
A:Reference number: Z18434; MUID:98141693; PMID:9484589
A:Accession: T03183
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-208 <BAH>
A:Cross-references: EMBL:AF003534; NID:g2738385; PINN:AAB94481.1; PID:g2738454
C:Superfamily: RING finger homology
F:159-202/Domain: RING finger homology <RRN>

Query Match 40.9%; Score 126; DB 2; Length 208;
Best Local Similarity 41.2%; Pred. No. 1.6e-08;
Matches 21; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 5 RMSTYSPAGVPYSESLARAGFYTGVDVKKCCGGLMDNMKRGDSP 55
| : : : | : : : | : : : | : : : | : : : | : : : |
DB 40 RLNSFQWPIQLPSKQQLSRAGFLYINIGDQVCGFCYDLTKEMKRSNDP 90

RESULT 9
T42628
neuronal apoptosis inhibitory protein 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T42628
R:Faraghi, Z.; Diez, E.; Gros, P.; Mackenzie, A.
Mamm. Genome 10, 761-763, 1999
A:Title: CDNA cloning and the 5' genomic organization of Naip2, a candidate gene for murine
A:Reference number: Z22179; MUID:99315342; PMID:10384056
A:Accession: T42628
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1447 <YAR>
A:Cross-references: EMBL:AF102871; NID:g3860228; PID:g3860229; PINN:AAC73002.1
C:Genetics:
A:Gene: Naip2

Query Match 40.6%; Score 125; DB 2; Length 1447;
Best Local Similarity 40.7%; Pred. No. 1.3e-07;
Matches 22; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 2 ELRYMSTYSPAGVPYSESLARAGFYTGVDVKKCCGGLMDNMKRGDSP 55
| | : : : | : : : | : : : | : : : | : : : | : : : |
DB 278 EELRLDSFKMPRNSANGVALARAGLFTYTGKIDVCGSCGGLKMGEDDP 331

```

RESULT 10  
JC7568  
Kidney inhibitor of apoptosis protein - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001  
C:Accession: JC7568  
R:Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.  
Biochem. Biophys. Res. Commun. 279, 820-831, 2000  
A:Title: KIAA, a novel member of the inhibitor of apoptosis protein family.  
A:Reference number: JC7568; MUID: 21095253; PMID:11162435  
A:Contents: Fetal kidney  
A:Accession: JC7568  
A:Molecule type: mRNA  
A:Residues: 1-298 <LIN>  
C:Comment: This protein, a new member of the inhibitor of apoptosis protein family, F

C:Genetics:  
A:Gene: KIAA  
A:Map position: 20q13.3  
C:Keywords: apoptosis

Query Match 40.3%; Score 124; DB 2; Length 298;  
Best Local Similarity 44.4%; Pred. No. 4.1e-06;  
Matches 24; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

RESULT 11  
A:5679  
Inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CPGV  
C:Species: Cydia pomonella granulosis virus CPGV  
C:Date: 21-Sep-1993 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000  
C:Accession: A45679  
R:Crook, N.E.; Clem, R.J.; Miller, L.K.  
J. Virol. 67, 2168-2174, 1993  
A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.  
A:Reference number: A45679; MUID:93188168; PMID:8445726  
A:Accession: A45679  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-275 <CRO>  
A:Cross-references: GB:L05494; NID:g289583; PIDN:AAA3835.1; PID:g289584  
A>Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBI:P:127015)  
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 34.6%; Score 106.5; DB 2; Length 275;  
Best Local Similarity 35.2%; Pred. No. 6.5e-06;  
Matches 19; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

RESULT 12  
S68452  
apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 17-Nov-2000  
C:Accession: S68452; S78528  
R:Lisbon, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Charton-Horvat, G.; Farahat  
Nature 379, 349-353, 1996  
A:Title: Suppression of apoptosis in mammalian cells by NIP and a related family of  
A:Reference number: A58182; MUID:96149249; PMID:8552191  
A:Accession: S68452  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-496 <LIS>

Query Match 33.18; Score 102; DB 2; Length 150;

Search completed: May 5, 2003, 16:08:07  
Job time : 7.01959 secs

Search completed: May 5, 2003, 16:08:07  
Job time : 7.01959 secs



GenCore version 5.1.4-P5-4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:51:32 ; Search time 2.2811 Seconds

(without alignments)  
1000.040 Million cell updates/sec

Title: US-08-569-749-6

Perfect score: 308

Sequence: 1 CELYRMSTYSPFAGVPSE.....KYKFCGGLMDNKRGDSP 55

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	308	100.0	604	1	BIR2_HUMAN
2	301	97.7	618	1	BIR3_HUMAN
3	294	95.5	612	1	BIR3_MOUSE
4	287	93.2	600	1	BIR2_MOUSE
5	248	80.5	611	1	BIR_CHICK
6	158	51.3	497	1	BIR4_HUMAN
7	152	49.4	496	1	BIR4_MOUSE
8	151	49.0	496	1	BIR4_RAT
9	141	45.8	358	1	PIAP_PIG
10	137	44.5	1402	1	BIRG_MOUSE
11	137	44.5	1403	1	BIRE_MOUSE
12	136	44.2	1403	1	BIRF_MOUSE
13	133	43.2	268	1	IAP3_MOUSE
14	129	41.9	438	1	IAP1_MOUSE
15	128	41.6	1403	1	BIR1_HUMAN
16	126	40.9	239	1	ZFP_IRV6
17	125	40.9	1447	1	BIRB_MOUSE
18	124	40.3	298	1	BIR7_HUMAN
19	112	36.4	236	1	BIR8_HUMAN
20	112	36.4	1403	1	BIRA_MOUSE
21	109	35.4	236	1	BIR8_PANTR
22	107	34.7	236	1	BIR8_GORGO
23	106.5	34.6	275	1	IAP_GYCP
24	106	34.4	498	1	IAP2_DROME
25	94	30.5	275	1	IAP1_MOUSE
26	83.5	27.1	286	1	IAP1_MOUSE
27	75	24.4	224	1	IAPL_MOUSE
28	74.5	24.2	142	1	BIR5_MOUSE
29	74.5	24.2	997	1	BIR1_MOUSE
30	72.5	23.5	4829	1	BIR6_MOUSE
31	71.5	23.2	140	1	BIR5_MOUSE
32	68.5	22.2	224	1	IAPL_MOUSE
33	68.5	22.2	224	1	IAPL_MOUSE

34	68.5	22.2	224	1	IAPL_MOUSE	011452 african swi
35	68.5	22.2	238	1	IAPL_MOUSE	011453 african swi
36	62.5	20.3	142	1	BIR5_MOUSE	091497 rattus norv
37	57	18.5	707	1	ORC1_MOUSE	P54789 schizosacch
38	57	18.5	1401	1	WRN_MOUSE	C09053 mus musculu
39	56.5	18.3	1192	1	MTH1_MOUSE	O31255 mycobacteri
40	55.5	18.0	617	1	THRB_MOUSE	P18292 rattus norv
41	55.5	18.0	618	1	THRB_MOUSE	P18221 mus musculu
42	55	17.9	249	1	IAP2_MOUSE	P41454 autographa
43	54.5	17.7	244	1	Y28K_MOUSE	P20313 sulfolobus
44	54	17.5	203	1	CHPE_MOUSE	O87005 pseudomonas
45	54	17.5	958	1	YBS3_MOUSE	P38086 saccharomyc

## ALIGNMENTS

RESULT 1  
ID BIR2\_HUMAN STANDARD: PRT; 604 AA.  
AC Q13489; Q16628; Q9UP46; Q9HC27;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DI 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 1 (Inhibitor of apoptosis protein 1) (H1AP1) (H1AP2) (TNFR2-TNFR signaling complex protein 1) (IAP homolog C).  
DE BIRC2 OR API1 OR IAP1 OR MHC.  
GN Homo sapiens (Human).  
OS Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OC NCBI\_Taxid-9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-96128127; PubMed-8548810;  
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;  
RT "The TNFR2-TNFR signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";  
RL Cell 83:1243-1252(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-96149249; PubMed-8552191;  
RA Iliston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertov-Horvat G., Farhani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.S.;  
RT "Suppression of apoptosis in mammalian cells by M1P and a related family of IAP genes.";  
RL Nature 379:349-353(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX TISSUE-Fetal liver;  
RA MEDLINE-96209843; PubMed-8643514;  
RT Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-99252096; PubMed-10233894;  
RA Horrevorts A.J., Fortlijn R.D., van Zonneveld A.J., de Vries C.J., ten Cate J.W., Pannekoek H.;  
RT "Vascular endothelial genes that are responsive to tumor necrosis factor-alpha in vitro are expressed in atherosclerotic lesions, including inhibitor of apoptosis protein-1, stannin, and two novel genes.";  
RL Blood 93:3418-3431(1999).  
RN [5]  
RP SEQUENCE OF 362-441 FROM N.A.  
RX MEDLINE-20519161; PubMed-11066071;  
RA Baens M., Steyts A., Dierlam J., De Wolf-Peters C., Marynen P.;  
RT "Structure of the M1P gene and molecular characterization of the genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone

RT B-cell lymphomas of MALT type." ;  
 RL Genes Chromosomes Cancer 29:281-291 (2000).  
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
 CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
 CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
 CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
 CC -1- SUBUNIT: Interacts with SMAC and with PRIS2; these interactions  
 CC inhibit apoptotic suppressor activity.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN  
 CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,  
 CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.  
 CC -1- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation  
 CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid  
 CC tissue). This translocation is found in approximately 50% of  
 CC cytogenetically abnormal low-grade MALT lymphoma and involves  
 CC MAL1 and BIRC2.  
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -----  
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 CC -----  
 DR EMBL: I49432; AAC41943.1; -  
 DR EMBL: U45878; AAC50371.1; -  
 DR EMBL: U37546; AAC50507.1; -  
 DR EMBL: AF070674; AAC83232.1; -  
 DR EMBL: AF178945; AAG09369.1; -  
 DR HSSP: Q13490; IOBH.  
 DR Genew: HGNC:591; BIRC3.  
 DR MIM: 601712; -  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR001841; Znf\_Ring.  
 DR Pfam: PF000197; zf-C3HC4; 1.  
 DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00653; BIR; 3.  
 DR SMART: SM00238; BIR; 3.  
 DR SMART: SM00114; CARD; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE: PS50209; CARD; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 KW Apoptosis; Zinc-finger; Repeat; Chromosomal translocation.  
 FT REPEAT 29 96 BIR 1.  
 FT REPEAT 169 235 BIR 2.  
 FT REPEAT 255 322 BIR 3.  
 FT DOMAIN 439 529 CARD.  
 FT ZN\_FING 557 592 CARD.  
 FT SITE 442 443 RING-TYPE.  
 FT BREAKPOINT FOR TRANSLOCATION TO FORM  
 FT BIRC2-MALT1.  
 FT CONFLICT 18 18 N -> Y (IN REF. 4).  
 FT CONFLICT 119 119 N -> H (IN REF. 2).  
 FT CONFLICT 153 153 D -> E (IN REF. 2).  
 FT CONFLICT 163 163 H -> P (IN REF. 2).  
 FT CONFLICT 165 165 A -> P (IN REF. 2).  
 FT CONFLICT 191 191 K -> R (IN REF. 2).  
 FT CONFLICT 191 191 F -> L (IN REF. 2).  
 FT CONFLICT 364 364 Q -> P (IN REF. 2).  
 FT CONFLICT 552 552 Q -> P (IN REF. 2).  
 SQ SEQUENCE 604 AA; 68371 MW; 8581A0BA9AAB4A7 CRC64;  
 Query Match 100.0%; Score 308; DB 1; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-33;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRNSTVSTFPAGVPSERSIARAGFYTYGVNDKVKCFCCGLMDNKRQDSP 55  
 DB 28 CELYRNSTVSTFPAGVPSERSIARAGFYTYGVNDKVKCFCCGLMDNKRQDSP 82  
 RESULT 2  
 BIR3\_HUMAN  
 ID BIR3\_HUMAN STANDARD; PRT; 618 AA.  
 AC Q13490; Q16516;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Baculoviral iAP repeat-containing protein 3 (inhibitor of apoptosis  
 DE protein 2) (HIAIP2) (HIAIP-2) (C-IAP1) (TNFR2-TRAF signaling complex  
 DE BIRC3 OR API2 OR IAP2 OR MIH2).  
 GN BIRC3 OR API2 OR IAP2 OR MIH2.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96128127; PubMed-8548810;  
 RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;  
 RT "The TNFR2-TRAF signaling complex contains two novel proteins related  
 RT to baculoviral inhibitor of apoptosis proteins";  
 RL Cell 83:1243-1252(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Liver;  
 RX MEDLINE-96149249; PubMed-8552191;  
 RA Liston P., Roy N., Ramal K., Lefebvre C., Balrd S., Chertom-Horvat G.,  
 RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
 RT "Suppression of apoptosis in mammalian cells by NAIP and a related  
 RT family of IAP genes";  
 RL Nature 379:349-353(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Fetal liver;  
 RX MEDLINE-96209843; PubMed-8643514;  
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
 RT "Cloning and expression of apoptosis inhibitory protein homologs that  
 RT function to inhibit apoptosis and/or bind tumor necrosis factor  
 RT receptor-associated factors";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Uterus;  
 RA Strussberg R.;  
 RT Submitted (Oct-2001) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RP STRUCTURE BY NMR OF 266-363.  
 RX MEDLINE-99332054; PubMed-10404221;  
 RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;  
 RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)  
 RT repeat";  
 RL Nat. Struct. Biol. 6:648-651(1999).  
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
 CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
 CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
 CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
 CC -1- SUBUNIT: Interacts with SMAC and with PRIS2; these interactions  
 CC inhibit apoptotic suppressor activity.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.  
 CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,  
 CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD  
 CC LEUKOCYTES.  
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

[illegible]

```

RN      121
RP      SEQUENCE FROM N.A
RC      TISSUE=Skkeletal muscle;
RX      MEDLINE=38110590; PubMed=9441758;
RA      Liston P., Lefevre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT      "Genomic characterization of the mouse inhibitor of apoptosis protein
RT      1 and 2 genes.";
RL      Genomics 46:495-503(1997).
CC      -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC      WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC      FORM AN HETEROERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC      NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC      -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC      inhibit apoptotic suppressor activity (By similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC      LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC      -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC      -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC      -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC      -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC      -----
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CC      or send an email to license@isb.sib.ch)
CC      -----
DR      EMBL; L49433; AAC42078.1; -;
DR      EMBL; U88909; AAC53532.1; -;
DR      HSSP; Q13490; IQBH.
DR      MCD; MGI:1197009; Birc3.
DR      InterPro: IPR001370; BIR.
DR      InterPro: IPR001375; CARD.
DR      InterPro: IPR001841; ZnF_fing.
DR      Pfam; PF00097; Zf-C3HC4; 1.
DR      Pfam; PF00619; CARD; 1.
DR      Pfam; PF00653; BIR; 3.
DR      SMART; SMO0238; BIR; 3.
DR      SMART; SMO0114; CARD; 1.
DR      SMART; SMO0184; RING; 1.
DR      PROSITE; PS01282; BIR_REPEAT_1; 3.
DR      PROSITE; PS0143; BIR_REPEAT_2; 3.
DR      PROSITE; PS50209; CARD; 1.
DR      PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR      PROSITE; PS50089; ZF_RING_2; 1.
DR      Apoptosis; zinc-finger; Repeat.
FT      REPEAT 46 113
FT      REPEAT 177 243 BIR 1.
FT      REPEAT 262 329 BIR 2.
FT      DOMAIN 447 537 BIR 3.
FT      ZN_FING 565 600 CARD.
FT      CONFLICT 380 380 RING-TYPE.
FT      CONFLICT 380 380 E -> K (IN REF. 2).
SQ      SEQUENCE 612 AA; 69676 MM; ED08969D93C6C610D CRC64;

Query Match 95.5%; Score 294; DB 1; Length 612;
Best Local Similarity 94.5%; Pred. No. 4.6e-31;
Matches 52; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 CELYMSYTFSPAGVPSERSLARAGFYTYGVNDKVCFCGGLMDMDMKRGDSP 55
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 45 CELYMSYTSNAPPRGVPYSERSLARAGFYTYGVNDKVCFCGGLMDMDMKRGDSP 99

RESULT 4
ID      BIR2_MOUSE
AC      008863;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
ST      STANDARD; PRT; 600 AA.

```

DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis  
CN BIRC2 OR API1 OR IAP1.  
OS Mus musculus (mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Skeletal muscle;  
RA MEDLINE=98110590; PubMed=9441758;  
RT Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;  
RT "Genomic characterization of the mouse inhibitor of apoptosis protein  
1 and 2 genes".  
RL Genomics 46:495-503(1997).  
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).  
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25, these interactions  
CC inhibit apoptotic suppressor activity (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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CC -----  
DR EMBL: U88908; AAC3531.1; -  
DR HSSP: Q13490; IQBH.  
DR MGD: MGI:1197007; Birc2.  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR001315; CARD.  
DR InterPro: IPR001841; ZnF\_fing.  
DR Pfam: PF00097; zf-C3HC4; 1.  
DR Pfam: PF00653; BIR; 3.  
DR SMART: SM00238; BIR; 3.  
DR SMART: SM00114; CARD; 1.  
DR SMART: SM00184; RING; 1.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE: PS0209; CARD; 1.  
DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE: PS0089; ZF\_RING\_2; 1.  
KW Apoptosis; Zinc-finger; Repeat.  
FT REPEAT 27 94 BIR 1.  
FT REPEAT 167 233 BIR 2.  
FT REPEAT 253 320 BIR 3.  
FT DOMAIN 436 525 CARD.  
FT ZN\_FING 553 588 RING-TYPE.  
SQ SEQUENCE 600 AA; 67198 MW; ADVF73B6849317D1 CRC64;  
  
Query Match 93.2%; Score 287; DB 1; Length 600;  
Best Local Similarity 90.9%; Pred. No. 3.8e-30;  
Matches 50; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
OY 1 CELYRSTSTSTPAGVPSERSLARAGFYTGNDVKYKCCGCLMDNKRKQSP 55  
DB 26 CELYRSTSTSTPAGVPSERSLARAGFYTGNDVKYKCCGCLMDNKRKQSP 80  
  
RESULT 5  
BIR\_CHICK  
ID BIR\_CHICK STANDARD; PRT; 611 AA.

AC 090660;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Inhibitor of apoptosis protein (IAP) (inhibitor of T cell apoptosis  
DE protein).  
GN ITA.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxId=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Spleen;  
RA MEDLINE=97101112; PubMed=8945639;  
RT Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;  
RT "ITA, a vertebrate homologue of IAP that is expressed in T  
RT lymphocytes".  
RL DNA Cell Biol. 15:981-988(1996).  
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.  
CC -1- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN  
CC BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.  
CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF  
CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.  
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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CC -----  
DR EMBL: U27466; AAB48118.1; -  
DR HSSP: Q13490; IQBH.  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR001315; CARD.  
DR InterPro: IPR001841; ZnF\_fing.  
DR Pfam: PF00097; zf-C3HC4; 1.  
DR Pfam: PF00653; BIR; 3.  
DR SMART: SM00238; BIR; 3.  
DR SMART: SM00114; CARD; 1.  
DR SMART: SM00184; RING; 1.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE: PS0209; CARD; 1.  
DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE: PS0089; ZF\_RING\_2; 1.  
KW Apoptosis; Zinc-finger; Repeat; Nuclear protein.  
FT REPEAT 30 97 BIR 1.  
FT REPEAT 176 242 BIR 2.  
FT REPEAT 262 329 BIR 3.  
FT DOMAIN 446 536 CARD.  
FT ZN\_FING 564 599 RING-TYPE.  
SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;  
  
Query Match 80.5%; Score 248; DB 1; Length 611;  
Best Local Similarity 81.5%; Pred. No. 5.3e-25;  
Matches 44; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
  
OY 1 CELYRSTSTSTPAGVPSERSLARAGFYTGNDVKYKCCGCLMDNKRKQSP 54  
DB 29 CELYRSTSTSTPAGVPSERSLARAGFYTGNDVKYKCCGCLMDNKRKQSP 82  
  
RESULT 6

BIR4\_HUMAN  
ID BIR4\_HUMAN STANDARD: PRT: 497 AA.  
AC P98170; Q9NQ14;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)  
DE (IAP-like protein) (HILP).  
GN BIR4 OR API3 OR IAP3 OR XIAP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal brain;  
RX MEDLINE=96149249; PubMed=8552191;  
RA Liston P., Roy N., Tama K., Lefebvre C., Balrd S., Cherton-Horvat G., Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";  
RL Nature 379:349-353(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal heart;  
RX MEDLINE=96256286; PubMed=8654366;  
RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., Van Dongen J.L., Gillfillan M.C., Shleis H., Hardwick J.M., Thompson C.B.;  
RT "A conserved family of cellular genes related to the baculovirus IAP gene and encoding apoptosis inhibitors.";  
RL EMBO J. 15:2685-2694(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Graffham D.;  
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.  
RN [4]  
RP FUNCTION.  
RX MEDLINE=97373959; PubMed=9230442;  
RA Deveraux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;  
RT "X-linked IAP is a direct inhibitor of cell-death proteases.";  
RL Nature 388:300-304(1997).  
RN [5]  
RP MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.  
RX MEDLINE=21634829; PubMed=11604410;  
RA Verhagen A.M., Silke J., Ekert P.G., Pakusch M., Kaufmann H., Connolly L.M., Day C.L., Tikoo A., Burke R., Wobbel C., Moritz R.L., Simpson R.J., Vaux D.L.;  
RT "HtrA2 promotes cell death through its serine protease activity and its ability to antagonize inhibitor of apoptosis proteins.";  
RL J. Biol. Chem. 277:445-454(2002).  
RN [6]  
RP STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.  
RX MEDLINE=21020961; PubMed=11140637;  
RA Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T., Herrmann J., Wu J.C., Pesik S.W.;  
RT "Structural basis for binding of Smac/DIABLO to the XIAP BIR3 domain.";  
RL Nature 408:1004-1008(2000).  
RN [7]  
RP FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9.  
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- TISSUE SPECIFICITY: UBIQUITOUS, EXCEPT PERIPHERAL BLOOD LEUCOCYTES.  
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3 and -7, while the third BIR is involved in caspase-9 inhibition. The interactions with SMAC and PRSS25 are mediated by the second and third BIR domains.  
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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DR EMBL: U45880; AAC50373.1; -  
DR EMBL: U32974; AAC50518.1; -  
DR EMBL: AL121601; CAB95312.1; -  
DR PDB: 1G3F; 10-JAN-01.  
DR Genew; HGNC:592; BIR4.  
DR MIM: 300079; -  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR001841; Znf\_ring.  
DR Pfam: PF00697; Zf-C3HC4; 1.  
DR Pfam: PF00653; BIR; 3.  
DR SMART; SM00238; BIR; 3.  
DR SMART; SM00184; RING; 1.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE: PS50089; ZF\_RING\_2; 1.  
KW Apoptosis; Zinc-finger; Repeat; Thiol protease inhibitor;  
KW 3D-structure.  
FT REPEAT 26 93 BIR 1.  
FT REPEAT 163 230 BIR 2.  
FT REPEAT 265 330 BIR 3.  
FT ZN\_FING 450 485 RING-TYPE.  
FT MUTAGEN 214 214 D->S: REDUCED INTERACTION WITH PRSS25.  
FT MUTAGEN 314 314 E->S: DECREASED INTERACTION WITH SMAC AND WITH PRSS25.  
FT CONFLICT 162 162 S -> C (IN REF. 1).  
FT CONFLICT 423 423 Q -> P (IN REF. 2).  
SQ SEQUENCE 497 AA; 56684 MW; 9D394C16D45EB635 CRC64;  
Query Match 51.3%; Score 156; DB 1; Length 497;  
Best Local Similarity 52.8%; Pred. No. 3, 2e-13;  
Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;  
QY 2 ELYRMSTVSTPAGVPSERSIARAGFYTYGVNDKYKCCGGLMDNMWRGDS 54  
DB 26 EENRLKTFANFSGSPVSASTIARAGFLTYTGSDIVKCSCHAAVDRMWDGDS 78  
RESULT 7  
BIR4\_MOUSE  
ID BIR4\_MOUSE STANDARD: PRT: 496 AA.  
AC Q60989; O08865;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)  
DE (IAP homolog A) (MIAP3) (MIAP-3).  
GN BIR4 OR API3 OR XIAP OR AI3A OR MIHA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;  
RX MEDLINE=96209843; PubMed=8643514;  
RA Uren A.G., Pakusch M., Hawkins C.J., Pule K.L., Vaux D.L.;  
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Farahani R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;



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RC TISSUE=Aorta; PubMed-9501011;
RX MEDLINE-98162622; Binder B.R., Lipp J.;
RA Stenlik C., de Martin R., Binder B.R., Lipp J.;
RT "Cytokine induced expression of porcine inhibitor of apoptosis
RT protein (Iap) family member is regulated by NF-kappa B.";
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U79142; AAC39171.1; -
DR HSSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS01282; BIR_REPEAT_2; 2.
DR PROSITE: PS00209; CARD; 1.
DR PROSITE: PS00518; zf_RING_1; FALSE_NEG.
DR PROSITE: PS00518; zf_RING_2; 1.
DR Apoptosis; Zinc-finger Repeat.
KW REPEAT 4 70 BIR 1.
FT REPEAT 90 157 BIR 2.
FT DOMAIN 193 283 CARD.
FT ZN_FING 311 346 RING-TYPE.
SQ SEQUENCE 358 AA; 40977 MW; EB226FA9A6190A4 CRC64;

Query Match 45.8%; Score 141; DB 1; Length 358;
Best Local Similarity 49.0%; Pred. No. 4e-11;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

OY 5 RMSTSTPAGVPSERSIARAGFTYTGNDKVCFCGGLMDNKRKGDSP 55
DB 93 RKFTCNMPSIPVHPEQLASAGFYMGHSDVCKCCGCGI RCMWGGDP 143

RESULT 10
BIR_MOUSE STANDARD: PRT; 1402 AA.
AC Q9JIB3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis
DE Inhibitory protein 7).
GN BIRC1G OR NAIP7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20414747; PubMed-10958627;
RA Endlitz M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.

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CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF242433; AAF82749.1; -
DR HSSP: Q13490; IQBH.
DR MGD: MGI:1858256; Birc1g.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS01282; BIR_REPEAT_2; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR Apoptosis; Repeat; Multigene family.
KW REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1402 AA; 159662 MW; C1DFEBA359893E0D CRC64;

Query Match 44.5%; Score 137; DB 1; Length 1402;
Best Local Similarity 46.3%; Pred. No. 5.4e-10;
Matches 25; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

OY 2 ELRSTSTPAGVPSERSIARAGFTYTGNDKVCFCGGLMDNKRKGDSP 55
DB 278 ELRMDMFMDOESVGEALVRAGFTYTKKDIYRCFCGCGLEKMAEGDP 331

RESULT 11
BIR_MOUSE STANDARD: PRT; 1403 AA.
AC Q9R016; Q9R029; P81703; O09122; O09121;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1e (Neuronal apoptosis
DE Inhibitory protein 5).
GN BIRC1E OR NAIP5 OR NAIP-RS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99431676; PubMed-10501978;
RA Huang S., Scharf J.M., Growney J.D., Endlitz M.G., Dietrich W.F.;
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct
RT functional transcripts.";
RL Mamm. Genome 10:1032-1035(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/Sv;
RX MEDLINE-99417674; PubMed-10486205;
RA Endlitz M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,
RA Kunzel L.M., Miller W., Dietrich W.F.;
RT "Comparative sequence analysis of the mouse and human Lgn1/SKA
RT interval.";
RL Genomics 60:137-151(1999).
RN [3]
RP SEQUENCE OF 82-168 FROM N.A.
RX STRAIN=129/Sv;
RX MEDLINE-97131520; PubMed-8975718;
RA Scharf J.M., Damron D., Firsella A., Bruno S., Beggs A.H.,
RA Kunzel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies

```

```

RT within the 1gnt critical interval and contains multiple copies of Naip
RT exon 5."
RL Genomics 38:405-417(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF135492; AAD56764.1; -.
DR EMBL: AF131205; AAD56760.1; -.
DR HSSP: Q13490; 10BH.
DR MGD: MGI:1298220; B1rcle.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
FT CONFLICT 92 92 K -> R (IN REF. 1).
FT CONFLICT 144 144 S -> R (IN REF. 1).
FT CONFLICT 242 242 T -> G (IN REF. 2).
FT CONFLICT 472 472 F -> A (IN REF. 2).
FT CONFLICT 516 516 A -> D (IN REF. 2).
FT CONFLICT 521 521 V -> T (IN REF. 2).
FT CONFLICT 533 533 V -> A (IN REF. 2).
FT CONFLICT 538 538 E -> D (IN REF. 2).
FT CONFLICT 1092 1092 H -> L (IN REF. 2).
FT CONFLICT 1129 1129 R -> Q (IN REF. 2).
FT CONFLICT 1137 1137 V -> I (IN REF. 2).
FT CONFLICT 1242 1242 D -> N (IN REF. 2).
FT CONFLICT 1276 1276 D -> N (IN REF. 2).
SQ SEQUENCE 1403 AA; 159695 MW; B27F65043BCEC42 CRC64;

Query Match 44.5%; Score 137; DB 1; Length 1403;
Best Local Similarity 46.3%; Pred. No. 5.4e-10;
Matches 25; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 2 ELYRMSTYSTFPAGVPYSESLARAGFYTGVDKVCFCGGLMDMKRGDSP 55
DB 278 EELRMDKFMKQPSVPYGFALVRAGFYTGKRDIVRCFCGGLCKEMKAGDDP 331

RESULT 12
BIRF_MOUSE STANDARD; PRT; 1403 AA.
AC Q9UB6; P81704; 009122; 009121;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1f (Neuronal apoptosis
DE Inhibitory protein 6)
GN BIRCLF OR NAIP OR NAIP-RS4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20414747; PubMed=10958627;

```

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RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
RA "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
RN [2]
RP SEQUENCE OF 82-168 FROM N.A.
RX STRAIN=129/SVJ;
RX MEDLINE=97131520; PubMed=8975718;
RA Scharf J.M., Damron D., Fritsella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RA "The mouse region syntenic for human spinal muscular atrophy lies
RT within the 1gnt critical interval and contains multiple copies of Naip
RT exon 5.";
RL Genomics 38:405-417(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF242431; AAP82751.1; -.
DR EMBL: U66327; AAC52975.1; -.
DR HSSP: Q13490; 10BH.
DR MGD: MGI:1298222; B1rc1f.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1403 AA; 159823 MW; 9D491250358C4B9 CRC64;

Query Match 44.2%; Score 136; DB 1; Length 1403;
Best Local Similarity 46.3%; Pred. No. 7.3e-10;
Matches 25; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 2 ELYRMSTYSTFPAGVPYSESLARAGFYTGVDKVCFCGGLMDMKRGDSP 55
DB 278 EELRMDKFMKQPSVPYGFALVRAGFYTGKRDIVRCFCGGLCKEMKAGDDP 331

RESULT 13
IAP3_NPVOP STANDARD; PRT; 268 AA.
AC P41437;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis inhibitor 3 (IAP-3).
GN IAP3 OR IAP.
OS Oryza pseudoturgata multicaulis polyhedrosis virus (OPNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxId=164623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94187094; PubMed=8139034;
RX Birnbaum M.J., Clem R.J., Miller L.K.;
RX "An apoptosis-inhibiting gene from a nuclear polyhedrosis virus
RT encoding a polypeptide with Cys/His sequence motifs.";
RL J. VIROL. 68:2521-2528(1994).
RN [2]

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RT atrophy candidate genes SMN and NAIP.";  
RL Genomics 48:121-127(1998).  
RN [3]  
RP SEQUENCE OF 386-623 FROM N.A.  
RA der Steege G., Draaijers T.G., Grootsoorten P.M., Ozinga J.,  
RA Anzeveno R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,  
RA Buys C.H.C.M.;  
RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 222-1403 FROM N.A.  
RA Jones K., Graves T., McPherson J.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP FUNCTION.  
RC TISSUE-Liver;  
RX MEDLINE=96149249; Pubmed=8552191;  
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertton-Horvat G.,  
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RT "Suppression of apoptosis in mammalian cells by NAIP and a related  
RT family of IAP genes.";  
RL Nature 379:349-353(1996).  
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
CC SIGNALS.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY  
CC NEURONS. FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN  
CC SPINAL CORD.  
CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN  
CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY (TYPE I (SMA TYPE 1), SMAS  
CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE 1  
CC (WERDNIG-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE  
CC III (WOLFF-BART-KUGELBERG-WEILANDER DISEASE) BASED UPON THE AGE OF  
CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE  
CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO  
CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000  
CC NEWBORNS.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.  
CC -----  
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CC -----  
DR EMBL: U19251; AAC52045.1; -;  
DR EMBL: U80017; AAC52047.1; -;  
DR EMBL: U21913; AA64504.1; -;  
DR EMBL: AC005031; AAC62261.1; -;  
DR HSSP: Q13490; IOBH.  
DR Genew; HGNC:7634; BIRC1.  
DR MIM: 600355; -;  
DR InterPro: IPR001370; BIR.  
DR Pfam: PF00653; BIR\_3.  
DR SMART: SM00238; BIR\_3.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE: PS0837; NACHT; 1.  
KM Apoptosis; Repeat.  
FT REPEAT 60 127 BIR 1.  
FT REPEAT 159 227 BIR 2.  
FT REPEAT 278 345 BIR 3.  
FT DOMAIN 464 758 NACHT.  
FT CONFLICT 222 223 PK -> YR (IN REF. 4).  
FT CONFLICT 386 387 VP -> ST (IN REF. 3).  
FT CONFLICT 535 535 M -> V (IN REF. 3).  
FT CONFLICT 553 553 Y -> H (IN REF. 3).  
FT CONFLICT 1228 1231 MISSING (IN REF. 4).  
SQ SEQUENCE 1403 AA; 159613 MW; 566304C154DA5E64 CRC64;

Matches 22; Conservative 11; Mismatches 21; Indels 0; Gaps 0;  
QY 2 ELTRMSTYTFPPAGVPYSEKSLARAGFTYTGVDKVCPCCGMLDNWKRQDSP 55  
Db 278 EEELRDSFKDMPRESAAGVAALAKAGLFTYGIINDIYOCFSCGCGCLEKRWQGGDDP 331  
Search completed: May 5, 2003, 16:02:44  
Job time: 4.2811 secs

Query Match 41.6%; Score 128; DB 1; Length 1403;  
Best Local Similarity 40.7%; Pred. No. 8.3e-09;



OY 1 CELYRMSTSTFPAGVPVSRSLARAGFYTGNDVKYKCCGCLMDNMKRGDSP 55  
 DB 28 CELYRMSTSTFPAGVPVSRSLARAGFYTGNDVKYKCCGCLMDNMKRGDSP 82

## RESULT 2

ID Q9ESR8 PRELIMINARY: PRT: 589 AA.  
 AC Q9ESR8; 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Inhibitor of apoptosis protein 2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN (1)

RP SEQUENCE FROM N.A.  
 RA Holcik M., Lefebvre C.A., Hicke K., Korneluk R.G.;  
 RT "Cloning and characterization of the Rat Homologs of the Inhibitor of  
 RT Apoptosis Protein 1, 2, and 3 Genes."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL: AF183431; AAG22971.1; -  
 DR HSSP: O13490; 10BH.  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR001841; Znf\_fing.  
 DR Pfam: PF00653; BIR; 3.  
 DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00238; BIR; 3.  
 DR SMART: SM00114; CARD; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
 DR PROSITE: PS50209; CARD; 1.  
 DR Zinc-finger.  
 KW SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD2853 CRC64;

Query Match 95.5%; Score 294; DB 11; Length 589;  
 Best Local Similarity 94.5%; Pred. No. 7.2e-31;  
 Matches 52; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CELYRMSTSTFPAGVPVSRSLARAGFYTGNDVKYKCCGCLMDNMKRGDSP 55  
 DB 24 CELYRMSTSTFPAGVPVSRSLARAGFYTGNDVKYKCCGCLMDNMKRGDSP 78

## RESULT 3

ID Q9QZC6 PRELIMINARY: PRT: 589 AA.  
 AC Q9QZC6; 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE Inhibitor of apoptosis protein 2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN (1)

RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RA Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.;  
 RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AF190020; AAF04585.1; -  
 DR HSSP: Q13490; 10BH.  
 DR InterPro: IPR001370; BIR.

DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR001841; Znf\_fing.  
 DR Pfam: PF00653; BIR; 3.  
 DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00238; BIR; 3.  
 DR SMART: SM00114; CARD; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
 DR PROSITE: PS50209; CARD; 1.  
 DR Zinc-finger.  
 KW SEQUENCE 589 AA; 66777 MW; E6812FEE3EA3A142 CRC64;

Query Match 95.5%; Score 294; DB 11; Length 589;  
 Best Local Similarity 94.5%; Pred. No. 7.2e-31;  
 Matches 52; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CELYRMSTSTFPAGVPVSRSLARAGFYTGNDVKYKCCGCLMDNMKRGDSP 55  
 DB 24 CELYRMSTSTFPAGVPVSRSLARAGFYTGNDVKYKCCGCLMDNMKRGDSP 78

## RESULT 4

ID Q921N0 PRELIMINARY: PRT: 374 AA.  
 AC Q921N0; 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Similar to baculoviral IAP repeat-containing 2.  
 DE BIRC2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)

RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC011338; AAH11338.1; -  
 DR MGD: MGI:1197007; BIRC2.  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR; 3.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; UNKNOWN\_3.  
 DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
 KW SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7E46F3 CRC64;

Query Match 92.2%; Score 284; DB 11; Length 374;  
 Best Local Similarity 90.9%; Pred. No. 9.3e-30;  
 Matches 50; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 CELYRMSTSTFPAGVPVSRSLARAGFYTGNDVKYKCCGCLMDNMKRGDSP 55  
 DB 26 CELYRMSTSTFPAGVPVSRSLARAGFYTGNDVKYKCCGCLMDNMKRGDSP 80

## RESULT 5

ID Q9DDN2 PRELIMINARY: PRT: 324 AA.  
 AC Q9DDN2; 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE Apoptosis inhibitor ch-IAP1 (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN (1)

RP SEQUENCE FROM N.A.  
 RA Pendleton C.N., Bargmann W.J., Varadarajan J., Bose H.R. Jr.;

"The apoptosis inhibitor ch-IAP1 is a direct transcriptional target of v-Rel and c-Rel."

RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF311289; AAG42316.1; -

DR HSSP: Q13490; 108H.

DR InterPro: IPR001370; BIR.

DR Pfam: PF00653; BIR; 3.

DR SMART: SM00238; BIR; 3.

DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.

DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.

DR NON\_TER 324 324

SO SEQUENCE 324 AA; 36567 MW; 5E2B89DEAE3733F3 CRC64;

Query Match 80.5%; Score 248; DB 13; Length 324;  
Best Local Similarity 81.5%; Pred. No. 5.3e-25;  
Matches 44; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CELYRSTSTPAGVPVSESLARAGFYTTGVNDKVCFCGCGMLDNMRGDS 54  
DB 29 CELYRSTSTPAGVPVSESLARAGFYTTGVNDKVCFCGCGMLDNMRGDS 82

RESULT 6  
ID 057319 PRELIMINARY; PRT; 610 AA.

AC 057319

DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE Inhibitor of apoptosis protein 1 (IAP) (inhibitor of T cell apoptosis  
PROTEIN).

DE IAP1.

GN Gallus gallus (Chicken).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
Gallus.

OC NCB1\_TaxID-9031;

OX NCB1\_TaxID-9031;

RN [1]

RP SEQUENCE FROM N.A.  
STRAIN-WHITE LEGHORN; TISSUE-EMBRYONIC FIBROBLAST;  
MEDLINE-98038801; PubMed-9372964;

RX You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;  
"ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a  
mediator of the antiapoptotic activity of the v-Rel oncoprotein.";  
Mol. Cell. Biol. 17:7328-7341(1997)

RT Mol. Cell. Biol. 17:7328-7341(1997)

RL -1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED  
CELLS.

CC -1- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF  
THE V-REL-TRANSFORMED CELLS.

CC -1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE  
SPLEEN, THYMUS, BURSAS, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS  
IN TESTIS, BRAIN AND SKELETAL MUSCLE.

CC -1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION  
PROCESS.

CC -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.

CC -1- SIMILARITY: MEMBER OF THE IAP FAMILY.

CC -1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF  
APOPTOSIS PROTEIN REPEAT).

CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

DR EMBL: AF008592; AAB88044.1; -

DR HSSP: Q13490; 108H.

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001315; CARD.

DR InterPro: IPR001841; znf\_ring.

DR Pfam: PF00653; BIR; 3.

DR Pfam: PF00619; CARD; 1.

DR Pfam: PF00097; zf-C3HC4; 1.

DR SMART: SM00238; BIR; 3.

DR SMART: SM00114; CARD; 1.

DR SMART: SM00184; RING; 1.

DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.

DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.

DR PROSITE: PS50209; CARD; 1.

KW Apoptosis; Zinc-finger; Repeat

FT REPEAT 30 97 BIR\_REPEAT\_1.

FT REPEAT 176 242 BIR\_REPEAT\_2.

FT REPEAT 262 329 BIR\_REPEAT\_3.

FT ZN\_FING 563 597 C3HC4-TYPE.

SO SEQUENCE 610 AA; 68924 MW; ADE47619650BA44A6 CRC64;

Query Match 80.5%; Score 248; DB 13; Length 610;  
Best Local Similarity 81.5%; Pred. No. 1.1e-24;  
Matches 44; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CELYRSTSTPAGVPVSESLARAGFYTTGVNDKVCFCGCGMLDNMRGDS 54  
DB 29 CELYRSTSTPAGVPVSESLARAGFYTTGVNDKVCFCGCGMLDNMRGDS 82

RESULT 7  
ID 080WD2 PRELIMINARY; PRT; 628 AA.

AC 080WD2

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE IAP1.

GN IAP1.

OS Brachydanio rerio (Zebrafish) (zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
Cyprinidae; Danio.

OC NCB1\_TaxID-7955;

RN [1]

RP SEQUENCE FROM N.A.  
MEDLINE-20373792; PubMed-10917738;

RX Inohara N., Nunez G.;  
"Genes with homology to mammalian apoptosis regulators identified in  
zebrafish.";  
Cell death Differ. 7:509-510(2000).

RT Cell death Differ. 7:509-510(2000).

RL [2]

RN [2]

RP SEQUENCE FROM N.A.  
Inohara N., Nunez G.;  
Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

RX EMBL: AF442500; AAL33679.1; -

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001315; CARD.

DR InterPro: IPR001841; znf\_ring.

DR Pfam: PF00653; BIR; 3.

DR Pfam: PF00619; CARD; 1.

DR Pfam: PF00097; zf-C3HC4; 1.

DR SMART: SM00238; BIR; 3.

DR SMART: SM00114; CARD; 1.

DR SMART: SM00184; RING; 1.

DR PROSITE: PS01282; BIR\_REPEAT\_1; UNKNOWN\_2.

DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.

DR PROSITE: PS50089; zf\_RING\_2; 1.

DR PROSITE: PS50209; CARD; 1.

SO SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87C8A95 CRC64;

Query Match 62.3%; Score 197; DB 13; Length 628;  
Best Local Similarity 61.1%; Pred. No. 3.7e-17;  
Matches 33; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 2 ELYRSTSTPAGVPVSESLARAGFYTTGVNDKVCFCGCGMLDNMRGDS 55  
DB 29 ELYRSTSTPAGVPVSESLARAGFYTTGVNDKVCFCGCGMLDNMRGDS 82

RESULT 8  
ID 080WH2 PRELIMINARY; PRT; 405 AA.

AC 080WH2

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

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DE XIAP.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF439767; AAL32047.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_rling.
DR Pfam: PF00653; BIR. 3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR. 3.
DR SMART: SM00184; RING. 1.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 405 AA; 45564 MW; A366E342D83BECNB CRC64;

Query Match
Best Local Similarity 51.3%; Score 158; DB 13; Length 405;
Matches 26; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 5 RMSTYSTFPAGVPSERSLARAGFYTGVDKYKCFCCGGLMDNMRKGDSP 55
ID 140 RLSTFPMWPDSPYRPEDLAEGAGTYIGIDNVQCFCCGGGLSGWEGDDP 190
DB 140 RLSTFPMWPDSPYRPEDLAEGAGTYIGIDNVQCFCCGGGLSGWEGDDP 190

RESULT 9
Q8UVF8 PRELIMINARY; PRT; 493 AA.
ID 08UVF8
AC 08UVF8:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
GN IAP3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Identification of chicken inhibitor of apoptosis protein XIAP
RT (IAP).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF451854; AAL47170.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_rling.
DR Pfam: PF00653; BIR. 3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR. 3.
DR SMART: SM00184; RING. 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;

Query Match
Best Local Similarity 51.3%; Score 158; DB 13; Length 493;
Matches 29; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

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QY 2 ELYRMSTYSTFPAGVPSERSLARAGFYTGVDKYKCFCCGGLMDNMRKGDSP 54
ID 26 EHRRLGTFVFPDPCPSASALRAGFYTGEDDKYKCFCHYVEGMEGDS 78
DB 26 EHRRLGTFVFPDPCPSASALRAGFYTGEDDKYKCFCHYVEGMEGDS 78

RESULT 10
Q9ESFO PRELIMINARY; PRT; 496 AA.
ID 09ESFO
AC 09ESFO:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF183429; AAG22969.1; -.
DR HSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_rling.
DR Pfam: PF00653; BIR. 3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR. 3.
DR SMART: SM00184; RING. 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
KW Zinc-finger.
SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AEC5B798 CRC64;

Query Match
Best Local Similarity 49.0%; Score 151; DB 11; Length 496;
Matches 27; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 2 ELYRMSTYSTFPAGVPSERSLARAGFYTGVDKYKCFCCGGLMDNMRKGDSP 54
ID 26 EHRRLGTFVFPDPCPSASALRAGFYTGEDDKYKCFCHYVEGMEGDS 78
DB 26 EHRRLGTFVFPDPCPSASALRAGFYTGEDDKYKCFCHYVEGMEGDS 78

RESULT 11
Q9EQ05 PRELIMINARY; PRT; 501 AA.
ID 09EQ05
AC 09EQ05:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=MISTAR; TISSUE=OVARY;
RA Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
RT protein in the rat corpus luteum."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF304333; AAG41192.1; -.
DR HSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_rling.
DR Pfam: PF00653; BIR. 3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR. 3.

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RA  Rawden L.L., Glassberg K.J., Diggs J., Shaw R., Farmerie W.,
RA  Moyer R.W.;
RT  "Complete Genomic Sequence of the Anisacta moorei Entomopoxvirus:
RT  Analysis and Comparison with other Poxviruses.";
RL  J. Virol. 74:120-139(2000).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Rawden A.L., Glassberg K.J., Diggs J., Shaw R., Farmerie W.,
RA  Moyer R.W.;
RL  Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF250284; AAG02727.1; -.
DR  HSSP; Q13490; 1QBH.
DR  InterPro: IPR001370; BIR.
DR  InterPro: IPR001841; ZnF_ring.
DR  Pfam: PF00653; BIR; 2.
DR  SMART; SM00338; BIR; 2.
DR  SMART; SM00184; RING; 1.
DR  PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR  PROSITE; PS50143; BIR_REPEAT_2; 2.
SQ  SEQUENCE 264 AA; 30547 MW; 2EB7ZDA4B58D920A CRC64;

Qy  5 RMSTYTFPAGVPSERSLAFAGEFYTGVDNKKVCFCCGLMLDMNKRQDSP 55
Db  110 RLKRYKEMPISMPSTKELTAGGFYTGKSDKVCFCFCGSLNKNETDDP 160

RESULT 14
Q01A70
AC  Q01A70
ID  Q01A70
AC  Q01A70;
ID  Q01A70;
DE  01-OCT-2000 (TREMblrel. 15, Created)
DE  01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE  01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE  Inhibitor of apoptosis 1 (Fragment).
OS  Gallus gallus (Chicken).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC  Gallus.
OX  NCBI_TaxID=9031;
RX  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-BRED LECHORN; TISSUE-SPLEEN;
RC  MEDLINE-21158006; PubMed-11261557;
RA  Zhou H., Liu W., Lamont S.J.;
RT  "Genetic variation among chicken lines and mammalian species in
RT  specific genes.";
RL  Poult. Sci. 80:284-288(2001).
DR  EMBL; AF221082; AAF5319.1; -.
DR  HSSP; Q13490; 1QBH.
DR  InterPro: IPR001370; BIR.
DR  Pfam: PF00653; BIR; 2.
DR  SMART; SM00338; BIR; 2.
DR  PROSITE; PS01282; BIR_REPEAT_1; 2.
DR  PROSITE; PS50143; BIR_REPEAT_2; 2.
FT  NON_TER 1
FT  NON_TER 1
SQ  SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

Query Match 46.88; Score 144; DB 13; Length 195;
Best Local Similarity 51.08; Pred. No. 2,7e-11;
Matches 28; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy  5 RMSTYTFPAGVPSERSLAFAGEFYTGVDNKKVCFCCGLMLDMNKRQDSP 55
Db  119 RVKFIIMNPFIPVQPGQLADAGFYTGGRNDVACFCDCGSLNKNESDDP 169

RESULT 15
Q01A69

```





GenCore version 5.1.4\_p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 15:50:57 ; Search time 10.8353 Seconds

(without alignments)  
676.383 Million cell updates/sec

Title: US-08-569-749-6

Perfect score: 308  
Sequence: 1 CELXRMSSTSTFPAGVPVSE.....KVACFCGCLMLDMWRKQDSP 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308	100.0	55	AAW13548	Human c-IAP2 repea
2	308	100.0	604	AAW19747	Human inhibitor of
3	308	100.0	604	AAW19582	Human apoptosis in
4	308	100.0	604	AAW13546	Human c-IAP2. Hom
5	308	100.0	604	AAW69295	Human HIAP-1 prote
6	308	100.0	604	AAW52703	Human cellular inh
7	308	100.0	604	AAI33997	Human cellular inh
8	308	100.0	604	ABG55664	Human inhibitor of
9	308	100.0	1140	AAU97837	Human cysteine pro
10	308	100.0	1141	AAW50694	Human APT2-MLT chl

11	301	97.7	55	AAW13547	Human c-IAP1 repea
12	301	97.7	306	AAU02925	Angiotensin conver
13	301	97.7	618	AAW19746	Human inhibitor of
14	301	97.7	618	AAW19583	Human apoptosis in
15	301	97.7	618	AAW13545	Human c-IAP1. Hom
16	301	97.7	618	AAW69296	Human HIAP-2 prote
17	301	97.7	618	AAI33998	Human cellular inh
18	301	97.7	618	ABG55665	Human inhibitor of
19	294	95.5	591	AAW19586	Mouse apoptosis in
20	294	95.5	612	ABG55668	Mouse inhibitor of
21	294	95.5	612	AAW13555	Murine c-IAP. Mus
22	294	95.5	612	AAW69299	Murine HIAP-2 prot
23	287	93.2	600	AAW69298	Murine HIAP-1 prot
24	287	93.2	602	AAW19585	Mouse apoptosis in
25	287	93.2	602	ABG55667	Mouse inhibitor of
26	158	51.3	497	AAW19581	Human apoptosis in
27	158	51.3	497	AAW69294	Human XIAP protein
28	158	51.3	497	AAW99985	Human X-linked inh
29	158	51.3	497	AAW59451	Human XIAP protein
30	158	51.3	497	ABG55663	Human inhibitor of
31	152	49.4	496	AAW19745	Mouse inhibitor of
32	152	49.4	496	AAW19584	Mouse apoptosis in
33	152	49.4	496	AAW69297	Murine XIAP protei
34	152	49.4	496	ABG55666	Mouse inhibitor of
35	151	49.0	438	AAW04583	Human inhibitor of
36	146	47.4	464	AAU75747	Human inhibitor of
37	131	42.5	438	AAW48191	Drosophila mutant
38	130.5	42.4	263	ABW09488	AMEP Baculovirus-
39	129	41.9	434	AAW48195	Drosophila melanog
40	129	41.9	438	ABW61858	Drosophila melanog
41	129	41.9	438	ABW67347	Drosophila wild-ty
42	129	41.9	438	AAW48188	Drosophila mutant
43	129	41.9	438	AAW48189	Drosophila mutant
44	129	41.9	438	AAW48190	Drosophila mutant
45	129	41.9	438	AAW48192	Drosophila mutant

#### ALIGNMENTS

```

RESULT 1
AAW13548
ID AAW13548 standard; Protein: 55 AA.
XX
AC AAW13548;
DT 22-JUL-1997 (first entry)
XX
DE Human c-IAP2 repeat 1.
XX
KW IAP; inhibitor; apoptosis; RING finger domain; reelinosis;
KW myocardial infarction; nephritis; HIV.
XX
OS Homo sapiens.
XX
PN W09706182-A1.
XX
PD 20-FEB-1997.
XX
PF 06-AUG-1996; 96WO-US12860.
XX
PR 08-DEC-1995; 95US-0569749.
PR 08-AUG-1995; 95US-0512946.
XX
( (TUL- ) TULARIK INC.
Goeddel DV, Rothe M.
WPL: 1997-154209/14.
Nucleic acids encoding cellular inhibitor of apoptosis proteins -
useful for apoptosis regulation in cells to reduce or increase
apoptosis and for pharmacological screening

```

XX Claim 3: Page 24; 35pp; English.

PS The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -

XX AAW61590/T61591) comprise a series of defined structural domain

CC repeats and/or a RING finger domain; in particular, at least two of

CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat

CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)

CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus

CC sequences derived from these human genes.

CC The nucleic acid is used for recombinant prodn. of human cellular

CC inhibitor of apoptosis protein which modulates apoptosis

CC regulation. The nucleic acids are useful in therapies where

CC increased cell-specific apoptosis is desired, e.g. in restinosis,

CC inflammatory disease states, myocardial infarction, glomerular

CC nephritis, transplant rejection and infectious diseases, e.g. HIV.

CC They can also be used in conditions requiring a reduction in

CC apoptosis.

CC

XX

SQ Sequence 55 AA;

Query Match 100.0%; Score 308; DB 18; Length 55;

Best Local Similarity 100.0%; Pred. No. 1.1e-34;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CELYRSTSTPAGVPVSESLARAGFYTGVDKVKCCGLMDNKRGDSP 55

DB 1 CELYRSTSTPAGVPVSESLARAGFYTGVDKVKCCGLMDNKRGDSP 55

RESULT 2

AAW19747

ID AAW19747 standard; Protein; 604 AA.

XX

AC AAW19747;

XX

DT 16-SEP-1997 (first entry)

XX

DE Human inhibitor of apoptosis protein homologue MIRC.

XX

KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIRC;

KW degenerative disease; infectious disease; autoimmune disease;

KW cancer; therapy; diagnosis.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Region 29..97

FT Region /label= BIR

FT Region 169..236

FT Region /label= BIR

FT Region 255..323

FT Region /label= BIR

FT Region 556..593

FT Region /label= RING\_finger

XX

PN WO9723501-A1.

XX

PD 03-JUL-1997.

XX

PF 20-DEC-1996; 96WO-AU00827.

XX

PR 22-DEC-1995; 95AU-0007275.

XX

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

XX

PI Vaux DL;

XX

DR WPI: 1997-350966/32.

DR N-PSDB; AAT72712.

XX

PT Isolated protein homologues of viral inhibitors of apoptosis - used

PT to modulate apoptosis for treatment of degenerative, infectious or

PT autoimmune diseases and cancer

XX

PS Claim 9: Page 58-62; 136pp; English.

XX

CC Mammalian IAP homologue C (MIRC) (AAW19747) is a human homologue of

CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid

CC sequence was deduced from a cDNA clone (see also AAT72712) isolated

CC from a human foetal liver cDNA library using primers based on

CC human EST sequences that resembled the BIR repeats of Orf1a

CC pseudotsuguta polyhedrosis virus IAP. IAP homologues (see also

CC AAW19745-46 and AAW19748-52) and their derivatives and chemical

CC analogues can be used in methods for modulating apoptosis in animal

CC cells, specifically for treatment, by inhibition, of degenerative

CC and infectious disease or, by promotion, of cancer and autoimmune

CC disease.

XX

SQ Sequence 604 AA;

Query Match 100.0%; Score 308; DB 18; Length 604;

Best Local Similarity 100.0%; Pred. No. 1.7e-33;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CELYRSTSTPAGVPVSESLARAGFYTGVDKVKCCGLMDNKRGDSP 55

DB 28 CELYRSTSTPAGVPVSESLARAGFYTGVDKVKCCGLMDNKRGDSP 82

RESULT 3

AAW19582

ID AAW19582 standard; Protein; 604 AA.

XX

AC AAW19582;

XX

DT 02-SEP-1997 (first entry)

XX

DE Human apoptosis inhibitor HIRAP-1.

XX

KW Apoptosis inhibitor; HIRAP-1; HIV; AIDS; neurodegeneration;

KW myelodysplastic syndrome; ischemia; myocardial infarction; stroke;

KW reperfusion injury; toxin-induced liver disease; gene therapy;

KW diagnosis.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Domain 29..96

FT Domain /label= BIR-1

FT Domain 169..235

FT Domain /label= BIR-2

FT Domain 255..322

FT Domain /label= BIR-3

FT Domain 546..591

FT Domain /label= Ring\_zinc\_finger

XX

PN WO9706255-A2.

XX

PD 20-FEB-1997.

XX

PF 05-AUG-1996; 96WO-IB01022.

XX

PR 22-DEC-1995; 95US-0576956.

XX

PR 04-AUG-1995; 95US-0511485.

XX

PA (UYOT-) UNIV OTTAWA.

XX

PI Baird S, Korneluk R, Liston P, Mackenzie AE;

XX

DR WPI: 1997-154262/14.

DR N-PSDB; AAT70837.

XX

PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used

PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection

PT of susceptibility to apoptotic disease

xx Claim 27; Page 72-74; 219pp; English.  
 ps  
 xx Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and  
 cc M-HIAP-2 (AA119581-86) are a new class of mammalian proteins that  
 cc are inhibitors of apoptosis (IAP) and which are characterized by  
 cc the presence of a ring zinc finger domain (see also AA119587) and at  
 cc least one BIR (baculovirus IAP repeat) domain (see also AA119588).  
 cc The HIAP amino acid sequences were deduced from cDNA clones (AA170837  
 cc and AA170838) from a human liver library. IAP polypeptides can be  
 cc expressed in host cells (in vitro or in vivo) and used in methods  
 cc for treating diseases and disorders involving apoptosis, esp. in a  
 cc human diagnosed as HIV-positive or as having AIDS, a  
 cc neurodegenerative disease, a myelodysplastic syndrome or an  
 cc ischemic injury, selected from myocardial infarction, stroke,  
 cc reperfusion injury, or a toxin-induced liver disease.  
 cc  
 xx Sequence 604 AA;  
 so

Query Match 100.0%; Score 308; DB 18; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-33;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGNDKVCFCGGLMDNKKRDS 55  
 DB 28 CELYRMSTYSTFPAGVPVSESLARAGFYTGNDKVCFCGGLMDNKKRDS 82

RESULT 4  
 AA113546  
 ID AA113546 standard; Protein; 604 AA.

AA113546;

22-JUL-1997 (first entry)

Human c-IAP2.

IAP: inhibitor; apoptosis; RING finger domain; restinosis;

myocardial infarction; nephritis; HIV.

Homo sapiens.

WO9706182-A1.

20-FEB-1997.

06-AUG-1996; 96WO-US12860.

08-DEC-1995; 95US-0569749.

08-AUG-1995; 95US-0512946.

(TULA-) TULARIK INC.

Goeddel DV, Rothe M;

WPI: 1997-154209/14.

N-PSDB; AAT61591.

Nucleic acids encoding cellular inhibitor of apoptosis proteins  
 useful for apoptosis regulation in cells to reduce or increase  
 apoptosis and for pharmacological screening

Disclosure: Page 21-23; 35pp; English.

The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -  
 AA113546/113547) comprise a series of defined structural domain  
 repeats and/or a RING finger domain; in particular, at least two of  
 cc a first domain repeat (AA113547 or AA113548), a second domain repeat  
 cc (AA113549 or AA113550), and a third domain repeat (AA113551 or AA113552)  
 cc and/or a RING finger domain (AA113553 or AA113554), or a consensus  
 cc sequences derived from these human genes.  
 cc The nucleic acid is used for recombinant prodn. of human cellular

inhibitor of apoptosis protein which modulates apoptosis  
 regulation. The nucleic acids are useful in therapies where  
 increased cell-specific apoptosis is desired, e.g. in restinosis,  
 inflammatory disease states, myocardial infarction, glomerular  
 nephritis, transplant rejection and infectious diseases, e.g. HIV.  
 They can also be used in conditions requiring a reduction in  
 apoptosis.

Query Match 100.0%; Score 308; DB 18; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-33;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGNDKVCFCGGLMDNKKRDS 55  
 DB 28 CELYRMSTYSTFPAGVPVSESLARAGFYTGNDKVCFCGGLMDNKKRDS 82

RESULT 5  
 AA169295  
 ID AA169295 standard; Protein; 604 AA.

AA169295;

13-NOV-1998 (first entry)

Human HIAP-1 protein.

Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;

proliferative disease; IAP; therapy; cancer; human; HIAP-1 protein.

Homo sapiens.

WO9835693-A2.

20-AUG-1998.

13-FEB-1998; 98WO-IB00781.

13-FEB-1997; 97US-0800929.

(UYOT-) UNIV OTTAWA.

Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;

Tsang B;

WPI: 1998-467164/40.

N-PSDB; AAV55039.

Inducing apoptosis in proliferative mammalian cells with inhibitor  
 of IAP or NAIP polypeptide - also methods for prognosis based on  
 presence of IAP and NAIP, specifically applied to cancers involving  
 p53 mutations

Disclosure: Fig 2; 147pp; English.

This sequence is the human HIAP-1 protein, which is a inhibitor of  
 apoptosis protein (IAP), and can be used in the method of the invention.  
 The method is for enhancing apoptosis in cells from a mammal with  
 proliferative disease by treatment with a compound that inhibits  
 biological activity of an IAP or NAIP polypeptide. The inhibitory  
 compounds are used to treat proliferative diseases, specially cancers of  
 ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
 liver nasopharynx, thyroid, central nervous system, prostate, colon,  
 rectum, cervix or endometrium, particularly to increase their sensitivity  
 to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
 detected in many cancers and are associated with poor prognosis.  
 resistance to chemotherapeutic agents and mutations in p53 (it is  
 suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
 genes). Transgenic animals are used for testing the effects of antisense  
 oligonucleotides and for screening for the inhibitors.

SQ Sequence 604 AA;  
 Query Match 100.0%; Score 308; DB 19; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-33;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYSTPAGVPVSESLARAGFYTGVDKVCFCGGLMDNKKRGDSP 55  
 |||||||  
 DB 28 CELYRMSTYSTPAGVPVSESLARAGFYTGVDKVCFCGGLMDNKKRGDSP 82

RESULT 6  
 AAY52703  
 ID AAY52703 standard; Protein; 604 AA.  
 AC AAY52703;  
 XX  
 XX

DT 26-JAN-2000 (first entry)

DE Human cellular inhibitor of apoptosis-2 protein.

KW Identification: genetic target; gene modulation; human;  
 KM antisense oligonucleotide; phosphorothioate; target validation;  
 XX nucleotide sequence-based technology; antisense drug discovery.

OS Homo sapiens.

PN W09953101-A1.

PD 21-OCT-1999.

PF 13-APR-1999; 99WO-US08268.

PR 13-APR-1998; 98US-0081483.

PR 28-APR-1998; 98US-0067638.

XX (ISIS-) ISIS PHARM INC.

PI Cowsett LM, Baker BF, McNeill J, Freier SM, Sasnor HM, Brooks DG;

DR Ohast C, Wyatt JR, Borchers AH, Vickers TA;

DR WPI: 1999-620446/53.

DR N-PSDB: AA241005.

PT Identifying compounds which modulate expression of nucleic acids, used

PS to provide compounds having defined physical, chemical or bioactive

CC properties, e.g. antisense activity

CC Example 20; Page 197-202; 264pp; English.

CC A method has been developed of defining a set of compounds that modulate

CC the expression of a target nucleic acid (tNA) sequence via binding of

CC the compounds with the tNA sequence. The method comprises generating a

CC library of virtual compounds in silico according to defined criteria,

CC and evaluating in silico the binding of the virtual compounds with the

CC tNA according to defined criteria. Also described are: (1) a method of

CC defining a set of oligonucleotides (ONS) that modulate the expression of

CC a tNA sequence via binding of the ONS with the tNA sequence comprising

CC generating a library of virtual compounds in silico according to defined

CC criteria, and evaluating in silico the binding of the virtual ONS with

CC the tNA according to defined criteria; and (2) a method of defining a

CC set of compounds that modulate the expression of a tNA sequence via

CC binding of the compounds with the tNA. The methods can be used for the

Query Match 100.0%; Score 308; DB 20; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-33;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYSTPAGVPVSESLARAGFYTGVDKVCFCGGLMDNKKRGDSP 55  
 |||||||  
 DB 28 CELYRMSTYSTPAGVPVSESLARAGFYTGVDKVCFCGGLMDNKKRGDSP 82

RESULT 7  
 AAY33997  
 ID AAY33997 standard; Protein; 604 AA.  
 AC AAY33997;  
 XX  
 XX

DT 26-NOV-1999 (first entry)

DE Human cellular inhibitor of apoptosis-2 sequence.

KW Cellular inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;  
 KM c-IAP-2; prophylaxis; infection; inflammation; tumor formation.

OS Homo sapiens.

PN US93958771-A.

PD 28-SEP-1999.

PF 03-DEC-1998; 98US-0205144.

PR 03-DEC-1998; 98US-0205144.

XX (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowsett LM, Ackermann EJ;

DR WPI: 1999-561046/47.

DR N-PSDB: AA222096.

PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2

PS useful for e.g. diagnostics, therapeutics, and as research reagents -

CC Example 13; Columns 45-50; 33pp; English.

CC The invention provides antisense compounds of 8-30 nucleotides that

CC inhibit the expression of human cellular inhibitor of Apoptosis-2

CC (c-IAP-2). The antisense compounds may be used for diagnostics,

CC therapeutics (for modulating the expression of c-IAP-2), prophylaxis

CC (e.g. to prevent or delay infection, inflammation, or tumor formation),

CC as research reagents (e.g. to distinguish between members of a biological

CC pathway) and in kits. The present sequence represents the human cellular

CC inhibitor of apoptosis-2.

CC Sequence 604 AA;

QY 1 CELYRMSTYSTPAGVPVSESLARAGFYTGVDKVCFCGGLMDNKKRGDSP 55  
 |||||||  
 DB 28 CELYRMSTYSTPAGVPVSESLARAGFYTGVDKVCFCGGLMDNKKRGDSP 82

RESULT 8

ABG65664

ID ABG65664 standard; Protein; 604 AA.

AC ABG65664;

XX 26-AUG-2002 (first entry)

DE Human inhibitor of apoptosis, HIAP1.

```

XX Human; antisense; inhibitor of apoptosis; H1NP1, H1AP2; XIAP;
KM cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KM pancreatic cancer; embryonic development; viral pathogenesis;
KM autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KM lupus erythematosus; herpes virus infection; pox virus infection;
KM adenovirus infection; proliferative disease.
XX
OS Homo sapiens.
PN WO200226968-A2.
PD 04-APR-2002.
XX
XX 27-SEP-2001; 2001WO-CA01379.
XX
XX 28-SEP-2000; 2000US-0672717.
XX
XX (UYOT-) UNIV OTTAWA.
XX (ABGE-) ABERA THERAPEUTICS INC.
XX
XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX WPI: 2002-479562/51.
XX DR N-PSDB; ABR93870.
XX
XX Novel antisense inhibitor of apoptosis nucleic acid useful for
XX PT enhancing apoptosis in a cell, for treating cancer and other
XX PT proliferative diseases
XX
XX PS Disclosure; Fig 2; 135pp; English.
XX
XX The invention relates to an inhibitor of apoptosis (IAP) antisense
XX CC nucleic acid (I) that inhibits IAP biological activity, regardless of
XX CC length of the antisense nucleic acid, the IAP proteins may be mouse
XX CC or human XIAP, H1AP1 or H1AP2. Also included are a pharmaceutical
XX CC composition comprising a mammalian IAP antisense molecule and a method of
XX CC enhancing apoptosis in a cell, comprising administering a negative
XX CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
XX CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
XX CC mammal diagnosed with a proliferative disease. The method is useful for
XX CC treating a patient diagnosed with a proliferative disease like cancer.
XX CC The IAP antisense molecule is useful to treat, ameliorate, improve,
XX CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
XX CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
XX CC conditions where apoptosis is involved or implicated (e.g. embryonic
XX CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
XX CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
XX CC virus, pox virus and adenovirus). The present sequence is a human IAP
XX CC protein sequence.
XX
XX SQ Sequence 604 AA:
XX
XX Query Match 100.0%; Score 308; DB 23; Length 604;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-33;
XX Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CELYRMSTSTPAGVPVSESLARAGFYTGVDKRCFCGGLMDNKKRGDSP 55
XX |||||||
XX DB 28 CELYRMSTSTPAGVPVSESLARAGFYTGVDKRCFCGGLMDNKKRGDSP 82
XX
XX RESULT 9
XX AAU97837
XX ID AAU97837 standard; Protein; 1140 AA.
XX
XX AAU97837;
XX
XX 27-AUG-2002 (first entry)
XX
XX Human cysteine protease fusion protein AP12-MLT (CPG2).
XX DE Cysteine protease; CPG2; cell-cell adhesion; lymphoma; osteoporosis;
XX

```

```

KM Rheumatoid arthritis; inflammatory disease; irritable bowel disease;
KM respiratory disease; asthma; autoimmune disease; bone disease;
KM atherosclerosis; neoplastic disease; melanoma; prostate; lung tumour;
KM ovary tumour; myeloproliferative disorder; leukaemia; metastasis;
KM heart disease; myocardial infarction; cardiac failure; metastasis;
KM reperfusion injury; neurodegenerative disease; Alzheimer's disease;
KM Parkinson's disease; neurological disorder; stroke; muscular dystrophy;
KM liver disease; cataract; infection; transgenic animal; gene; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200233058-A2.
XX
XX PD 25-APR-2002.
XX
XX 22-OCT-2001; 2001WO-GB04698.
XX
XX 20-OCT-2000; 2000GB-0025816.
XX PR 29-JAN-2001; 2001GB-0002260.
XX
XX (INPH-) INPHARMATICA LTD.
XX
XX Fagan RJ, Phelps CB, Gutteridge A, Nicholls RQ;
XX WPI: 2002-46311/49.
XX DR N-PSDB; ABR52387.
XX
XX New proteins identified as cysteine proteases for diagnosing,
XX PT preventing and treating neoplastic, inflammatory, autoimmune diseases
XX PT and neurological disorders
XX
XX PS Claim 1; Fig 15; 129pp; English.
XX
XX This sequence represents a polypeptide (I) termed BAA63099.1 (CPG1),
XX CC AAD6161.1 (CPG2) or AAD38507.2 (CPG3), identified as a cysteine
XX CC protease, its fragment having cysteine protease activity or having an
XX CC antigenic determinant in common with the polypeptide, or its functional
XX CC equivalent. (I) is useful as a cysteine protease and for effecting
XX CC cell-cell adhesion. A nucleic acid (II) encoding (I) is useful for
XX CC expressing a protein that possesses cysteine protease activity. (II),
XX CC (III), a vector (III) comprising (II), a ligand (IV) which binds (I) and
XX CC a compound (V) that alters the activity of (I), are useful for treating
XX CC diseases in which the expression of the natural gene or the activity of
XX CC the polypeptide is higher or lower in a diseased patient when compared
XX CC to the level of expression or activity in a healthy patient. (I) - (V)
XX CC are useful in therapy or diagnosis of disease and in the manufacture of
XX CC a medicament for treating lymphoma, rheumatoid arthritis, osteoporosis,
XX CC inflammatory disease, such as irritable bowel disease, respiratory
XX CC disease such as asthma, autoimmune disease, bone disease,
XX CC atherosclerosis, neoplastic diseases, such as melanoma, prostate, lung
XX CC and ovary tumours, myeloproliferative disorder, leukaemia, metastasis,
XX CC heart disease, myocardial infarction, cardiac failure, reperfusion
XX CC injury, neurodegenerative diseases such as Alzheimer's disease,
XX CC Parkinson's disease, neurological disorder, stroke, muscular dystrophy,
XX CC liver disease, cataract, infection such as bacterial, parasitic,
XX CC Plasmodium and viral infection. A transgenic or knockout non-human animal
XX CC is useful as an animal model to screen for a compound effective to treat
XX CC a disease. This sequence encodes cysteine protease fusion protein
XX CC AP12-MLT (CPG2) described in the invention.
XX
XX SQ Sequence 1140 AA:
XX
XX Query Match 100.0%; Score 308; DB 23; Length 1140;
XX Best Local Similarity 100.0%; Pred. No. 3.6e-33;
XX Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CELYRMSTSTPAGVPVSESLARAGFYTGVDKRCFCGGLMDNKKRGDSP 55
XX |||||||
XX DB 28 CELYRMSTSTPAGVPVSESLARAGFYTGVDKRCFCGGLMDNKKRGDSP 82
XX
XX RESULT 10
XX AAB50694
XX

```

ID AAB50694 standard; Protein: 1141 AA.  
XX  
AC AAB50694;  
XX  
DT 19-MAR-2001 (first entry)  
XX  
DE Human API2-MLT chimeric protein sequence.  
XX  
KW Human; API2-MLT chimera; chimeric; apoptosis inhibitor 2; MLT; API2;  
KW mucosa-associated lymphoid tissue lymphoma associated translocation;  
KW chromosome 11 region q21-22.3; chromosome 18 region q21.1-22;  
KW molecular characterisation; chromosome translocation; carcinogenesis;  
KW fusion protein; malignancy.  
XX  
OS Chimeric - Homo sapiens.  
OS Synthetic.  
XX  
PN WO200073500-A1.  
XX  
PD 07-DEC-2000.  
XX  
PE 26-MAY-2000; 2000WO-EP04796.  
XX  
PR 27-MAY-1999; 99EP-0201683.  
XX  
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
XX  
PI Baens M, Marynen P, Dierlamm J;  
XX  
DR WPI; 2001-061556/07.  
DR N-PSDB; AAC90972.  
XX  
XX  
PT Determining if a tissue sample has a chromosome (11:18) translocation  
PT associated with malignancies by amplifying a nucleic acid sample using  
PT primers complementary to chromosome 11 region q21-22.3 and chromosome  
PT 18 region q21.1-22.  
XX  
XX  
PS Claim 12; Fig 5; 47pp; English.  
XX  
CC The present invention describes a method for determining if a tissue  
CC sample comprises a cell with a chromosome (11:18) translocation  
CC associated with malignancies such as mucosa-associated lymphoid tissue  
CC (MALT) lymphomas. The method comprises subjecting a sample nucleic acid  
CC to amplification using primers complementary to sequences which are on  
CC chromosome 11 region q21-22.3 and on chromosome 18 region q21.1-22. The  
CC method can be used for determining if a tissue sample or analogue  
CC comprises a chromosome (11:18) translocation associated with malignancies  
CC such as mucosa-associated lymphoid tissue lymphomas. The nucleic acid or  
CC the antibody may be used as a probe for detection, for hybridisation to  
CC southern blot cell DNAs or for in situ hybridisation of cells, or for  
CC determining the presence of complementary DNA. The present sequence  
CC represents the specifically claimed chimeric human apoptosis inhibitor 2  
CC (API2)/MALT-lymphoma associated translocation (MLT) protein.  
XX  
SQ Sequence 1141 AA;  
Query Match 100.0%; Score 308; DB 2; Length 1141;  
Best Local Similarity 100.0%; Pred. No. 3 6e-33;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CELYRMSTYTFPAGVPSERSLARAGFYTGVDKVCFCGGLMLNWKRGDSP 55  
DB 28 CELYRMSTYTFPAGVPSERSLARAGFYTGVDKVCFCGGLMLNWKRGDSP 82

RESULT 11  
AAU01347  
ID AAM13547 standard; Protein: 55 AA.  
XX  
AC AAM13547;  
XX  
XX  
DT 22-JUL-1997 (first entry)  
XX

DE Human c-IAP1 repeat 1.  
XX  
XX IAP; inhibitor; apoptosis; RING finger domain; restinosis;  
KW myocardial infarction; nephritis; HIV.  
XX  
OS Homo sapiens.  
XX  
PN WO9706182-A1.  
XX  
PD 20-FEB-1997.  
XX  
PE 06-AUG-1996; 96WO-US12860.  
XX  
PR 08-DEC-1995; 95DS-0569749.  
PR 08-AUG-1995; 95US-0512946.  
XX  
XX (TULA-) TULARIK INC.  
XX  
PA Goeddel DV, Rothe M;  
XX  
PI WPI; 1997-154209/14.  
XX  
DR Nucleic acids encoding cellular inhibitor of apoptosis proteins  
PT useful for apoptosis regulation in cells to reduce or increase  
PT apoptosis and for pharmacological screening  
XX  
XX  
PS Claim 3; Page 23; 35pp; English.  
XX  
XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -  
CC AAT61590/T61591) comprise a series of defined structural domain  
CC repeats and/or a RING finger domain; in particular, at least two of  
CC a first domain repeat (AAM13547 or AAM13548), a second domain repeat  
CC (AAM13549 or AAM13550), and a third domain repeat (AAM13551 or AAM13552)  
CC and/or a RING finger domain (AAM13553 or AAM13554), or a consensus  
CC sequences derived from these human genes.  
CC The nucleic acid is used for recombinant prodn. of human cellular  
CC inhibitor of apoptosis protein which modulates apoptosis  
CC regulation. The nucleic acids are useful in therapies where  
CC increased cell-specific apoptosis is desired, e.g. in restinosis,  
CC inflammatory disease states, myocardial infarction, glomerular  
CC nephritis, transplant rejection and infectious diseases, e.g. HIV.  
CC They can also be used in conditions requiring a reduction in  
CC apoptosis.  
XX  
SQ Sequence 55 AA;  
Query Match 97.7%; Score 301; DB 18; Length 55;  
Best Local Similarity 98.2%; Pred. No. 1e-33;  
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CELYRMSTYTFPAGVPSERSLARAGFYTGVDKVCFCGGLMLNWKRGDSP 55  
DB 1 CELYRMSTYTFPAGVPSERSLARAGFYTGVDKVCFCGGLMLNWKRGDSP 55

RESULT 12  
AAU02925  
ID AAU02925 standard; Protein: 306 AA.  
XX  
AC AAU02925;  
XX  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Angiotensin converting enzyme (ACEV) splice variant protein #25.  
XX  
XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;  
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;  
KW platelet-derived endothelial cell growth factor; cardiovascular disease;  
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1c;  
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;  
KW myocardial infarction; coronary arterial thrombosis; renal disease;  
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;  
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;

KM nonarctoidotic pulmonary granulomatous disease; endothelial abnormality;  
 KW vascular disorder; asbestosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200136632-A2.  
 XX  
 PD 25-MAY-2001.  
 XX  
 PF 17-NOV-2000; 2000WO-IL00766.  
 XX  
 PR 17-NOV-1999; 99IL-0132978.  
 XX  
 PR 10-DEC-1999; 99IL-0133455.  
 XX  
 PA (COMP-) COMPUGEN LTD.  
 XX  
 PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;  
 XX  
 DR MPI: 2001-336004/35.  
 DR N-PSDB; AAS06025.  
 XX  
 PS Novel alternative splicing variants e.g. variant of angiotensin  
 PT converting enzyme (ACEV), useful in identifying candidate compounds  
 PT capable of binding to the variant and to detect anti-variant antibodies.  
 XX  
 PS Claim 4; Fig 25; 51pp; English.  
 XX  
 CC The sequence represents an angiotensin converting enzyme splice variant  
 CC (ACEV) polypeptide. The polypeptides of the invention include variants of  
 CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,  
 CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase  
 CC inhibitor 1C, cellular tumour antigen P53, and vasodilator intestinal  
 CC polypeptide receptor 2. The polypeptides and their associated nucleic  
 CC acids are useful for identification of variant sequences and detection of  
 CC candidate compounds capable of binding to the molecules. The sequences of  
 CC the invention can be used in the treatment and diagnosis of various  
 CC disorders including cardiovascular diseases such as arteriosclerosis,  
 CC myocardial infarction and coronary arterial thrombosis, renal diseases  
 CC such as diabetic nephropathy, muscular diseases such as hypertrophy,  
 CC immune disorders such as immune complex nephritis, multiple sclerosis,  
 CC cancer, sarcoidosis, nonarctoidotic pulmonary granulomatous diseases such  
 CC as asbestosis and vascular pathologies involving an endothelial  
 CC abnormality such as deep vein thrombosis.  
 XX  
 SQ Sequence 306 AA;  
 XX  
 Query Match 97.7%; Score 301; DB 22; Length 306;  
 Best Local Similarity 98.2%; Pred. No. 7.2e-33;  
 Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNMKRGDSP 55  
 DB 45 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNMKRGDSP 99  
 XX  
 RESULT 13  
 AAM19746  
 ID AAM19746 standard; Protein; 618 AA.  
 XX  
 AC AAM19746;  
 XX  
 DT 16-SEP-1997 (first entry)  
 XX  
 DE Human inhibitor of apoptosis protein homologue MIHB.  
 XX  
 KW Inhibitor of apoptosis protein; IAP; mammalian XAP homologue; MIHB;  
 KW degenerative disease; infectious disease; autoimmune disease;  
 KW cancer; therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers

FT Region 46..113  
 FT /label= BIR  
 FT Region 184..250  
 FT /label= BIR  
 FT Region 269..337  
 FT /label= BIR  
 FT Region 569..606  
 FT /label= RING\_finger  
 XX  
 PN MO9723501-A1.  
 XX  
 PD 03-JUL-1997.  
 XX  
 PF 20-DEC-1996; 96WO-AU00827.  
 XX  
 PR 22-DEC-1995; 95AU-0007275.  
 XX  
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 XX  
 PI Vaux DL;  
 XX  
 DR MPI: 1997-350966/32.  
 DR N-PSDB; AAT72711.  
 XX  
 PS Claim 8; Page 51-54; 136pp; English.  
 XX  
 CC Mammalian IAP homologue B (MIHB) (AAM19746) is a human homologue of  
 CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid  
 CC sequence was deduced from a cDNA clone (see also AAT72711) isolated  
 CC from a human foetal liver cDNA library using primers based on  
 CC human EST sequences that resembled the BIR repeats of Oryz1.  
 CC pseudotungta polyhedrosis virus IAP. IAP homologues (see also  
 CC AAM19745 and AAM19747-52) and their derivatives and chemical analogues  
 CC can be used in methods for modulating apoptosis in animal cells,  
 CC specifically for treatment, by inhibition, of degenerative and  
 CC infectious disease or, by promotion, of cancer and autoimmune  
 CC disease.  
 XX  
 SQ Sequence 618 AA;  
 XX  
 Query Match 97.7%; Score 301; DB 18; Length 618;  
 Best Local Similarity 98.2%; Pred. No. 1.6e-32;  
 Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNMKRGDSP 55  
 DB 45 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNMKRGDSP 99  
 XX  
 RESULT 14  
 AAM19583  
 ID AAM19583 standard; Protein; 618 AA.  
 XX  
 AC AAM19583;  
 XX  
 DT 02-SEP-1997 (first entry)  
 XX  
 DE Human apoptosis inhibitor HIAP-2.  
 XX  
 KW Apoptosis inhibitor; HIAP-2; HIV; AIDS; neurodegeneration;  
 KW myelodysplastic syndrome; leukaemia; myocardial infarction; stroke;  
 KW reperfusion injury; toxin-induced liver disease; gene therapy;  
 KW diagnosis.  
 XX  
 OS Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 46..113  
 FT /label= BIR-1

```
FT Domain 184.250
FT /label= BIR-2
FT Domain 269.336
FT /label= BIR-3
FT Domain 560.605
FT /label= Ring_zinc_finger
PN MO9706255-A2.
XX 20-FEB-1997.
XX 05-AUG-1996; 96WO-IB01022.
XX 22-DEC-1995; 95US-0576956.
XX 04-AUG-1995; 95US-0511485.
XX (UYOT-) UNIV OTTAWA.
XX
XX PI Balrd S, Korneluk RG, Liston P, Mackenzie AE;
XX WPI: 1997-154262/14.
XX DR N-PSDB: AAT70838.
XX
XX PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
XX to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
XX of susceptibility to apoptotic disease
XX
XX PS Claim 27; Page 75-77; 219pp; English.
XX
XX CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
XX M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
XX are inhibitors of apoptosis (IAP) and which are characterised by
XX the presence of a ring zinc finger domain (see also AAW19587) and at
XX least one BIR (baculovirus IAP repeat) domain (see also AAW19588)
XX CC The XIAP amino acid sequences were deduced from cDNA clones (AAT70837
XX and AAT70838) from a human liver library. IAP polypeptides can be
XX expressed in host cells (in vitro or in vivo) and used in methods
XX for treating diseases and disorders involving apoptosis, esp. in a
XX human diagnosed as HIV-positive or as having AIDS, a
XX neurodegenerative disease, a myelodysplastic syndrome or an
XX CC ischemic injury, selected from myocardial infarction, stroke,
XX reperfusion injury, or a toxin-induced liver disease.
XX
XX SQ Sequence 618 AA:
XX
XX Query Match 97.7%; Score 301; DB 18; Length 618;
XX Best Local Similarity 98.2%; Pred. No. 1.6e-32;
XX Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 55
Db 45 CELYRMSTYSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 99
RESULT 15
AAW13545
ID AAW13545 standard; Protein: 618 AA.
XX
XX AC AAW13545;
XX
XX DT 22-JUL-1997 (first entry)
XX
XX DE Human c-IAP1.
XX
XX KW IAP; inhibitor; apoptosis; RING finger domain; restinosis;
XX myocardial infarction; nephritis; HIV.
XX
XX OS Homo sapiens.
XX
XX PN MO9706182-A1.
XX
XX PD 20-FEB-1997.
XX
```

```
PF 06-AUG-1996; 96WO-US12860.
XX
XX PR 08-DEC-1995; 95US-0569749.
XX 08-AUG-1995; 95US-0512946.
XX
XX PA (TULA-) TULARIK INC.
XX
XX PI Goedel DV, Rothe M;
XX
XX DR WPI: 1997-154209/14.
XX DR N-PSDB: AAT61590.
XX
XX PT Nucleic acids encoding cellular inhibitor of apoptosis proteins
XX useful for apoptosis regulation in cells to reduce or increase
XX apoptosis and for pharmacological screening
XX
XX PS Disclosure; Page 18-20; 35pp; English.
XX
XX CC The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
XX AAT61590/T61591) comprise a series of defined structural domain
XX repeats and/or a RING finger domain; in particular, at least two of
XX a first domain repeat (AAW13547 or AAW13548), a second domain repeat
XX (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
XX and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
XX sequences derived from these human genes.
XX CC The nucleic acid is used for recombinant prodn. of human cellular
XX inhibitor of apoptosis protein which modulates apoptosis
XX regulation. The nucleic acids are useful in therapies where
XX increased cell-specific apoptosis is desired, e.g. in restinosis,
XX CC inflammatory disease states, myocardial infarction, glomerular
XX nephritis, transplant rejection and infectious diseases, e.g. HIV.
XX CC They can also be used in conditions requiring a reduction in
XX apoptosis.
XX
XX SQ Sequence 618 AA:
XX
XX Query Match 97.7%; Score 301; DB 18; Length 618;
XX Best Local Similarity 98.2%; Pred. No. 1.6e-32;
XX Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 55
Db 45 CELYRMSTYSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 99
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GenCore version 5.1.4\_P5\_4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:59:02 ; Search time 3.12673 Seconds

(without alignments)  
432.866 Million cell updates/sec

Title: US-08-569-749-8

Perfect score: 267

Sequence: 1 LAKAGFYITGPDVACFAC.....WEKDNAMSEHLRHPKCP 46

Scoring table:

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Searched: 262574 seqs, 29422922 residues

262574

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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#### SUMMARIES

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1	267	100.0	46	4 US-08-569-749-8	Sequence 8, Appl1
2	267	100.0	46	5 PCT-US96-12860-8	Sequence 8, Appl1
3	267	100.0	604	4 US-08-569-749-4	Sequence 4, Appl1
4	267	100.0	604	5 PCT-US96-12860-4	Sequence 4, Appl1
5	264	98.9	67	2 US-08-511-485-22	Sequence 22, Appl1
6	264	98.9	604	2 US-08-511-485-6	Sequence 6, Appl1
7	264	98.9	604	3 US-09-212-971-6	Sequence 6, Appl1
8	264	98.9	604	4 US-08-800-929A-6	Sequence 6, Appl1
9	264	98.9	604	4 US-09-617-053A-6	Sequence 6, Appl1
10	248	92.9	46	5 US-08-569-749-7	Sequence 7, Appl1
11	248	92.9	46	5 PCT-US96-12860-7	Sequence 7, Appl1
12	248	92.9	67	2 US-08-511-485-23	Sequence 23, Appl1
13	248	92.9	438	5 PCT-US95-05922A-2	Sequence 2, Appl1
14	248	92.9	618	2 US-08-511-485-8	Sequence 8, Appl1
15	248	92.9	618	4 US-09-212-971-8	Sequence 8, Appl1
16	248	92.9	618	4 US-08-800-929A-8	Sequence 8, Appl1
17	248	92.9	618	4 US-08-569-749-2	Sequence 2, Appl1
18	248	92.9	618	4 US-09-617-053A-8	Sequence 8, Appl1
19	248	92.9	618	4 US-09-069-023-29	Sequence 29, Appl1
20	248	92.9	618	5 PCT-US96-12860-2	Sequence 2, Appl1
21	247	92.5	612	4 US-09-212-971-14	Sequence 14, Appl1
22	247	92.5	612	4 US-08-800-929A-14	Sequence 14, Appl1
23	247	92.5	612	4 US-08-569-749-14	Sequence 14, Appl1
24	247	92.5	612	4 US-09-617-053A-14	Sequence 14, Appl1
25	247	92.5	612	4 PCT-US96-12860-14	Sequence 14, Appl1
26	235	88.0	600	3 US-09-212-971-12	Sequence 12, Appl1
27	235	88.0	600	4 US-08-800-929A-12	Sequence 12, Appl1

28	235	88.0	600	4 US-09-617-053A-12	Sequence 12, Appl1
29	182	68.2	68	2 US-08-511-485-21	Sequence 21, Appl1
30	182	68.2	497	2 US-08-511-485-4	Sequence 4, Appl1
31	182	68.2	497	3 US-09-212-971-4	Sequence 4, Appl1
32	182	68.2	497	4 US-08-800-929A-4	Sequence 4, Appl1
33	182	68.2	497	4 US-09-617-053A-4	Sequence 4, Appl1
34	177	66.3	68	2 US-08-511-485-20	Sequence 20, Appl1
35	177	66.3	496	2 US-08-511-485-10	Sequence 10, Appl1
36	177	66.3	496	3 US-09-212-971-10	Sequence 10, Appl1
37	177	66.3	496	4 US-08-800-929A-10	Sequence 10, Appl1
38	177	66.3	496	4 US-09-617-053A-10	Sequence 10, Appl1
39	145	54.3	67	2 US-08-511-485-15	Sequence 15, Appl1
40	145	54.3	236	4 US-08-121-979-4	Sequence 4, Appl1
41	145	54.3	236	4 US-09-332-319-4	Sequence 4, Appl1
42	145	54.3	236	4 US-09-239-867-2	Sequence 2, Appl1
43	145	54.3	498	4 US-08-511-485-13	Sequence 13, Appl1
44	141	52.8	66	2 US-08-511-485-25	Sequence 25, Appl1
45	141	52.8	236	4 US-09-239-867-4	Sequence 4, Appl1

#### ALIGNMENTS

##### RESULT 1

US-08-569-749-8  
Sequence 8, Application US/08569749

Patent No. 6187557

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Goeddel, David V

TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,749

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brenner, David J.

REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)781-1989

TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 46 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-569-749-8

Query Match

Best Local Similarity 100.0%; Score 267; DB 4; Length 46;

Pred. No. 2; 1e-28;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAKAGFYITGPDVACFACGKLSNWEKDNAMSEHLRHPKCP 46

DB 1 LAKAGFYITGPDVACFACGKLSNWEKDNAMSEHLRHPKCP 46

```
RESULT 2
PCT-US96-12860-8
; Sequence 8, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/513,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-12860-8

Query Match          100.0%; Score 267; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 2,1e-23;
Matches 46; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LAKAGFYITGPDGVACFACGKLSNWEPKDNAMSEHLRHPKCP 46
DB 1 LAKAGFYITGPDGVACFACGKLSNWEPKDNAMSEHLRHPKCP 46

RESULT 3
US-08-569-749-4
; Sequence 4, Application US/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Goeddel, David V
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

```
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-4

Query Match          100.0%; Score 267; DB 4; Length 604;
Best Local Similarity 100.0%; Pred. No. 3.6e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAKAGFYITGPDGVACFACGKLSNWEPKDNAMSEHLRHPKCP 46
DB 189 LAKAGFYITGPDGVACFACGKLSNWEPKDNAMSEHLRHPKCP 234

RESULT 4
PCT-US96-12860-4
; Sequence 4, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 604 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-12860-4

Query Match          100.0%; Score 267; DB 5; Length 604;
Best Local Similarity 100.0%; Pred. No. 3.6e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 LAKAGFYIIGDRVACACGKLSNMEPKDNAMSEHLRHPKCP 46  
DB 189 LAKAGFYIIGDRVACACGKLSNMEPKDNAMSEHLRHPKCP 234

## RESULT 5

US-08-511-485-22  
Sequence 22, Application US/08511485  
Patent No. 5919912  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511.485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 67 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-511-485-22

Query Match 98.9%; Score 264; DB 2; Length 67;  
Best Local Similarity 97.8%; Pred. No. 7.9e-28;  
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGDRVACACGKLSNMEPKDNAMSEHLRHPKCP 46  
DB 21 LAKAGFYIIGDRVACACGKLSNMEPKDNAMSEHLRHPKCP 66

## RESULT 6

US-08-511-485-6  
Sequence 6, Application US/08511485  
Patent No. 5919912  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street

CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511.485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 604 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-511-485-6

Query Match 98.9%; Score 264; DB 2; Length 604;  
Best Local Similarity 97.8%; Pred. No. 8.8e-27;  
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGDRVACACGKLSNMEPKDNAMSEHLRHPKCP 46  
DB 189 LAKAGFYIIGDRVACACGKLSNMEPKDNAMSEHLRHPKCP 234

## RESULT 7

US-09-212-971-6  
Sequence 6, Application US/09212971B  
Patent No. 6107041  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K.  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212.971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER FILING DATE: 1996-04-26  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 604  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-212-971-6

Query Match 98.9%; Score 264; DB 3; Length 604;  
Best Local Similarity 97.8%; Pred. No. 8.8e-27;  
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRAVACFACGKLSNWEKDNAMSEHLRHFPKCP 46  
DB 189 LARAGFYIIGPDRAVACFACGKLSNWEKDNAMSEHLRHFPKCP 234

RESULT 8  
US-08-800-929A-6  
Sequence 6, Application US/08800929A  
Patent No. 6133437  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF  
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
NUMBER OF INVENTION: DISEASE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elding LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996  
APPLICATION NUMBER: 60/017,354  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bleker-Brady, Kristina  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 604 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-800-929A-6

Query Match 98.9%; Score 264; DB 4; Length 604;  
Best Local Similarity 97.8%; Pred. No. 8.8e-27;  
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRAVACFACGKLSNWEKDNAMSEHLRHFPKCP 46  
DB 189 LARAGFYIIGPDRAVACFACGKLSNWEKDNAMSEHLRHFPKCP 234

RESULT 9  
US-09-617-053A-6  
Sequence 6, Application US/09617053A  
Patent No. 6300492  
GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
FILE REFERENCE: 07891/009003  
CURRENT APPLICATION NUMBER: US/09/617,053A  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 604  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-617-053A-6

Query Match 98.9%; Score 264; DB 4; Length 604;  
Best Local Similarity 97.8%; Pred. No. 8.8e-27;  
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRAVACFACGKLSNWEKDNAMSEHLRHFPKCP 46  
DB 189 LARAGFYIIGPDRAVACFACGKLSNWEKDNAMSEHLRHFPKCP 234

RESULT 10  
US-08-569-749-7  
Sequence 7, Application US/08569749  
Patent No. 6187357  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Goedel, David V  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HORBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-7

Query Match 92.9%; Score 248; DB 4; Length 46;

Best Local Similarity 91.3%; Pred. No. 6.6e-26;  
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNNEPKDNANSEHLRHPKCP 46  
Db 1 LAKAGFYIIGPDRVACFACGKLSNNEPKDNANSEHLRHPKCP 46

RESULT 11  
PCT-US96-12860-7

Sequence 7, Application PC/TUS9612860  
GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1 30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

PCT-US96-12860-7  
Query Match 92.9%; Score 248; DB 5; Length 46;  
Best Local Similarity 91.3%; Pred. No. 6.6e-26;  
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNNEPKDNANSEHLRHPKCP 46  
Db 1 LAKAGFYIIGPDRVACFACGKLSNNEPKDNANSEHLRHPKCP 46

RESULT 12  
US-08-511-485-23  
Sequence 23, Application US/08511485  
Patent No. 5919912  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street

ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-292  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744

CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 67 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein

US-08-511-485-23  
Query Match 92.9%; Score 248; DB 2; Length 67;  
Best Local Similarity 91.3%; Pred. No. 1e-25;  
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNNEPKDNANSEHLRHPKCP 46  
Db 21 LAKAGFYIIGPDRVACFACGKLSNNEPKDNANSEHLRHPKCP 66

RESULT 13  
PCT-US95-05922A-2  
Sequence 2, Application PC/TUS9505922A  
GENERAL INFORMATION:  
APPLICANT: HE, ET AL.  
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GIUFFILAN,  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05922A  
FILING DATE: 11 MAY 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-292  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 438 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
PCT-US95-05922A-2

Query Match 92.9%; Score 248; DB 5; Length 438;  
Best Local Similarity 91.3%; Pred. No. 7.9e-25;  
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDGVACFCAGKLSNWEKDNAMSEHLRHPKCP 46  
DB 24 LARAGFYIIGPDGVACFCAGKLSNWEKDNAMSEHLRHPKCP 69

## RESULT 14

US-08-511-485-8  
Sequence 8, Application US/08511485  
Patent No. 5919912  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY PRIMERS,  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-511-485-8

Query Match 92.9%; Score 248; DB 2; Length 618;  
Best Local Similarity 91.3%; Pred. No. 1.2e-24;  
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDGVACFCAGKLSNWEKDNAMSEHLRHPKCP 46  
DB 204 LARAGFYIIGPDGVACFCAGKLSNWEKDNAMSEHLRHPKCP 249

RESULT 15  
US-09-212-971-8

Sequence 8, Application US/09212971B  
Patent No. 6107041  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212,971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017,354  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-212-971-8

Query Match 92.9%; Score 248; DB 3; Length 618;  
Best Local Similarity 91.3%; Pred. No. 1.2e-24;  
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDGVACFCAGKLSNWEKDNAMSEHLRHPKCP 46  
DB 204 LARAGFYIIGPDGVACFCAGKLSNWEKDNAMSEHLRHPKCP 249

Search completed: May 5, 2003, 16:09:11  
Job time : 4.12673 secs

GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:02:07 ; Search time 5.67051 Seconds

(Without alignments)  
699,970 Million cell updates/sec

Title: US-08-569-749-8

Sequence: 1 LAKAGFYIIGPGDRVACFAC.....WEKDKNMSHLRHPKCPF 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328255 segs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/2/pubppa/US08\_NIW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/2/pubppa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubppa/PCUS\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubppa/US09\_NEW\_PUB.pep:\*  
10: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	264	98.9	67	9 US-09-201-936-22	Sequence 22, Appl
2	264	98.9	604	9 US-09-201-936-6	Sequence 6, Appl
3	264	98.9	604	10 US-09-974-592-6	Sequence 62, Appl
4	259	97.0	306	10 US-09-778-927A-62	Sequence 6, Appl
5	248	92.9	67	9 US-09-201-936-23	Sequence 23, Appl
6	248	92.9	438	1 US-08-464-588-2	Sequence 2, Appl
7	248	92.9	618	10 US-09-201-936-8	Sequence 8, Appl
8	248	92.9	618	10 US-09-974-592-8	Sequence 14, Appl
9	247	92.5	612	10 US-09-974-592-14	Sequence 14, Appl
10	244	91.4	551	9 US-09-201-936-42	Sequence 42, Appl
11	235	88.0	600	10 US-09-974-592-12	Sequence 12, Appl
12	235	88.0	602	9 US-09-201-936-40	Sequence 40, Appl
13	182	68.2	68	9 US-09-201-936-21	Sequence 21, Appl
14	182	68.2	110	9 US-09-965-967-21	Sequence 21, Appl
15	182	68.2	497	9 US-09-201-936-4	Sequence 4, Appl
16	182	68.2	497	10 US-09-974-592-4	Sequence 4, Appl
17	177	66.3	68	9 US-09-201-936-20	Sequence 20, Appl
18	177	66.3	496	9 US-09-201-936-10	Sequence 10, Appl
19	177	66.3	496	10 US-09-974-592-10	Sequence 10, Appl

20	145	54.3	67	9 US-09-201-936-15	Sequence 15, Appl
21	145	52.8	498	9 US-09-201-936-13	Sequence 13, Appl
22	141	52.8	66	9 US-09-201-936-25	Sequence 25, Appl
23	141	52.8	107	9 US-09-965-967-20	Sequence 20, Appl
24	141	52.8	278	9 US-09-964-899-39	Sequence 39, Appl
25	141	52.8	1403	8 US-08-913-322-22	Sequence 22, Appl
26	141	52.8	1403	8 US-08-913-322-22	Sequence 24, Appl
27	140	52.4	66	9 US-09-201-936-24	Sequence 24, Appl
28	136	50.9	68	9 US-09-201-936-27	Sequence 27, Appl
29	135	50.6	68	9 US-09-201-936-28	Sequence 28, Appl
30	135	50.6	68	9 US-10-041-859-18	Sequence 18, Appl
31	135	50.6	172	9 US-10-041-859-12	Sequence 12, Appl
32	132	49.4	68	9 US-09-201-936-19	Sequence 19, Appl
33	131	49.1	68	9 US-09-201-936-18	Sequence 18, Appl
34	131	49.1	68	9 US-09-201-936-29	Sequence 29, Appl
35	131	49.1	68	9 US-10-041-859-17	Sequence 17, Appl
36	131	49.1	172	9 US-10-041-859-11	Sequence 11, Appl
37	131	49.1	275	9 US-09-201-936-12	Sequence 12, Appl
38	130	48.7	68	9 US-09-201-936-26	Sequence 26, Appl
39	129	48.3	68	9 US-10-041-859-19	Sequence 19, Appl
40	129	48.3	109	9 US-09-965-967-30	Sequence 30, Appl
41	129	48.3	172	9 US-10-041-859-13	Sequence 13, Appl
42	127	47.6	68	9 US-10-041-859-14	Sequence 14, Appl
43	127	47.6	172	9 US-10-041-859-8	Sequence 8, Appl
44	127	47.6	346	9 US-10-041-859-2	Sequence 2, Appl
45	126	47.2	68	9 US-10-041-859-15	Sequence 15, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-201-936-22
; Sequence 22, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-201-936-22

Query Match      98.9%; Score 264; DB 9; Length 67;
Best Local Similarity 97.8%; Pred. No. 1.7e-26;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAKAGFYIIGPGDRVACFACGKLSNWEKDKNMSHLRHPKCPF 46
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      21 LAKAGFYIIGPGDRVACFACGKLSNWEKDKNMSHLRHPKCPF 66

RESULT 2
US-09-201-936-6
; Sequence 6, Application US/09201936
```

```
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
EARLIER FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 604
TYPE: PRF
ORGANISM: Homo sapiens
US-09-201-936-6
```

```
Query Match          98.9%; Score 264; DB 9; Length 604;
Best Local Similarity 97.8%; Pred. No. 1.9e-25;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 LAKAGFYIIGPGRVACFACGKLSNMPEKDNMSEHLRHFPCPF 46
||:|||||
DB 189 LARAGFYIIGPGRVACFACGKLSNMPEKDNMSEHLRHFPCPF 234

RESULT 3
US-09-974-592-6
Sequence 6, Application US/09974592
Patent No. US20020120121A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 07891/009004
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 604
TYPE: PRF
ORGANISM: Homo sapiens
US-09-974-592-6
```

```
Query Match          98.9%; Score 264; DB 10; Length 604;
Best Local Similarity 97.8%; Pred. No. 1.9e-25;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LAKAGFYIIGPGRVACFACGKLSNMPEKDNMSEHLRHFPCPF 46
||:|||||
DB 189 LARAGFYIIGPGRVACFACGKLSNMPEKDNMSEHLRHFPCPF 234
```

```
RESULT 4
US-09-778-927A-62
Sequence 62, Application US/09778927A
Patent No. US20020068342A1
GENERAL INFORMATION:
APPLICANT: KHOSRAVI, Rami et al.
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
FILE REFERENCE: 2786-0160P
CURRENT APPLICATION NUMBER: US/09/778,927A
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: IL 134453
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: IL135341
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 62
LENGTH: 306
TYPE: PRF
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(306)
OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-927A-62
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```
Query Match          97.0%; Score 259; DB 10; Length 306;
Best Local Similarity 95.7%; Pred. No. 3.8e-25;
Matches 44; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 LAKAGFYIIGPGRVACFACGKLSNMPEKDNMSEHLRHFPCPF 46
||:|||||
DB 204 LARAGFYIIGPGRVACFACGKLSNMPEKDNMSEHLRHFPCPF 249
```

```
RESULT 5
US-09-201-936-23
Sequence 23, Application US/09201936
Patent No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 67
TYPE: PRF
ORGANISM: Homo sapiens
US-09-201-936-23
```

```
Query Match          92.9%; Score 248; DB 9; Length 67;
Best Local Similarity 91.3%; Pred. No. 1.8e-24;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 LAKAGFYIIGPGRVACFACGKLSNMPEKDNMSEHLRHFPCPF 46
||:|||||
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DB 21 LARAGFYIIGPDRVACFACGKLSNMEPKDAMSEHRRHFPNCPF 66

RESULT 6

US-08-464-588-2

Sequence 2, Application US/08464588

Publication No. US20030073159A1

GENERAL INFORMATION:

APPLICANT: HE, ET AL.

TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARILLA, BYRNE, BAIN, GILFILLAN,

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,588

FILING DATE: June 5, 1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05922

FILING DATE: 11 MAY 1995

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-387

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 438 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS:

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

US-08-464-588-2

Query Match 92.9%; Score 248; DB 1; Length 438;

Best Local Similarity 91.3%; Pred. No. 1.4e-23;

Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNMEPKDAMSEHRRHFPNCPF 46

11:|||||

DB 24 LARAGFYIIGPDRVACFACGKLSNMEPKDAMSEHRRHFPNCPF 69

RESULT 7

US-09-201-936-8

Sequence 8, Application US/09201936

Publication No. US20020187946A1

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: Mackenzie, Alexander E.

APPLICANT: Baird, Stephen

APPLICANT: Liston, Peter

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

FILE REFERENCE: 07891/003003

CURRENT APPLICATION NUMBER: US/09/201,936

CURRENT FILING DATE: 1998-12-01

EARLIER APPLICATION NUMBER: 09/011,356

EARLIER FILING DATE: 1998-02-04

EARLIER APPLICATION NUMBER: PCT/IB96/01022

US-09-201-936-8

EARLIER FILING DATE: 1996-08-05

EARLIER APPLICATION NUMBER: 08/576,956

EARLIER FILING DATE: 1995-12-22

EARLIER APPLICATION NUMBER: 08/511,485

EARLIER FILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 8

LENGTH: 618

TYPE: PRT

ORGANISM: Homo sapiens

US-09-201-936-8

Query Match 92.9%; Score 248; DB 9; Length 618;

Best Local Similarity 91.3%; Pred. No. 2.1e-23;

Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNMEPKDAMSEHRRHFPNCPF 46

11:|||||

DB 204 LARAGFYIIGPDRVACFACGKLSNMEPKDAMSEHRRHFPNCPF 249

RESULT 9

US-09-974-592-14

Sequence 14, Application US/09974592

Patent No. US20020120121A1

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: Mackenzie, Alexander E.

APPLICANT: Liston, Peter

APPLICANT: Baird, Stephen

APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND

TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

```

; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-974-592-14

Query Match
Best Local Similarity 92.5%; Score 247; DB 10; Length 612;
Best Local Similarity 91.3%; Pred. No. 2,7e-23;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
Db 197 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 242

RESULT 10
US-09-201-936-42
; Sequence 42, Application US/09201936
; Publication No. US20020187946a1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-42

Query Match
Best Local Similarity 91.4%; Score 244; DB 9; Length 591;
Best Local Similarity 91.3%; Pred. No. 6,3e-23;
Matches 42; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
Db 176 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 221

RESULT 11
US-09-974-592-12
; Sequence 12, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
```

```

; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-974-592-12

Query Match
Best Local Similarity 88.0%; Score 235; DB 10; Length 600;
Best Local Similarity 89.1%; Pred. No. 9e-22;
Matches 41; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
Db 187 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 232

RESULT 12
US-09-201-936-40
; Sequence 40, Application US/09201936
; Publication No. US20020187946a1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-40

Query Match
Best Local Similarity 88.0%; Score 235; DB 9; Length 602;
Best Local Similarity 89.1%; Pred. No. 9e-22;
Matches 41; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
Db 189 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 234

RESULT 13
US-09-201-936-21
; Sequence 21, Application US/09201936
; Publication No. US20020187946a1
; GENERAL INFORMATION:
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RESULT 8
AAW19582
ID AAW19582 standard; Protein: 604 AA.
XX
AC AAW19582;
XX
DT 02-SEP-1997 (first entry)
XX
DE Human apoptosis inhibitor HIAP-1.
XX
KW Apoptosis inhibitor; HIAP-1; HIV; AIDS; neurodegeneration;
KW myelodysplastic syndrome; ischaemia; myocardial infarction; stroke;
KW reperfusion injury; toxin-induced liver disease; gene therapy;
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 29..96
FT Domain /label= BIR-1
FT Domain 169..235
FT Domain /label= BIR-2
FT Domain 255..322
FT Domain /label= BIR-3
FT Domain 546..591
FT Domain /label= Ring_zinc_finger
XX
PN W09706255-A2.
XX
PD 20-FEB-1997.
XX
PF 05-AUG-1996; 96WO-IB01022.
XX
PR 22-DEC-1995; 95US-0576956.
PR 04-AUG-1995; 95US-0511485.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX
DR WPI: 1997-154262/14.
DR N-PSDB; AAT70837.
XX
PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
PT of susceptibility to apoptotic disease
XX
PS Claim 27; Page 72-74; 219pp; English.
XX
CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC are inhibitors of apoptosis (IAP) and which are characterised by
CC the presence of a ring zinc finger domain (see also AAW19587) and at
CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC The HIAP amino acid sequences were deduced from cDNA clones (AAT70837
CC and AAT70838) from a human liver library. IAP polypeptides can be
CC expressed in host cells (in vitro or in vivo) and used in methods
CC for treating diseases and disorders involving apoptosis, esp. in a
CC human diagnosed as HIV-positive or as having AIDS, a
CC neurodegenerative disease, a myelodysplastic syndrome or an
CC ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease.
XX
SQ Sequence 604 AA;
Query Match 98.9%; Score 264; DB 18; Length 604;
Best Local Similarity 97.8%; Pred. No. 3.2e-25;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LAKAGFYIIGPDRAVACFACGKLSNWPKDNAMSEHLRHPKCPF 46
DB 189 LARAGFYIIGPDRAVACFACGKLSNWPKDNAMSEHLRHPKCPF 234
```

```
RESULT 9
AAG69295
ID AAG69295 standard; Protein: 604 AA.
XX
AC AAG69295;
XX
DT 13-NOV-1998 (first entry)
XX
DE Human HIAP-1 protein.
XX
KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; human; HIAP-1 protein.
XX
OS Homo sapiens.
XX
PN W09835693-A2.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-IB00781.
XX
PR 13-FEB-1997; 97US-0800929.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
PI Tsang B;
XX
DR WPI: 1998-467164/40.
DR N-PSDB; AAV55039.
XX
PT Inducing apoptosis in proliferative mammalian cells with inhibitor
PT of IAP or NAIP polypeptide - also methods for prognosis based on
PT presence of IAP and NAIP, specifically applied to cancers involving
PT p53 mutations
XX
PS Disclosure; Fig 2; 147pp; English.
XX
CC This sequence is the human HIAP-1 protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.
XX
SQ Sequence 604 AA;
Query Match 98.9%; Score 264; DB 19; Length 604;
Best Local Similarity 97.8%; Pred. No. 3.2e-25;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LAKAGFYIIGPDRAVACFACGKLSNWPKDNAMSEHLRHPKCPF 46
DB 189 LARAGFYIIGPDRAVACFACGKLSNWPKDNAMSEHLRHPKCPF 234
```

DT 26-AUG-2002 (first entry)  
XX  
DE Human inhibitor of apoptosis, HIAP1.  
XX  
KW Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
KW pancreatic cancer; embryonic development; viral pathogenesis;  
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
KW lupus erythematosus; herpes virus infection; pox virus infection;  
KW adenovirus infection; proliferative disease.  
XX  
OS Homo sapiens.  
XX  
PN WO20026968-A2.  
XX  
PD 04-APR-2002.  
XX  
PE 27-SEP-2001; 2001WO-CA01379.  
XX  
PR 28-SEP-2000; 2000US-0672717.  
XX  
PA (UYOT-) UNIV OTTAWA.  
XX (AEGE-) AEGERA THERAPEUTICS INC.  
XX  
PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
XX  
DR MPI: 2002-479562/51.  
XX N-PSDB; AAK93870.  
XX  
PT Novel antisense inhibitor of apoptosis nucleic acid useful for  
PT enhancing apoptosis in a cell, for treating cancer and other  
PT proliferative diseases  
XX  
PS Disclosure; Fig 2; 135pp; English.  
XX  
XX The invention relates to an inhibitor of apoptosis (IAP) antisense  
XX nucleic acid (I) that inhibits IAP biological activity, regardless of  
XX length of the antisense nucleic acid, the IAP proteins may be mouse  
XX or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
XX composition comprising a mammalian IAP antisense molecule and a method of  
XX enhancing apoptosis in a cell, comprising administering a negative  
XX regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
XX antisense inhibitor is useful for enhancing apoptosis in a cell in a  
XX mammal diagnosed with a proliferative disease. The method is useful for  
XX treating a patient diagnosed with a proliferative disease like cancer.  
XX The IAP antisense molecule is useful to treat, ameliorate, improve,  
XX sustain or prevent proliferative diseases (e.g. ovarian cancer,  
XX adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
XX conditions where apoptosis is involved or implicated (e.g. embryonic  
XX development, viral pathogenesis, autoimmune disorders, neurodegenerative  
XX diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
XX virus, pox virus and adenovirus). The present sequence is a human IAP  
XX protein sequence.  
XX  
SQ Sequence 604 AA;  
XX  
Query Match 98.9%; Score 264; DB 23; Length 604;  
Best Local Similarity 97.8%; Pred. No. 3.2e-25;  
Matches 45; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 LAKAGFYITGPDGVACFACGKLSNWEPRDNAMSEHLRHFPCPF 46  
DB 189 LARAGFYITGPDGVACFACGKLSNWEPRDNAMSEHLRHFPCPF 234  
RESULT 11  
AAU02925  
ID AAU02925 standard; Protein: 306 AA.  
XX  
AC AAU02925;  
XX  
DT 12-SEP-2001 (first entry)  
XX

DE Angiotensin converting enzyme (ACEV) splice variant protein #25.  
XX  
XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;  
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;  
KW platelet-derived endothelial cell growth factor; cardiovascular disease;  
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;  
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;  
KW myocardial infarction; coronary arterial thrombosis; renal disease;  
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;  
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;  
KW noncardiogenic pulmonary granulomatous disease; endothelial abnormality;  
KW vascular disorder; asbestosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200136632-A2.  
XX  
PD 25-MAY-2001.  
XX  
PE 17-NOV-2000; 2000WO-IL00766.  
XX  
PR 17-NOV-1999; 99IL-0132978.  
XX 10-DEC-1999; 99IL-0133455.  
XX  
PA (COMP-) COMPUGEN LTD.  
XX  
PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;  
XX  
DR MPI: 2001-336004/35.  
XX N-PSDB; AAS06025.  
XX  
PT Novel alternative splicing variants e.g. variant of angiotensin  
PT converting enzyme (ACEV), useful in identifying candidate compounds  
PT capable of binding to the variant and to detect anti-variant antibodies  
XX  
XX Claim 4; Fig 25; 519pp; English.  
XX  
XX The sequence represents an angiotensin converting enzyme splice variant  
XX (ACEV) polypeptide. The polypeptides of the invention include variants of  
XX granulocyte colony stimulating factor receptor, glucagon, interleukin 6,  
XX platelet-derived endothelial cell growth factor, cyclin-dependent kinase  
XX inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal  
XX polypeptide receptor 2. The polypeptides and their associated nucleic  
XX acids are useful for identification of variant sequences and detection of  
XX candidate compounds capable of binding the molecules. The sequences of  
XX the invention can be used in the treatment and diagnosis of various  
XX disorders including cardiovascular diseases such as arteriosclerosis,  
XX myocardial infarction and coronary arterial thrombosis, renal diseases  
XX such as diabetic nephropathy, muscular diseases such as hypertrophy,  
XX immune disorders such as immune complex nephritis, multiple sclerosis,  
XX cancer, sarcoidosis, noncardiogenic pulmonary granulomatous diseases such  
XX as asbestosis and vascular pathologies involving an endothelial  
XX abnormality such as deep vein thrombosis.  
XX  
SQ Sequence 306 AA;  
XX  
Query Match 97.0%; Score 259; DB 22; Length 306;  
Best Local Similarity 95.7%; Pred. No. 6.7e-25;  
Matches 44; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 LAKAGFYITGPDGVACFACGKLSNWEPRDNAMSEHLRHFPCPF 46  
DB 204 LARAGFYITGPDGVACFACGKLSNWEPRDNAMSEHLRHFPCPF 249  
RESULT 12  
AAW13549  
ID AAW13549 standard; Protein: 46 AA.  
XX  
AC AAW13549;  
XX  
DT 22-JUL-1997 (first entry)  
XX

```

XX DE Human c-IAP1 repeat 2.
XX PD
XX KW IAP; inhibitor; apoptosis; RING finger domain; restinosis;
XX KW myocardial infarction; nephritis; HIV.
XX OS
XX PA Homo sapiens.
XX PN MO9706182-A1.
XX PD 20-FEB-1997.
XX PE
XX PF 06-AUG-1996; 96WO-US12860.
XX PR 08-DEC-1995; 95US-0569749.
XX PR 08-AUG-1995; 95US-0512946.
XX PA (TULAR-) TULARIK INC.
XX PI
XX PI Goeddel DV, Rothe M;
XX DR WPI: 1997-154209/14.
XX PT Nucleic acids encoding cellular inhibitor of apoptosis proteins
XX PT useful for apoptosis regulation in cells to reduce or increase
XX PT apoptosis and for pharmacological screening
XX PS
XX PS Claim 3; Page 24; 35pp; English.
XX CC The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
XX CC AAT61590/T61591) comprise a series of defined structural domain
XX CC repeats and/or a RING finger domain, in particular, at least two of
XX CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat
XX CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
XX CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
XX CC sequence derived from these human genes.
XX CC The nucleic acid is used for recombinant prodn. of human cellular
XX CC inhibitor of apoptosis protein which modulates apoptosis
XX CC regulation. The nucleic acids are useful in therapies where
XX CC increased cell-specific apoptosis is desired, e.g. in restinosis,
XX CC inflammatory disease states, myocardial infarction, glomerular
XX CC nephritis, transplant rejection and infectious diseases, e.g. HIV.
XX CC They can also be used in conditions requiring a reduction in
XX CC apoptosis.
XX SQ Sequence 46 AA:
XX
XX Query Match 92.9%; Score 248; DB 18; Length 46;
XX Best Local Similarity 91.3%; Pred. NO. 2.3e-24;
XX Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 LAKAGFYTGPGDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46
DB 1 LARAGFYTGPGDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46

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XX XX 14-NOV-1996.
XX PD
XX PF 11-MAY-1995; 95WO-US05922.
XX PR 11-MAY-1995; 95WO-US05922.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI
XX PI He WM, Hudson FL, Rosen CA;
XX DR WPI: 1996-518608/51.
XX DR N-ESDB; AAT43709.
XX PT Polynucleotide encoding human inhibitor of apoptosis gene 1 - useful
XX PT for treating degenerative diseases, as antiviral defence mechanism
XX PT and preventing cell death during trauma and strokes
XX PS Claim 1; Page 40-41; 53pp; English.
XX CC Human inhibitor of apoptosis 1 (hiap-1) (AAW04583) is a protein
XX CC useful for treating degenerative diseases, rheumatoid arthritis,
XX CC septic shock, as an antiviral defence mechanism, and for
XX CC preventing cell death during strokes or trauma. Its amino acid
XX CC sequence was deduced from a cDNA clone (AAT43709) that can be obt'd.
XX CC from human Jurkat cell lines or human osteoclastoma stromal cell
XX CC lines. Recombinant hiap-1 can be produced in prokaryotic or
XX CC eukaryotic host cells, or expressed in vivo. It can also be used
XX CC to screen for modulators of hiap-1 activity.
XX SQ Sequence 438 AA:
XX
XX Query Match 92.9%; Score 248; DB 17; Length 438;
XX Best Local Similarity 91.3%; Pred. NO. 2.5e-23;
XX Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 LAKAGFYTGPGDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46
DB 24 LARAGFYTGPGDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 69

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RESULT 13
AAW04583
ID AAW04583 standard; Protein; 438 AA.
XX
XX AAW04583;
AC
XX
XX 07-FEB-1997 (first entry)
DE Human inhibitor of apoptosis gene 1.
XX
XX Inhibitor of apoptosis 1; hiap-1; degenerative disease;
XX KW rheumatoid arthritis; septic shock; antiviral; trauma; stroke;
XX KW cell death; oncogenesis; cancer; diagnosis; therapy.
XX OS Homo sapiens.
XX PN WO9635703-A1.

```

```

RESULT 14
AAW19746
ID AAW19746 standard; Protein; 618 AA.
XX
XX AAW19746;
AC
XX
XX 16-SEP-1997 (first entry)
DE Human inhibitor of apoptosis protein homologue M1HB.
XX
XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; M1HB;
XX KW degenerative disease; infectious disease; autoimmune disease;
XX KW cancer; therapy; diagnosis.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 46..113
XX FT /label= BIR
XX FT 184..250
XX FT /label= BIR
XX FT 269..337
XX FT /label= BIR
XX FT 569..606
XX FT /label= RING_finger
XX PN WO9723501-A1.
XX PD 03-JUL-1997.
XX PF 20-DEC-1996; 96WO-AU00827.

```

```
PR 22-DEC-1995; 95AU-0007275.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Vaux DL;
XX
XX WPI: 1997-350966/32.
XX N-PSDB; AAT72711.
XX
XX Isolated protein homologues of viral inhibitors of apoptosis - used
XX to modulate apoptosis for treatment of degenerative, infectious or
XX autoimmune diseases and cancer
XX
XX Claim 8; Page 51-54; 136pp; English.
XX
XX Mammalian IAP homologue B (MIHB) (AAW19746) is a human homologue of
XX baculovirus inhibitor of apoptosis protein (IAP). Its amino acid
XX sequence was deduced from a cDNA clone (see also AAT72711) isolated
XX from a human foetal liver cDNA library using primers based on
XX human EST sequences that resembled the BIR repeats of Oryza
XX pseudotsugata polyhedrosis virus IAP. IAP homologues (see also
XX AAW19745 and AAW19747-52) and their derivatives and chemical analogues
XX can be used in methods for modulating apoptosis in animal cells,
XX specifically for treatment, by inhibition, of degenerative and
XX infectious disease or, by promotion, of cancer and autoimmune
XX disease.
XX
XX Sequence 618 AA:
SQ
Query Match 92.9%; Score 248; DB 10; Length 618;
Best Local Similarity 91.3%; Pred. No. 3.6e-23;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 LARAGFYIIGPGRVACFACGKLSWNEPKDNMSEHLRHPKCP 46
DB 204 LARAGFYIIGPGRVACFACGKLSWNEPKDNMSEHLRHPKCP 249
RESULT 15
AAW19583
ID AAW19583 standard; Protein; 618 AA.
XX
XX AAW19583;
XX
XX 02-SEP-1997 (first entry)
XX
XX Human apoptosis inhibitor HIAP-2.
XX
XX Apoptosis inhibitor; HIAP-2; HIV; AIDS; neurodegeneration;
XX myelodysplastic syndrome; ischemia; myocardial infarction; stroke;
XX reperfusion injury; toxin-induced liver disease; gene therapy;
XX diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 46..113
XX FT /label= BIR-1
XX FT 184..250
XX FT /label= BIR-2
XX FT 269..336
XX FT /label= BIR-3
XX FT 560..605
XX FT /label= Ring_zinc_finger
XX
XX WO9706255-A2.
XX
XX 20-FEB-1997.
XX
XX 05-AUG-1996; 96WO-IB01022.
XX
XX 22-DEC-1995; 95US-0576956.
XX 04-AUG-1995; 95US-0511485.
PR
```

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XX
XX (UYOT-) UNIV OTTAWA.
XX
XX Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX
XX WPI: 1997-154262/14.
XX N-PSDB; AAT70838.
XX
XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
XX to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
XX of susceptibility to apoptotic disease
XX
XX Claim 27; Page 75-77; 219pp; English.
XX
XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
XX M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
XX are inhibitors of apoptosis (IAP) and which are characterised by
XX the presence of a ring zinc finger domain (see also AAW19587) and at
XX least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
XX The HIAP amino acid sequences were deduced from cDNA clones (AAT70837
XX and AAT70838) from a human liver library. IAP polypeptides can be
XX expressed in host cells (in vitro or in vivo) and used in methods
XX for treating diseases and disorders involving apoptosis, esp. in a
XX human diagnosed as HIV-positive or as having AIDS, a
XX neurodegenerative disease, a myelodysplastic syndrome or an
XX ischemic injury, selected from myocardial infarction, stroke,
XX reperfusion injury, or a toxin-induced liver disease.
XX
XX Sequence 618 AA:
SQ
Query Match 92.9%; Score 248; DB 18; Length 618;
Best Local Similarity 91.3%; Pred. No. 3.6e-23;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 LARAGFYIIGPGRVACFACGKLSWNEPKDNMSEHLRHPKCP 46
DB 204 LARAGFYIIGPGRVACFACGKLSWNEPKDNMSEHLRHPKCP 249
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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:50:57 ; Search time 9.06221 Seconds  
(without alignments)  
676.383 Million cell updates/sec

Title: US-08-569-749-8

Perfect score: 267  
Sequence: 1 LAKAPFYIIGPDRAVACFRAC.....WEKDNANSEHLRHPKCF 46

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	267	100.0	46	AAW13550	Human c-IAP2 repa
2	267	100.0	604	AAW19747	Human inhibitor of
3	267	100.0	604	AAW13546	Human c-IAP2. Hom
4	267	100.0	604	AAW52703	Human cellular inh
5	267	100.0	604	AAV33997	Human cellular inh
6	267	100.0	1140	AAU97837	Human cysteine pro
7	267	100.0	1141	AAW50694	Human APT-2. MUR chl
8	264	98.9	604	AAW19582	Human HIAP-1 prote
9	264	98.9	604	AAW69295	Human HIAP-1 prote
10	264	98.9	604	ABG55664	Human inhibitor of

11	259	97.0	306	AAU02925	Angiotensin conver
12	248	92.9	46	AAW13549	Human c-IAP1 repa
13	248	92.9	438	AAW04583	Human inhibitor of
14	248	92.9	618	AAW19746	Human inhibitor of
15	248	92.9	618	AAW19583	Human apoptosis in
16	248	92.9	618	AAW13545	Human c-IAP1. Hom
17	248	92.9	618	AAW69296	Human HIAP-2 prote
18	248	92.9	618	AAW33998	Human cellular inh
19	248	92.9	618	AAW65665	Human inhibitor of
20	247	92.5	612	AAW13555	Murine c-IAP. Mus
21	247	92.5	612	AAW69299	Murine HIAP-2 prot
22	244	91.4	591	AAW19586	Mouse apoptosis in
23	244	91.4	591	ABG55668	Mouse inhibitor of
24	235	88.0	600	AAW69298	Murine HIAP-1 prot
25	235	88.0	602	AAW19585	Mouse apoptosis in
26	235	88.0	602	ABG55667	Mouse inhibitor of
27	182	68.2	497	AAW19581	Human apoptosis in
28	182	68.2	497	AAW69294	Human XIAP protein
29	182	68.2	497	AAW99985	Human X-linked inh
30	182	68.2	497	AAW59451	Human XIAP protein
31	182	68.2	497	ABG55663	Human inhibitor of
32	178	66.7	464	AAW75747	Human inhibitor of
33	177	66.3	496	AAW19745	Mouse inhibitor of
34	177	66.3	496	AAW19584	Mouse apoptosis in
35	177	66.3	496	AAW69297	Murine XIAP protei
36	177	66.3	496	ABG55666	Mouse inhibitor of
37	145	54.3	236	AAW81440	Human TIAP (an inh
38	145	54.3	236	AAE00365	Human IAP-1-like pro
39	145	54.3	236	AAE00366	Chimpanzee IAP-1lik
40	145	54.3	236	AAU75066	Human testes spect
41	145	54.3	498	AAW19748	Drosophila inhibit
42	145	54.3	498	ABG55663	Drosophila melanog
43	144	53.9	236	AAE00367	Goat IAP-1-like p
44	141	52.8	278	AAO20511	Protein of AIP rel
45	141	52.8	1232	AAW98217	Neuronal apoptosis

ALIGNMENTS

RESULT 1	AAW13550	standard; Protein: 46 AA.
ID	AAW13550	
XX	AAW13550:	
AC	22-JUL-1997 (first entry)	
DT	XX	
XX	Human c-IAP2 repeat 2.	
DE	XX	
XX	IAP, inhibitor; apoptosis; RING finger domain; restinosis;	
KW	myocardial infarction; nephritis; HIV.	
KX	XX	
OS	Homo sapiens.	
XX	XX	
PN	MO9706182-AI.	
XX	20-FEB-1997.	
PD	XX	
XX	06-AUG-1996; 96WO-0512860.	
PF	XX	
PR	08-DEC-1995; 95US-0569749	
PR	08-AUG-1995; 95US-0512846.	
XX	(TULIA-) TULIRIK INC.	
PA	XX	
PI	Goeddel DV, Rothe M;	
XX	WPI, 1997-154209/14.	
DR	XX	
XX	Nucleic acids encoding cellular inhibitor of apoptosis proteins	
PT	useful for apoptosis regulation in cells to reduce or increase	
PT	apoptosis and for pharmacological screening	



XX  
PS Claim 3; Page 24; 35pp; English.

XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -  
XX AAT61590/761591) comprise a series of defined structural domain  
CC repeats and/or a RING finger domain; in particular, at least two of  
CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat  
CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)  
CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus  
CC sequences derived from these human genes.  
CC The nucleic acid is used for recombinant prodn. of human cellular  
CC inhibitor of apoptosis protein which modulates apoptosis  
CC regulation. The nucleic acids are useful in therapies where  
CC increased cell-specific apoptosis is desired, e.g. in restinosis,  
CC inflammatory disease states, myocardial infarction, glomerular  
CC nephritis, transplant rejection and infectious diseases, e.g. HIV.  
CC They can also be used in conditions requiring a reduction in  
CC apoptosis.

SO Sequence 46 AA;

Query Match 100.0%; Score 267; DB 18; Length 46;  
Best Local Similarity 100.0%; Pred. No. 8.5e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKAGFYITGPDGVACFACGKLSNWEKDNAMSEHLRHPKCP 46  
DB 1 LKAGFYITGPDGVACFACGKLSNWEKDNAMSEHLRHPKCP 46

RESULT 2  
AAW19747  
ID AAW19747 standard; Protein; 604 AA.  
XX AAW19747;  
XX  
XX 16-SEP-1997 (first entry)  
DE Human inhibitor of apoptosis protein homologue MIHC.  
DE  
XX  
XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHC;  
KW degenerative disease; infectious disease; autoimmune disease;  
KW cancer; therapy; diagnosis.  
XX  
XX Homo sapiens.

OS  
FH Key Location/Qualifiers  
FT Region 29..97  
FT Region /label= BIR  
FT Region 169..236  
FT Region /label= BIR  
FT Region 255..323  
FT Region /label= BIR  
FT Region 556..593  
FT Region /label= RING\_finger

XX WO9723501-A1.  
XX  
XX 03-JUL-1997.  
XX  
XX  
XX 20-DEC-1996; 96WO-AU00827.  
XX  
XX  
XX 22-DEC-1995; 95AU-0007275.  
XX  
XX  
XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX  
XX Vaux DL;  
XX  
XX WPI; 1997-350966/32.  
XX  
XX N-PSDB; AAT72712.  
XX  
XX Isolated protein homologues of viral inhibitors of apoptosis - used  
PT to modulate apoptosis for treatment of degenerative, infectious or

PT autoimmune diseases and cancer

XX  
XX Claim 9; Page 58-62; 136pp; English.

XX Mammalian IAP homologue C (MIHC) (AAW19747) is a human homologue of  
CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid  
CC sequence was deduced from a cDNA clone (see also AAT72712) isolated  
CC from a human foetal liver cDNA library using primers based on  
CC human EST sequences that resembled the BIR repeats of Orygia  
CC pseudotsuguta polyhedrosis virus IAP. IAP homologues (see also  
CC AAW19745-46 and AAW19748-52) and their derivatives and chemical  
CC analogues can be used in methods for modulating apoptosis in animal  
CC cells, specifically for treatment, by inhibition, of degenerative  
CC and infectious disease or, by promotion, of cancer and autoimmune  
CC disease.

SO Sequence 604 AA;

Query Match 100.0%; Score 267; DB 18; Length 604;  
Best Local Similarity 100.0%; Pred. No. 1.3e-25;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKAGFYITGPDGVACFACGKLSNWEKDNAMSEHLRHPKCP 46  
DB 189 LKAGFYITGPDGVACFACGKLSNWEKDNAMSEHLRHPKCP 234

RESULT 3  
AAW13546  
ID AAW13546 standard; Protein; 604 AA.  
XX AAW13546;  
XX  
XX 22-JUL-1997 (first entry)  
DE Human c-IAP2.  
DE  
XX  
XX IAP; inhibitor; apoptosis; RING finger domain; restinosis;  
KW myocardial infarction; nephritis; HIV.  
KW  
XX  
XX Homo sapiens.

OS  
FH Key Location/Qualifiers  
FT Region 29..97  
FT Region /label= BIR  
FT Region 169..236  
FT Region /label= BIR  
FT Region 255..323  
FT Region /label= BIR  
FT Region 556..593  
FT Region /label= RING\_finger

XX WO9706182-A1.  
XX  
XX 20-FEB-1997.  
XX  
XX  
XX 06-AUG-1996; 96WO-US12860.  
XX  
XX  
XX 08-DEC-1995; 95US-0569749.  
XX  
XX  
XX 08-AUG-1995; 95US-0512946.  
XX  
XX (TULA-) TULARIK INC.  
XX  
XX  
XX Goeddel DV; Rothe M;  
XX  
XX WPI; 1997-154209/14.  
XX  
XX N-PSDB; AAT61591.  
XX  
XX  
XX Nucleic acids encoding cellular inhibitor of apoptosis proteins  
PT useful for apoptosis regulation in cells to reduce or increase  
PT apoptosis and for pharmacological screening  
XX  
XX  
XX Disclosure; Page 21-23; 35pp; English.

XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -  
XX AAT61590/761591) comprise a series of defined structural domain  
CC repeats and/or a RING finger domain; in particular, at least two of  
CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat  
CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)  
CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus  
CC sequences derived from these human genes.  
CC The nucleic acid is used for recombinant prodn. of human cellular  
CC inhibitor of apoptosis protein which modulates apoptosis

CC regulation. The nucleic acids are useful in therapies where  
 CC increased cell-specific apoptosis is desired, e.g. in restitosis,  
 CC inflammatory disease states, myocardial infarction, glomerular  
 CC nephritis, transplant rejection and infectious diseases, e.g. HIV.  
 CC They can also be used in conditions requiring a reduction in  
 CC apoptosis.

SO Sequence 604 AA;

Query Match 100.0%; Score 267; DB 18; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-25;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46  
 |||  
 DB 189 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 234

#### RESULT 4

AAV52703  
 ID AAV52703 standard; Protein: 604 AA.

AC AAV52703;

DT 26-JAN-2000 (first entry)

DE Human cellular inhibitor of apoptosis-2 protein.

XX Identification; genetic target; gene modulation; human;

KW antisense oligonucleotide; phosphorothioate; target validation;

KW nucleotide sequence-based technology; antisense drug discovery.

OS Homo sapiens.

PN MO9953101-A1.

PD 21-OCT-1999.

PF 13-APR-1999; 99WO-US08268.

PR 13-APR-1998; 98US-0081483.

PR 28-APR-1998; 98US-0067638.

PA (ISIS-) ISIS PHARM INC.

PI Cowsett LM, Baker BF, McNeill J, Freiler SM, Sasnor HM, Brooks DG;

PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;

DR MPI: 1999-620446/53.

DR N-PSDB; AA241005.

XX Identifying compounds which modulate expression of nucleic acids, used

PT to provide compounds having defined physical, chemical or bioactive

PT properties, e.g. antisense activity

XX Example 20; Page 197-202; 26pp; English.

CC A method has been developed of defining a set of compounds that modulate

CC the expression of a target nucleic acid (tNA) sequence via binding of

CC a library of virtual compounds in silico according to defined criteria,

CC and evaluating in silico the binding of the virtual compounds with the

CC tNA according to defined criteria. Also described are: (1) a method of

CC defining a set of oligonucleotides (ONs) that modulate the expression of

CC a tNA sequence via binding of the ONs with the tNA sequence comprising

CC generating a library of virtual compounds in silico according to defined

CC criteria, and evaluating in silico the binding of the virtual ONs with

CC the tNA according to defined criteria; and (2) a method of defining a

CC set of compounds that modulate the expression of a tNA sequence via

CC binding of the compounds with the tNA. The methods can be used for the

CC generation and identification of synthetic compounds having defined

CC physical, chemical or bioactive properties. Information gathered from

CC assays of such compounds is used to identify nucleic acid sequences that

CC are tractable to a variety of nucleotide sequence-based technologies,  
 CC e.g. antisense drug discovery and target validation. AA240852 to  
 CC AA241220, and AAV52701 to AAV52706, represent sequences used in the  
 CC exemplification of the present invention.

SO Sequence 604 AA;

Query Match 100.0%; Score 267; DB 20; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-25;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46  
 |||  
 DB 189 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 234

#### RESULT 5

AAV33997  
 ID AAV33997 standard; Protein: 604 AA.

AC AAV33997;

DT 26-NOV-1999 (first entry)

DE Human cellular inhibitor of apoptosis-2 sequence.

XX Cellular inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;

KW c-IAP-2; prophylaxis; infection; inflammation; tumor formation.

OS Homo sapiens.

PN US5958771-A.

PD 28-SEP-1999.

PF 03-DEC-1998; 98US-0205144.

PR 03-DEC-1998; 98US-0205144.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowsett LM, Ackermann EJ;

DR MPI: 1999-561046/47.

DR N-PSDB; AA222096.

XX Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2

PT useful for e.g. diagnostics, therapeutics, and as research reagents -

XX Example 13; Columns 45-50; 33pp; English.

CC The invention provides antisense compounds of 8-30 nucleotides that

CC inhibit the expression of human Cellular Inhibitor of Apoptosis-2

CC (c-IAP-2). The antisense compounds may be used for diagnostics,

CC therapeutics (for modulating the expression of c-IAP-2), prophylaxis

CC (e.g. to prevent or delay infection, inflammation, or tumor formation),

CC as research reagents (e.g. to distinguish between members of a biological

CC pathway) and in kits. The present sequence represents the human cellular

CC inhibitor of apoptosis-2.

SO Sequence 604 AA;

Query Match 100.0%; Score 267; DB 20; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-25;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46  
 |||  
 DB 189 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 234

#### RESULT 6

AAU97837

ID AA097837 standard; Protein: 1140 AA.  
 AC AA097837;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Human cysteine protease fusion protein AP12-MLT (CPG2).  
 XX  
 KW Cysteine protease; CPG2; cell-cell adhesion; lymphoma; osteoporosis;  
 KW rheumatoid arthritis; inflammatory disease; irritable bowel disease;  
 KW respiratory disease; asthma; autoimmune disease; bone disease;  
 KW atherosclerosis; neoplastic disease; melanoma; prostate; lung tumour;  
 KW ovary tumour; myeloproliferative disorder; leukaemia; metastasis;  
 KW heart disease; myocardial infarction; cardiac failure; AP12-MLT;  
 KW reperfusion injury; neurodegenerative disease; Alzheimer's disease;  
 KW Parkinson's disease; neurological disorder; stroke; muscular dystrophy;  
 KW liver disease; cataract; infection; transgenic animal; gene; ds.  
 XX  
 OS Homo sapiens.  
 PN WO200233058-A2.  
 PD 25-APR-2002.  
 PE 22-OCT-2001; 2001WO-GB04698.  
 XX  
 PR 20-OCT-2000; 2000GB-0025816.  
 PR 29-JAN-2001; 2001GB-0002260.  
 XX  
 PA (INPR-) INPHARMATICA LTD.  
 PI Fagan RJ, Phelps CB, Gutteridge A, Nicholls RO;  
 DR N-PSDB; ABK52387.  
 PT New proteins identified as cysteine proteases for diagnosing,  
 PT preventing and treating neoplastic, inflammatory, autoimmune diseases  
 PT and neurological disorders  
 PT  
 PS Claim 1; Fig 15; 12pp; English.  
 XX  
 CC This sequence represents a polypeptide (I) termed BAA83099.1 (CPG1),  
 CC AAD6161.1 (CPG2) or AAB38507.2 (CPG3), identified as a cysteine  
 CC protease, its fragment having cysteine protease activity or having an  
 CC antigenic determinant in common with the polypeptide, or its functional  
 CC equivalent. (I) is useful as a cysteine protease and for effecting  
 CC cell-cell adhesion. A nucleic acid (II) encoding (I) is useful for  
 CC expressing a protein that possesses cysteine protease activity. (I),  
 CC (II), a vector (III) comprising (II), a ligand (IV) which binds (I) and  
 CC a compound (V) that alters the activity of (I), are useful for treating  
 CC diseases in which the expression of the natural gene or the activity of  
 CC the polypeptide is higher or lower in a diseased patient when compared  
 CC to the level of expression or activity in a healthy patient. (I) - (X)  
 CC are useful in therapy or diagnosis of disease and in the manufacture of  
 CC a medicament for treating lymphoma, rheumatoid arthritis, osteoporosis,  
 CC inflammatory disease, such as irritable bowel disease, respiratory  
 CC disease such as asthma, autoimmune disease, bone disease,  
 CC atherosclerosis, neoplastic diseases, such as melanoma, prostate, lung  
 CC and ovary tumours, myeloproliferative disorder, leukaemia, metastasis,  
 CC heart disease, myocardial infarction, cardiac failure, reperfusion  
 CC injury, neurodegenerative diseases such as Alzheimer's disease,  
 CC Parkinson's disease, neurological disorder, stroke, muscular dystrophy,  
 CC liver disease, cataract, infection such as bacterial, parasitic,  
 CC plasmodium and viral infection. A transgenic or knockout non-human animal  
 CC is useful as an animal model to screen for a compound effective to treat  
 CC a disease. This sequence encodes cysteine protease fusion protein  
 CC AP12-MLT (CPG2) described in the invention.  
 CC  
 SQ Sequence 1140 AA;  
 Query Match 100.0%; Score 267; DB 23; Length 1140;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-25;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LAKAGFYITGPDGVACFACGKLSNWEPRKDAMSEHLRHPKCP 46;  
 DB 189 LAKAGFYITGPDGVACFACGKLSNWEPRKDAMSEHLRHPKCP 234

## RESULT 7

ID AAB50694 standard; Protein: 1141 AA.  
 XX  
 AC AAB50694;  
 XX  
 DT 19-MAR-2001 (first entry)  
 XX  
 DE Human AP12-MLT chimeric protein sequence.

KW Human; AP12-MLT chimera; chimeric; apoptosis inhibitor 2; MLT; AP12;  
 KW mucosa-associated lymphoid tissue lymphoma associated translocation;  
 KW chromosome 11 region q21-22.3; chromosome 18 region q21.1-22;  
 KW molecular characterisation; chromosome translocation; carcinogenesis;  
 KW fusion protein; malignancy.  
 XX  
 OS Chimeric - Homo sapiens.  
 OS Synthetic.  
 PN WO200073500-A1.  
 PD 07-DEC-2000.  
 PE 26-MAY-2000; 2000WO-EP04796.  
 XX  
 PR 27-MAY-1999; 99EP-0201683.  
 XX  
 PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOC.  
 PI Baens M, Marynen P, Dierlamm J;  
 DR N-PSDB; AAC90972.  
 PT Determining if a tissue sample has a chromosome (11:18) translocation  
 PT associated with malignancies by amplifying a nucleic acid sample using  
 PT primers complementary to chromosome 11 region q21-22.3 and chromosome  
 PT 18 region q21.1-22  
 PS Claim 12; Fig 5; 47pp; English.

CC The present invention describes a method for determining if a tissue  
 CC sample comprises a cell with a chromosome (11:18) translocation  
 CC associated with malignancies such as mucosa-associated lymphoid tissue  
 CC (MALT) lymphomas. The method comprises subjecting a sample nucleic acid  
 CC to amplification using primers complementary to sequences which are on  
 CC chromosome 11 region q21-22.3 and on chromosome 18 region q21.1-22. The  
 CC method can be used for determining if a tissue sample or analogue  
 CC comprises a chromosome (11:18) translocation associated with malignancies  
 CC such as mucosa-associated lymphoid tissue lymphomas. The nucleic acid or  
 CC the antibody may be used as a probe for detection, for hybridisation to  
 CC southern blot cell DNAs or for in situ hybridisation of cells, or for  
 CC determining the presence of complementary DNA. The present sequence  
 CC represents the specifically claimed chimeric human apoptosis inhibitor 2  
 CC (AP12)/MALT-lymphoma associated translocation (MLT) protein.

SQ Sequence 1141 AA;

Query Match 100.0%; Score 267; DB 22; Length 1141;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-25; Mismatches 0; Indels 0;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAKAGFYITGPDGVACFACGKLSNWEPRKDAMSEHLRHPKCP 46  
 DB 189 LAKAGFYITGPDGVACFACGKLSNWEPRKDAMSEHLRHPKCP 234

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:51:32 ; Search time 1.90783 Seconds

(Without alignments)  
1000.040 Million cell updates/sec

Title: US-08-569-749-8

Sequence: 1 IAKAGFYIGPGDRVACAC.....WEIKDNAMSEHLRHFPCPF 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	267	100.0	604	BIR2_HUMAN	Q13489 homo sapien.
2	254	95.1	358	PIAP_PIG	O62640 sus scrofa
3	248	92.9	618	BIR3_HUMAN	Q13490 homo sapien
4	247	92.5	612	BIR3_MOUSE	O62210 mus musculu
5	235	88.0	600	BIR2_MOUSE	O08863 mus musculu
6	186	69.7	611	BIR_CHICK	O90660 gallus gall
7	182	68.2	497	BIR1_HUMAN	P88170 homo sapien
8	177	66.3	496	BIR4_MOUSE	O60989 mus musculu
9	175	65.5	436	BIR4_RAT	O91016 ratu
10	145	54.3	236	BIR8_HUMAN	O96P09 homo sapien
11	145	54.3	236	BIR8_PANTR	O95M72 pan troglod
12	145	54.3	498	IAP2_DROME	Q24307 drosophila
13	144	53.9	236	BIR8_GORGO	Q35M71 gorilla gor
14	141	52.8	1402	BIR3_MOUSE	Q9J1B3 mus musculu
15	141	52.8	1403	BIR1_HUMAN	Q13075 homo sapien
16	141	52.8	1403	BIR4_MOUSE	O9QW45 mus musculu
17	141	52.8	1403	BIR4_MOUSE	O91016 mus musculu
18	141	52.8	1403	BIR4_MOUSE	O91016 mus musculu
19	138	51.7	1447	BIR8_MOUSE	Q9J1B6 mus musculu
20	135	50.6	268	IAP3_NPYOP	Q9J4K4 mus musculu
21	131	48.3	275	IAP_GVCP	P41457 oryza psen
22	129	48.3	438	IAP1_DROME	Q24306 drosophila
23	122.5	45.9	4829	BIR6_HUMAN	O9NR09 homo sapien
24	121	45.3	298	BIR7_HUMAN	O96C55 homo sapien
25	112	41.9	239	ZFP_IRV6	P47732 chilo lride
26	105.5	39.5	140	BIR5_MOUSE	O70201 mus musculu
27	105.5	39.5	142	BIR5_RAT	O9J1B7 ratu
28	103	38.6	997	BIR1_SCHPO	O14064 schlosacch
29	93	34.8	286	IAP1_NPYAC	P41455 autographa
30	92.5	34.6	142	BIR5_HUMAN	O15392 homo sapien
31	90	33.7	275	IAP1_NPYOP	O10236 oryza psen
32	72.5	27.2	224	IAPL_ASEB7	O65138 african swi
33	69.5	26.0	224	IAPL_ASEW1	O11452 african swi

## ALIGNMENTS

34	66.5	24.9	224	1	IAPL_ASFC3	O11451 african swi
35	66.5	24.9	224	1	IAPL_ASFC3	O12407 african swi
36	66.5	24.9	238	1	IAPL_ASEW2	O11453 african swi
37	60	22.3	249	1	IAP2_NPYAC	P41454 autographa
38	59.5	22.3	404	1	FEPA_MERTM	O50497 methanobact
39	57.5	21.5	278	1	HUPJ_RHOCA	O03009 rhodobacter
40	56.5	21.2	706	1	SMZA_DROME	O24323 drosophila
41	56.5	21.2	2236	1	PYRL_DROME	P05990 drosophila
42	56	21.0	1004	1	ATB1_ARTSF	P28774 attemia san
43	55	20.6	1433	1	CATB_YEAST	P39113 saccharomyc
44	54	20.2	181	1	VG79_HSV11	O00148 ictaluriid h
45	54	20.2	606	1	WDRL_HUMAN	O75083 homo sapien

  

RESULT 1	BIR2_HUMAN	STANDARD:	PRT:	604 AA.
ID	BIR2_HUMAN	Q9UP46; Q9HC27;		
AC	Q13489; 016628; Q9UP46; Q9HC27;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Baculoviral IAP repeat-containing protein 1 (inhibitor of apoptosis protein 1) (H1AP1) (H1AP-1) (C-IAP2) (TNFR2-TRAF signaling complex protein 1) (TAP homolog C).			
DE	BIR2 OR API1 OR IAP1 OR MHIC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96128127; PubMed=8548810;			
RA	Roche M., Pan M.-G., Henzel W.J., Ayres F.M., Goeddel D.V.;			
RT	"The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins."			
RL	Cell 83:1243-1252(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96149249; PubMed=8552191;			
RA	Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,			
RT	Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;			
RL	"Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes."			
RN	Nature 379:349-353(1996).			
RP	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96209843; PubMed=8643514;			
RA	Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;			
RT	"Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors."			
RL	Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99252096; PubMed=10233894;			
RA	Horrevoets A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,			
RT	ten Cate J.W., Pannekoek H.;			
RL	"Vascular endothelial genes that are responsive to tumor necrosis factor-alpha in vitro are expressed in atherosclerotic lesions, including inhibitor of apoptosis protein-1, stannin, and two novel genes."			
RN	Blood 93:3418-3431(1999).			
RP	[5]			
RX	SEQUENCE OF 362-441 FROM N.A.			
RA	MEDLINE=20519161; PubMed=11066071;			
RT	Baens M., Steyis A., Dierlam J., De Wolf-Peters C., Marynen P.;			
RL	"Structure of the MTR gene and molecular characterization of the genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone			

RT B-cell lymphomas of MALT type.";  
RL Genes Chromosomes Cancer 29:281-291(2000).  
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
CC -1- SUBUNIT: Interacts with SMAC and with PRIS25; these interactions  
CC inhibit apoptotic suppressor activity.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN  
CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,  
CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.  
CC -1- DISEASE: Involved in t(11;18)(q21;q21) chromosomal translocation  
CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid  
CC tissue). This translocation is found in approximately 50% of  
CC cytogenetically abnormal low-grade MALT lymphoma and involves  
CC MALT1 and BIRC2.  
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL, L49432; AAC41943.1; -  
DR EMBL, U45878; AAC50371.1; -  
DR EMBL, U37546; AAC50507.1; -  
DR EMBL, AF070674; AAC83233.1; -  
DR EMBL, AF178945; AAC09369.1; -  
DR HSSP, Q13490; 10BH.  
DR GeneW, HGNC:591; BIRC3.  
DR MIM, 601712; -  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR001315; CARD.  
DR InterPro: IPR001841; Znf\_ring.  
DR Pfam, PF00097; zf-C3HC4; 1.  
DR Pfam, PF00619; CARD; 1.  
DR Pfam, PF00653; BIR; 3.  
DR SMART, SM00238; BIR; 3.  
DR SMART, SM00114; CARD; 1.  
DR SMART, SM00184; RING; 1.  
DR PROSITE, PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE, PS50143; BIR\_REPEAT\_2; 3.  
DR PROSITE, PS50209; CARD; 1.  
DR PROSITE, PS50518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE, PS50089; ZF\_RING\_2; 1.  
KW Apoptosis; zinc-finger; Repeat; Chromosomal translocation.  
FT REPEAT 29 96  
FT REPEAT 169 235  
FT REPEAT 255 322  
FT DOMAIN 439 529  
FT ZN\_FING 557 592  
FT SITE 442 443  
FT  
FT BIRC2-MALT1.  
FT  
FT CONFLICT 18 18 N->Y (IN REF. 4).  
FT CONFLICT 119 119 N->H (IN REF. 2).  
FT CONFLICT 153 153 D->E (IN REF. 2).  
FT CONFLICT 163 163 H->P (IN REF. 2).  
FT CONFLICT 165 165 A->P (IN REF. 2).  
FT CONFLICT 191 191 K->R (IN REF. 2).  
FT CONFLICT 364 364 F->L (IN REF. 2).  
FT CONFLICT 552 552 Q->P (IN REF. 2).  
SQ SEQUENCE 604 AA; 68371 MW; 8581A00BA9AAB4A7 CRC64;  
Query Match 100.0%; Score 267; DB 1; Length 604;  
Best Local Similarity 100.0%; Pred. No. 5.7e-27;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYITGPDVRVACFACGKLSNWEKPKDNAMSEHLNHPKCP 46  
DB 189 LAKAGFYITGPDVRVACFACGKLSNWEKPKDNAMSEHLNHPKCP 234  
RESULT 2  
ID PIAP\_PIG STANDARD; PRT; 358 AA.  
AC 062640;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Putative inhibitor of apoptosis.  
GN PIAP.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Aorta;  
RX MEDLINE=98162622; PubMed=9501011;  
RA Stehlik C., de Martin R., Binder B.R., Lipp J.;  
RT "Cytokine induced expression of porcine inhibitor of apoptosis  
RT protein (Iap) family member is regulated by NF-kappa B.";  
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).  
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC  
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CC  
CC EMBL, U79142; AAC39171.1; -  
DR HSSP, Q13490; 10BH.  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR001315; CARD.  
DR InterPro: IPR001841; Znf\_ring.  
DR Pfam, PF00097; zf-C3HC4; 1.  
DR Pfam, PF00619; CARD; 1.  
DR Pfam, PF00653; BIR; 2.  
DR SMART, SM00238; BIR; 2.  
DR SMART, SM00114; CARD; 1.  
DR SMART, SM00184; RING; 1.  
DR PROSITE, PS01282; BIR\_REPEAT\_1; 2.  
DR PROSITE, PS50143; BIR\_REPEAT\_2; 2.  
DR PROSITE, PS50209; CARD; 1.  
DR PROSITE, PS50518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE, PS50089; ZF\_RING\_2; 1.  
KW Apoptosis; zinc-finger; Repeat.  
FT REPEAT 4 70  
FT REPEAT 90 157  
FT DOMAIN 193 283  
FT ZN\_FING 311 346  
FT SITE 40977 MW; EB2268FA9A6190A4 CRC64;  
SQ SEQUENCE 358 AA; 40977 MW; EB2268FA9A6190A4 CRC64;  
Query Match 95.1%; Score 254; DB 1; Length 358;  
Best Local Similarity 93.5%; Pred. No. 1.6e-25;  
Matches 43; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 1 LAKAGFYITGPDVRVACFACGKLSNWEKPKDNAMSEHLNHPKCP 46  
DB 24 LAKAGFYITGPDVRVACFACGKLSNWEKPKDNAMSEHLNHPKCP 69  
RESULT 3

BIR3\_HUMAN  
ID BIR3\_HUMAN STANDARD: PRT: 618 AA.  
AC 013490: 016516;  
DT 01-NOV-1997 (rel. 35, Created)  
DT 01-NOV-1997 (rel. 35, Last sequence update)  
DE 15-JUN-2002 (rel. 41, Last annotation update)  
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS  
DE PROTEIN 2) (HIAIP2) (HIAIP-2) (C-IAP1) (TNFR2-TKAF signaling complex;  
DE protein 2) (IAP homolog B).  
GN BIR3 OR API2 OR IAP2 OR MIMB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96128127; PubMed=8548810;  
RA Rother M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;  
RT "The TNFR2-TKAF signaling complex contains two novel proteins related  
RT to baculoviral inhibitor of apoptosis proteins.";  
RL Cell 83:1243-1252(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96149249; PubMed=8552191;  
RA Liston P., Roy N., Tamal K., Lefebvre C., Balire S., Chertton-Horvat G.,  
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RT "Suppression of apoptosis in mammalian cells by NAIP and a related  
RT family of IAP genes.";  
RL Nature 379:349-353(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96209843; PubMed=8643514;  
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
RT "Cloning and expression of apoptosis inhibitory protein homologs that  
RT function to inhibit apoptosis and/or bind tumor necrosis factor  
RT receptor-associated factors.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX STRAUSBERG R.;  
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP STRUCTURE BY NMR OF 266-363.  
RX MEDLINE=99332054; PubMed=10404221;  
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;  
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)  
RT repeat.";  
RL Nat. Struct. Biol. 6:648-651(1999).  
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions  
CC inhibit apoptotic suppressor activity.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.  
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,  
CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD  
CC LEUCOCYTES.  
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;  
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/BIR3ID239.html".  
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CC EMBL: L49431; AAC41942.1; -  
CC EMBL: U45879; AAC50372.1; -  
CC EMBL: U37547; AAC50508.1; -  
CC EMBL: BC016174; AAH16174.1; -  
CC PDB: 1OBH; 20-OCT-99.  
CC GeneW: HGNC:590; BIR32.  
CC MIM: 601721; -  
CC InterPro: IPR001370; BIR.  
CC InterPro: IPR001315; CARD.  
CC InterPro: IPR001841; Znf\_Ring.  
CC Pfam: PF00097; zf-C3HC4; 1.  
CC Pfam: PF00619; CARD; 1.  
CC Pfam: PF00653; BIR; 3.  
CC SMART: SM00238; BIR; 3.  
CC SMART: SM00114; CARD; 1.  
CC SMART: SM00184; RING; 1.  
CC PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
CC PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
CC PROSITE: PS50209; CARD; 1.  
CC PROSITE: PS50089; zf\_RING\_1; FALSE\_NEG.  
CC PROSITE: PS50089; zf\_RING\_2; 1.  
CC Apoptosis; Zinc-finger; Repeat; 3d-structure.  
CC REPEAT 46 113 BIR 1.  
CC REPEAT 184 250 BIR 2.  
CC REPEAT 269 336 BIR 3.  
CC DOMAIN 453 543 CARD.  
CC ZN\_FING 571 606 CARD.  
CC CONFLICT 157 157 S -> P (IN REF. 2).  
CC CONFLICT 308 308 C -> G (IN REF. 2).  
CC CONFLICT 414 414 Q -> L (IN REF. 2).  
CC CONFLICT 514 514 L -> W (IN REF. 2).  
SQ SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

Query Match 92.9%; Score 248; DB 1; Length 618;  
Best Local Similarity 91.3%; Pred. No. 1,7e-24;  
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LARAGFYIIPGDRVACFACGCKLSNMPEKDNAMSEHLRHPKCP 46  
DB 204 LARAGFYIIPGDRVACFACGCKLSNMPEKDNAMSEHLRHPKCP 249

RESULT 4  
BIR3\_MOUSE  
ID BIR3\_MOUSE STANDARD: PRT: 612 AA.  
AC 062210: 008864;  
DT 01-NOV-1997 (rel. 35, Created)  
DT 01-NOV-1997 (rel. 35, Last sequence update)  
DE 15-JUN-2002 (rel. 41, Last annotation update)  
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS  
DE PROTEIN 2) (MIAP2) (MIAP-2).  
GN BIR3 OR API2 OR IAP2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
RX MEDLINE=96128127; PubMed=8548810;  
RA Rother M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;  
RT "The TNFR2-TKAF signaling complex contains two novel proteins related  
RT to baculoviral inhibitor of apoptosis proteins.";  
RL Cell 83:1243-1252(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE=skeletal muscle;  
MEDLINE=98110590; PubMed=9441758;  
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;  
RT "Genomic characterization of the mouse inhibitor of apoptosis protein

```

RT 1 and 2 genes.
CC Genomics 46:495-503(1997).
CC - FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC - SUBUNIT: Interacts with SMAC and with PR525; these interactions
CC inhibit apoptotic suppressor activity (by similarity).
CC - SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC - TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC - SIMILARITY: BELONGS TO THE IAP FAMILY.
CC - SIMILARITY: CONTAINS 3 BIR REPEATS.
CC - SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
DR EMBL: L49433; AAC42078.1; -.
DR EMBL: U88909; AAC53532.1; -.
DR HSSP: 013490; 10BH.
DR MGD: MGI:1197009; Birc3.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_Ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50089; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
DR REPEAT 46 113 BIR 1.
DR REPEAT 177 243 BIR 2.
DR REPEAT 262 329 BIR 3.
DR DOMAIN 447 537 CARD.
DR ZN_FING 565 600 RING-TYPE.
DR CONFLICT 380 E -> K (IN REF. 2).
DR SEQUENCE 612 AA; 69676 MW; E08969D93C6C610F CRC64;

Query Match
Best Local Similarity 92.5%; Score 247; DB 1; Length 612;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKAGFYITGPDGVACFACGKLSNWEKDNAMSEHLRHPKCP 46
DB 197 LAKAGFYITGPDGVACFACGKLSNWEKDNAMSEHLRHPKCP 242

RESULT 5
BIR2_MOUSE
ID BIR2_MOUSE STANDARD; PRT; 600 AA.
AC 008663;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
DE protein 1) (MIAP1) (MIAP-1).
GN BIRC2 OR API1 OR IAP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RC MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Pong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
CC Genomics 46:495-503(1997).
CC - FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
CC - SUBUNIT: Interacts with SMAC and with PR525; these interactions
CC inhibit apoptotic suppressor activity (by similarity).
CC - SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC - SIMILARITY: BELONGS TO THE IAP FAMILY.
CC - SIMILARITY: CONTAINS 3 BIR REPEATS.
CC - SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
DR EMBL: U88908; AAC53531.1; -.
DR HSSP: 013490; 10BH.
DR MGD: MGI:1197007; Birc2.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_Ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50089; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
DR REPEAT 27 94 BIR 1.
DR REPEAT 167 233 BIR 2.
DR REPEAT 253 320 BIR 3.
DR DOMAIN 436 525 CARD.
DR ZN_FING 553 588 RING-TYPE.
DR SEQUENCE 600 AA; 67198 MW; AD/F73E649317D1 CRC64;

Query Match
Best Local Similarity 88.0%; Score 235; DB 1; Length 600;
Matches 41; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKAGFYITGPDGVACFACGKLSNWEKDNAMSEHLRHPKCP 46
DB 187 LAKAGFYITGPDGVACFACGKLSNWEKDNAMSEHLRHPKCP 232

RESULT 6
BIR_CHICK
ID BIR_CHICK STANDARD; PRT; 611 AA.
AC 090660;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis
DE protein).
GN ITA.

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CC -----
DR EMBL: U45880; AAC50373.1; -
DR EMBL: U32974; AAC50518.1; -
DR EMBL: AL121601; CAB95312.1; -
DR PDB: 1G3F; 10-JAN-01.
DR Genew: HGNC:592; BIRC4.
DR MIM: 300079; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00653; BIR.3.
DR SMART: SM00238; BIR.3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS00143; BIR_REPEAT_2; 3.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat; Thiol protease inhibitor;
KW 3D-structure.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 265 330 BIR 3.
FT ZN_FING 450 485 BIR-3.
FT MOTAGEN 214 248 D->S: REDUCED INTERACTION WITH PRSS25.
FT MOTAGEN 314 314 E->S: DECREASED INTERACTION WITH SMAC AND
WITH PRSS25.
FT CONFLICT 162 162 S -> C (IN REF. 1).
FT CONFLICT 423 423 S -> P (IN REF. 2).
SQ SEQUENCE 497 AA; 56684 MM; 9D394C16D45EB635 CRC64;

Query Match 68.2%; Score 182; DB 1; Length 497;
Best Local Similarity 69.6%; Pred. No. 4,5e-16;
Matches 32; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

OY 1 LAKAGFYTGDRVACFACGKLSNWEPKDNMSEHLRHPKCP 46
DB 184 LASAGLYTIGADVOVCFCCGKLNWPCDRAMSEHRRHPCF 229

RESULT 8
BIR4_MOUSE
ID BIR4_MOUSE STANDARD; PRT; 496 AA.
AC 060989; 008865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP3) (MIAP-3).
GN BIRC4 OR API3 OR XIAP OR AIP4 OR AIP4 OR MTA.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Parahani R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
(CC (By similarity)).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
(CC inhibit apoptotic suppressor activity (By similarity)).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3

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CC -----
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRSS25 are mediated by the second
CC and third BIR domains (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
DR EMBL: U36842; AAC52594.1; -
DR EMBL: U08990; AAB58376.1; -
DR HSSP: Q13490; IOBH.
DR MGD: MGI:107572; Birc4.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00653; BIR.3.
DR SMART: SM00238; BIR.3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS00143; BIR_REPEAT_2; 3.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-TYPE.
FT CONFLICT 208 208 E -> K (IN REF. 2).
FT CONFLICT 317 317 E -> D (IN REF. 2).
FT CONFLICT 322 322 W -> C (IN REF. 2).
FT CONFLICT 346 346 S -> P (IN REF. 2).
FT CONFLICT 360 360 S -> P (IN REF. 2).
FT CONFLICT 388 388 I -> L (IN REF. 2).
FT CONFLICT 449 449 C -> S (IN REF. 2).
FT CONFLICT 462 462 V -> F (IN REF. 2).
FT CONFLICT 468 468 V -> A (IN REF. 2).
FT CONFLICT 490 490 K -> N (IN REF. 2).
SQ SEQUENCE 496 AA; 56079 MM; EC5FAE0799F2CDD8 CRC64;

Query Match 66.3%; Score 177; DB 1; Length 496;
Best Local Similarity 67.4%; Pred. No. 2e-15;
Matches 31; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

OY 1 LAKAGFYTGDRVACFACGKLSNWEPKDNMSEHLRHPKCP 46
DB 184 LASAGLYTIGADVOVCFCCGKLNWPCDRAMSEHRRHPCF 229

RESULT 9
BIR4_RAT
ID BIR4_RAT STANDARD; PRT; 496 AA.
AC 09016;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (RIAP3) (RIAP-3).
GN BIRC4 OR API3 OR XIAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Salto N.;

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RT "Rattus norvegicus X-linked inhibitor of apoptosis (riap) mRNA.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBD databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRSS25 are mediated by the second
CC and third BIR domains (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL; AB033366; BAA85304.1; -
DR HSSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01283; BIR_REPEAT_1; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger; Repeat.
DR REPEAT 26 93 BIR 1.
DR REPEAT 163 230 BIR 2.
DR REPEAT 264 329 BIR 3.
DR ZN_FING 449 484 RING-TYPE.
DR SEQUENCE 496 AA; 56072 MW; E250E3C77461A469 CRC64;

Query Match 65.5%; Score 175; DB 1; Length 496;
Best Local Similarity 67.4%; Pred. No. 3.6e-15;
Matches 31; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDYVACFACGKLSNWEKDNAMSEHLRHFPCPF 46
DB 184 LASAGLYTIGIDYVQCFCCGKLNKWEKCDRAWSEHRRHFNCF 229

RESULT 10
BIR8_HUMAN
ID BIR8_HUMAN STANDARD: PRT; 236 AA.
AC Q96P09; Q96P05;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2) (Testis-specific
DE inhibitor of apoptosis).
GN BIRC8 OR ILP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=11597143;
RA Lagace M., Xuan J.-Y., Young S.S., McRoberts C., Maier J.,
RA Rajcan-Separovic E., Korneluk R.G.;
RT "Genomic Organization of the X-linked Inhibitor of Apoptosis and

```

```

RT Identification of a novel testis-specific transcript.";
RL Genomics 77:181-188(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
RA Fratini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezoni P., Fearhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RL Mol. Cell. Biol. 21:4293-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SUBUNIT: Binds to caspase-9.
CC -1- TISSUE SPECIFICITY: Testis-specific in normal tissues.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BIR REPEAT.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF420440; AAL30369.1; -
DR EMBL; AF164682; AAK81892.1; -
DR Genew; HGNC:14878; BIRC8.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 1.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger.
DR REPEAT 7 70 BIR.
DR ZN_FING 189 224 RING-TYPE.
DR CONFLICT 196 196 Y -> H (IN REF. 2).
DR SEQUENCE 236 AA; 27115 MW; CB7F034B0DDFAD9D CRC64;

Query Match 54.3%; Score 145; DB 1; Length 236;
Best Local Similarity 50.0%; Pred. No. 1.3e-11;
Matches 23; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDYVACFACGKLSNWEKDNAMSEHLRHFPCPF 46
DB 23 LAKAGFYIIGEDKYVQCFHGGGLANWKPEDEWQHAKWFGCKY 68

RESULT 11
BIR8_PANTR
ID BIR8_PANTR STANDARD: PRT; 236 AA.
AC Q95W72;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2).
GN BIRC8 OR ILP2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
RA Fratini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezoni P., Fearhead H.O., Duckett C.S.;

```

RT "Molecular cloning of ILP-2, a novel member of the inhibitor of  
RT apoptosis protein family."  
RT Mol. Cell Biol. 21:4292-4301(2001).  
CC -1- FUNCTION: Protects against apoptosis mediated by BAX (By  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
CC -1- SUBUNIT: Binds to caspase-9 (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 BIR REPEAT.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC  
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CC  
CC EMBL: AY030052; AAK49776.1; -  
CC InterPro: IPR001370; BIR.  
CC InterPro: IPR001841; znf\_ring.  
CC Pfam: PF00653; BIR.1.  
CC Pfam: PF00657; zf-C3HC4.1.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 1.  
DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE: PS00889; ZF\_RING\_2; 1.  
KM Apoptosis; zinc-finger.  
FT REPEAT 7  
FT ZN\_RING 224  
SQ SEQUENCE 236 AA; 27136 MW; 64CCA3A251420E2D CRC64;  
Query Match 54.3%; Score 145; DB 1; Length 236;  
Best Local Similarity 50.0%; Pred. No. 1.3e-1x;  
Matches 23; Conservative 10; Mismatches 13; Indels 0; Gaps 0;  
QY 1 LAKAGFYIIGPGRVACFACGKLSMWEPRDNAMSEIRHPRKCP 46  
Db 23 LARAGFYAIGEDKVKCFHCGGGLAMKPKEDWEDHAKYKPGCKY 68  
RESULT 12  
ID IAP2\_DROME STANDARD; PRT; 498 AA.  
AC Q24307; Q24177; Q24115; Q24149; Q9V7G1;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis 2 inhibitor (inhibitor of apoptosis 2) (DIAP2) (DIAP) (IAP  
DE homolog A) (IAP-like protein) (DIIP).  
GN IAP2 OR ILP OR DIHA OR CG8293.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Moscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Embryo;  
RX MEDLINE-96128128; PubMed-8548811;  
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertok Horvat G.,  
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RT "Suppression of apoptosis in mammalian cells by NAIP and a related  
RT family of IAP genes".

RL Nature 379:349-353(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Canton-S;  
RX MEDLINE-96256286; PubMed-8654366;  
RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,  
RA Gillfillan M.C., Shleis H., Hardwick J.M., Thompson C.B.;  
RT "A conserved family of cellular genes related to the baculovirus iap  
RT gene and encoding apoptosis inhibitors".  
RL ENBO J. 15:2685-2694(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Canton-S;  
RA Rose J.L.;  
RT Thesis (1991), Vanderbilt University / Nashville, U.S.A.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Berkeley;  
RX MEDLINE-20196006; PubMed-10731132;  
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Ananthides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer J.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
RA Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostrel A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
RA Palazotto M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao G., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster".  
RL Science 287:2185-2195(2000).  
RN [6]  
RP SEQUENCE OF 17-498 FROM N.A.  
RC TISSUE-larva;  
RX MEDLINE-96209843; PubMed-8643514;  
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
RT "Cloning and expression of apoptosis inhibitor protein homologs that  
RT function to inhibit apoptosis and/or bind tumor necrosis factor  
RT receptor-associated factors".  
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND  
CC -1- H2O-DEPENDENT CELL DEATH IN THE EYE.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS THROUGHOUT  
CC DEVELOPMENT.  
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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CC -----
DR EMBL; L49441; AAC41610.1;
DR EMBL; U45881; AAC46988.1;
DR EMBL; U32373; AAC47155.1;
DR EMBL; M96581; NOT_ANNOTATED_CDS.
DR EMBL; AE003809; AAP58095.1;
DR EMBL; U38809; AAB08398.1;
DR HSSP; Q13490; IOBH.
DR FlyBase; FBgn0015247; Iap2.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS00143; BIR_REPEAT_2; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
DR REPEAT; 9; BIR 1.
DR REPEAT; 113; BIR 2.
DR REPEAT; 212; BIR 3.
DR ZN_FING; 451; 486
FT CONFLICT; 5; G -> V (IN REF. 2).
FT CONFLICT; 40; E -> K (IN REF. 2).
FT CONFLICT; 64; ER -> AG (IN REF. 3).
FT CONFLICT; 94; A -> D (IN REF. 6).
FT CONFLICT; 282; A -> S (IN REF. 3).
FT CONFLICT; 286; P -> Q (IN REF. 2 AND 5).
FT CONFLICT; 302; P -> T (IN REF. 6).
FT CONFLICT; 303; A -> T (IN REF. 2).
FT CONFLICT; 327; ALEVERPP -> DMRCASR (IN REF. 3).
FT CONFLICT; 369; 376
SO SEQUENCE; 498 AA; 54506 MW; 66EC36DA6ED24ADC; CRC64;

Query Match      54.3%; Score 145; DB 1; Length 498;
Best Local Similarity 55.6%; Pred. No. 2.8e-11;
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRAVACRACGKLSNWEKDNAMSEHLRHFKECP 45
DB 133 LAKAGFYIILRLDHVCVWNCVIAKMEKNDNAFEHKKRFPQCP 177

RESULT 13
BIR8_GORGO
ID BIR8_GORGO STANDARD; PRT; 236 AA.
AC Q95W71;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (IIP-2).
GN BIR8 OR IIP2.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Reffey S.B.,
RA Frittl A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezzoni P., Fearhead H.O., Duckett C.S.;

```

```

RT Molecular cloning of IIP-2, a novel member of the inhibitor of
RT apoptosis protein family.
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SUBUNIT: Binds to caspase-9 (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL; AY030053; AAK49777.1;
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.
DR PROSITE; PS00143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger.
DR REPEAT; 7; BIR.
DR ZN_FING; 189; 224
FT SEQUENCE; 236 AA; 27120 MW; C3A70B39BE442E4C; CRC64;

Query Match      53.9%; Score 144; DB 1; Length 236;
Best Local Similarity 47.8%; Pred. No. 1.8e-11;
Matches 22; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRAVACRACGKLSNWEKDNAMSEHLRHFKECP 46
DB 23 LAKAGFYALIGDEKTIQCFHCGLANWPKEDPWROHAKWPGCKY 68

RESULT 14
BIR8_MOUSE
ID BIR8_MOUSE STANDARD; PRT; 1402 AA.
AC Q9JIB3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis
DE inhibitory protein 7).
GN BIR8IG OR NAIP7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20414747; PubMed=10958627;
RA Endlitz M.G., Hadinoto V., Gromey J.D., Miller W., Dietrich W.F.;
RA "Genomic sequence analysis of the mouse Naip gene array."
RL Genome Res. 10:1095-1102(2000).
DE -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
DE SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
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CC EMBL: AF242433; AAF82749.1; -
DR HSP; Q13490; IQBH.
DR MGD; MG1:1858256; Birc1g.
DR InterPro; IPR001370; BIR.
DR Pfam; PF006653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT REPEAT 464 759 NACHT.
SQ DOMAIN 1402 AA; 159662 MW; CIDFFBA359803EOD CRC64;

Query Match 52.8%; Score 141; DB 1; Length 1402;
Best Local Similarity 52.2%; Pred. No. 2.6e-10;
Matches 24; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

OY 1 LAKAGFYTGDRVACFACGKLSMWEPRDNAMSEHLRHPKCP 46
DB 181 LSAAGFYTGKRDYVOCFSCGSLGNWEGDDPMKEHAKMPCPEF 226

RESULT 15
BIR1_HUMAN STANDARD; PRT; 1403 AA.
AC Q13075; Q13730; Q89796; Q75857;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE baculoviral IAP repeat-containing protein 1 (neuronal apoptosis
DE inhibitory protein).
GN BIRC1 OR NAIP.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=95112344; PubMed=7813013;
RA Roy N., Mahadevan M.S., McLean M., Shuttler G., Yaraqhi Z.,
RA Farahani R., Baird S., Besner-Johnston A., Lefebvre C., Kang X.,
RA Salih M., Aubry H., Tamai K., Guan X., Ioannou P., Crawford T.O.,
RA de Jong P.J., Surh L., Ikeda J., Korneluk R.G., Mackenzie A.;
RT "The gene for neuronal apoptosis inhibitory protein is partially
RT deleted in individuals with spinal muscular atrophy.";
RL Cell 80:167-178(1995).
RN [2]
RP SEQUENCE FROM N.A., AND REVISIONS.
RC TISSUE=Brain;
RX MEDLINE=98163755; PubMed=9503025;
RA Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farahani R.,
RA Xuan J.-Y., Kang X., Lefebvre C., Ikeda J.-E., Korneluk R.G.,
RA Mackenzie A.E.;
RT "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular
RT atrophy candidate genes SMN and NAIP.";
RL Genomics 48:121-127(1998).
RN [3]
RP SEQUENCE OF 386-623 FROM N.A.
RA der Steege G., Draaijers T.G., Grootscholten P.M., Olinga J.,
RA Anzeveno R., Velona I., Brane C., Schiefer H., van Omnen G.J.B.,
RA Buys C.H.C.M.;
RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 223-1403 FROM N.A.
RA Jones K., Graves T., McPherson J.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]

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RP FUNCTION.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertou-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.";
RL Nature 379:349-353(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY
CC NEURONS. FOUND IN LAYER AND PLACENTA, AND IN A LESSER EXTENT IN
CC SPINAL CORD.
CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN
CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE 1). SMAS
CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE 1
CC (WERNIG-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE
CC III (MOTIFART-KUGELBERG-WELANDER DISEASE) BASED UPON THE AGE OF
CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE
CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO
CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000
CC NEBORN.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL; U19251; AAC52045.1; -
DR EMBL; U80017; AAC52047.1; -
DR EMBL; U21913; AAA64504.1; -
DR EMBL; AC005031; AAC62261.1; -
DR HSP; Q13490; IQBH.
DR Genew; HGNC:7634; BIRC1.
DR MIM; 600355; -
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0837; NACHT; 1.
KW Apoptosis; Repeat.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 758 NACHT.
FT CONFLICT 222 223 VP -> YR (IN REF. 4).
FT CONFLICT 386 387 M -> V (IN REF. 3).
FT CONFLICT 535 535 Y -> H (IN REF. 3).
FT CONFLICT 553 553 Y -> H (IN REF. 3).
FT CONFLICT 1228 1231 MISSING (IN REF. 4).
SQ SEQUENCE 1403 AA; 159613 MW; 566304C154DB5E64 CRC64;

Query Match 52.8%; Score 141; DB 1; Length 1402;
Best Local Similarity 52.2%; Pred. No. 2.6e-10;
Matches 24; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

OY 1 LAKAGFYTGDRVACFACGKLSMWEPRDNAMSEHLRHPKCP 46
DB 299 LAKAGFYTGKRDYVOCFSCGSLGNWEGDDPMKEHAKMPCPEF 344

```

Search completed: May 5, 2003, 16:02:46  
 Job time : 2.90783 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:58:42 ; Search time 5.03456 Seconds

(without alignments)  
878.365 Million cell updates/sec

Title: US-08-569-749-8

Sequence: 1 LKAGFYIIGPGDRVACFAC.....WEIKDNAMSEHLRHPKCPF 46

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	264	98.9	604	S68449	apoptosis inhibitor
2	234	95.1	358	JC5964	apoptosis inhibitor
3	248	92.9	618	S68450	apoptosis inhibitor
4	182	68.2	497	S69544	apoptosis inhibitor
5	145	54.3	496	S68452	apoptosis inhibitor
6	145	54.3	497	S69545	apoptosis inhibitor
7	141	52.8	1232	A55478	apoptosis inhibitor
8	138	51.7	1447	T42628	neuronal apoptosis
9	135	50.6	268	T10304	neuronal apoptosis
10	131	49.1	275	A53989	inhibitor of apopt
11	131	49.1	275	A45679	inhibitor of apopt
12	122.5	45.9	4845	T31067	inhibitor-of-apopt
13	121	45.3	298	JC7568	BR repeat contain
14	112	41.9	208	T03183	kidney inhibitor o
15	103	38.6	997	T43523	probable apoptosis
16	100	37.5	150	T28409	cutl7 protein - fl
17	98	36.7	155	T30489	ORF MSV248 probabl
18	95	35.6	292	T41772	apoptosis inhibito
19	93	34.8	286	D36828	IAP1 orf27 - Bomby
20	90	33.7	275	T03100	orf13 protein - Au
21	74.5	27.9	329	T28403	apoptosis-inhibiti
22	68	25.5	155	T28403	ORF MSV242 probabl
23	62.5	23.4	223	T37471	apoptosis inhibito
24	60	22.5	249	S16652	hypothetical prote
25	60	22.5	249	H72858	apoptosis inhibito
26	59	22.1	355	T41814	IAP2 orf71 - Bomby
27	58	22.1	355	C64549	conserved hypochet
28	58	21.7	355	G71958	hypothetical prote
29	57.5	21.5	278	T30427	probable apoptosis
				S25690	hup1 protein - Rho

30	56.5	21.2	724	2	C49423	semaphorin II prec
31	56.5	21.2	2236	1	Q2F	rudimentary protei
32	56	21.0	1004	2	JH0470	Na+/K+-exchanging
33	55	20.6	313	2	T02534	hypothetical prote
34	55	20.6	462	2	T47287	hypothetical prote
35	55	20.6	469	2	AB0237	hypothetical prote
36	55	20.6	469	2	T47015	hypothetical prote
37	55	20.6	1433	2	S54587	hypothetical prote
38	54.5	20.4	546	2	A81807	CAT8 protein - yea
39	54	20.2	181	2	E36794	fumarate hydratase
40	54	20.2	606	2	T13152	hypothetical prote
41	54	20.2	843	1	A27340	MDR1 protein - hum
42	53.5	20.0	172	2	T34035	complement C7 prec
43	53.5	20.0	563	1	VCMY7	hypothetical prote
44	53.5	20.0	741	2	T40095	env polypeptide
45	53	19.9	838	2	A48440	zinc finger, C3HC4 ring-infected eryt

#### ALIGNMENTS

RESULT 1  
S68449  
apoptosis inhibitor hlap-1 - human  
C:Species: Homo sapiens (man)  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 21-Jul-2000  
C:Accession: S68449  
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Balrd, S.; Chertton-Horvat, G.; Faraha  
Nature 379, 349-353, 1996  
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of  
A:Reference number: A58182; MUID:96149249; PMID:8552191  
A:Accession: S68449  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-604 <LIS>  
A:Cross-references: EMBL:U45878; NID:g1184315; PIDN:AAC50371.1; PID:g1184316  
C:Function:  
A:Description: apoptotic suppressor  
C:Superfamily: RING finger homology  
C:Keywords: apoptosis; zinc finger  
F:553-597/Domain: RING finger homology <RMG>

Query Match 98.9% Score 264; DB 2; Length 604;  
Best Local Similarity 97.8%; Pred. No. 1.1e-24;  
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAGFYIIGPGDRVACFACGKLSNWEKDNAMSEHLRHPKCPF 46  
Db 189 LKAGFYIIGPGDRVACFACGKLSNWEKDNAMSEHLRHPKCPF 234

RESULT 2  
JC5964  
apoptosis inhibitor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 02-Sep-2000  
C:Accession: JC5964  
R:Stehlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.  
Biochem. Biophys. Res. Commun. 243, 827-832, 1998  
A:Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (Iap)  
A:Reference number: JC5964; MUID:98162622; PMID:9501011  
A:Accession: JC5964  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-358 <STE>  
C:Cross-references: GB:U79142; NID:92957174; PIDN:AAC39171.1; PID:92957175  
F:307-351/Domain: RING finger homology <RRN>

Query Match 95.1% Score 254; DB 2; Length 358;  
Best Local Similarity 93.5%; Pred. No. 1.2e-23;  
Matches 43; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAKAGFYITGPDRAVACFACGKLSNWEPRKDNAMSEHLRHFPCPF 46  
|||||  
Db 24 LAKAGFYITGPDRAVACFACGKLSNWEPRKDNAMSEHLRHFPCPF 69

RESULT 3  
S68450  
apoptosis inhibitor hlap-2 - human  
C:Species: Homo sapiens (man)  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 21-Jul-2000  
C:Accession: S68450  
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996  
A>Title: Suppression of apoptosis in mammalian cells by NALP and a related family of IAP  
A:Reference number: A58182; MUID:96149249; PMID:8552191  
A:Accession: S68450  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-618 <LIS>  
A:Cross-references: EMBL:U45879; NID:q1184317; PIDN:AAC50372.1; PID:q1184318  
C:Function:  
A:Description: apoptotic suppressor  
C:Superfamily: RING finger homology  
C:Keywords: apoptosis; zinc finger  
F:567-611/Domain: RING finger homology <RNG>

Query Match 92.9%; Score 248; DB 2; Length 618;  
Best Local Similarity 91.3%; Pred. No. 1.1e-22;  
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKAGFYITGPDRAVACFACGKLSNWEPRKDNAMSEHLRHFPCPF 46  
|||||  
Db 204 LAKAGFYITGPDRAVACFACGKLSNWEPRKDNAMSEHLRHFPCPF 249

RESULT 4  
S69544  
apoptosis inhibitor IAP homolog - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Nov-2000  
C:Accession: S69544; S68451  
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Giffillan, M.C. EMBO J. 15, 2685-2694, 1996  
A>Title: A conserved family of cellular genes related to the baculovirus iap gene and er  
A:Reference number: S69544; MUID:96256286; PMID:8654366  
A:Accession: S69544  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-497 <DUC>  
A:Cross-references: EMBL:U32974; NID:q1016687; PIDN:AAC50518.1; PID:q1016688  
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996  
A>Title: Suppression of apoptosis in mammalian cells by NALP and a related family of IAP  
A:Reference number: A58182; MUID:96149249; PMID:8552191  
A:Accession: S68451  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>  
A:Cross-references: EMBL:U45880; NID:q1184319; PIDN:AAC50373.1; PID:q1184320  
C:Genetics:  
A:Gene: IIP  
C:Function:  
A:Description: apoptotic suppressor  
C:Superfamily: apoptosis inhibitor IAP homology; RING finger homology  
C:Keywords: apoptosis; zinc finger  
F:446-490/Domain: RING finger homology <RRN>

Query Match 68.2%; Score 182; DB 2; Length 497;  
Best Local Similarity 69.6%; Pred. No. 1.2e-14;  
Matches 32; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 1 LAKAGFYITGPDRAVACFACGKLSNWEPRKDNAMSEHLRHFPCPF 46  
|||||

Db 184 LASAGLYTIGIDQVOCFCGCKLKWPCDRAMSEHLRHFPCPF 229

RESULT 5  
S68452  
apoptosis inhibitor dlap - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 17-Nov-2000  
C:Accession: S68452; S78528  
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996  
A>Title: Suppression of apoptosis in mammalian cells by NALP and a related family of  
A:Reference number: A58182; MUID:96149249; PMID:8552191  
A:Accession: S68452  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-496 <LIS>  
A:Cross-references: EMBL:U45881; NID:q1184313; PIDN:AAC46988.1; PID:q1184314  
R:Baird, S.D.  
submitted to the EMBL Data Library, January 1996  
A:Reference number: S78528  
A:Accession: S78528  
A:Molecule type: mRNA  
A:Residues: 1-36, 'AT', 37, 'K', 39, 'L', 41-44, 'H', 46-58, 'Q', 60-412, 'A', 414-427, 'A', 429-49  
A:Cross-references: EMBL:U45881; NID:q1184313; PIDN:AAC46988.1; PID:q1184314  
C:Genetics:  
A:Cross-references: FlyBase:FBgn0015247  
C:Function:  
A:Description: apoptotic suppressor  
C:Superfamily: apoptosis inhibitor IAP homology; RING finger homology  
C:Keywords: apoptosis; zinc finger  
F:445-489/Domain: RING finger homology <RNG>

Query Match 54.3%; Score 145; DB 2; Length 496;  
Best Local Similarity 55.6%; Pred. No. 4.2e-10;  
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 LAKAGFYITGPDRAVACFACGKLSNWEPRKDNAMSEHLRHFPCPF 45  
|||||  
Db 131 LAKAGFYITGPDRAVACFACGKLSNWEPRKDNAMSEHLRHFPCPF 175

RESULT 6  
S69545  
apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: S69545  
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Giffillan, EMBO J. 15, 2685-2694, 1996  
A>Title: A conserved family of cellular genes related to the baculovirus iap gene and  
A:Reference number: S69544; MUID:96256286; PMID:8654366  
A:Accession: S69545  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-497 <DUC>  
A:Cross-references: EMBL:U32973; NID:q1019116; PIDN:AAC47155.1; PID:q1019117  
C:Genetics:  
A:Gene: IIP  
C:Function:  
A:Description: apoptotic suppressor  
C:Superfamily: apoptosis inhibitor IAP homology; RING finger homology  
F:446-490/Domain: RING finger homology <RRN>

Query Match 54.3%; Score 145; DB 2; Length 497;  
Best Local Similarity 55.6%; Pred. No. 4.2e-10;  
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 LAKAGFYITGPDRAVACFACGKLSNWEPRKDNAMSEHLRHFPCPF 45  
|||||  
Db 133 LAKAGFYITGPDRAVACFACGKLSNWEPRKDNAMSEHLRHFPCPF 177

RESULT 7  
A55478





C:Species: Mus musculus (house mouse)  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
C:Accession: T31067  
R:Hauer, H.P.; Bardoff, M.; Pyrcowakis, G.; Jentsch, S.  
J. Cell Biol. 141, 1415-1422, 1998  
A:Title: A giant ubiquitin-conjugating enzyme related to IAP apoptosis inhibitors.  
A:Reference number: Z20963; MUID:98292517; PMID:9628897  
A:Accession: T31067  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-4645 <HAU>  
A:Cross-References: EMBL:Y17667; NID:g3319989; PIDN:CAA76720.1; PID:g3319990  
A:Note: localized to the Golgi compartment and the vesicular system  
C:Keywords: membrane-associated protein

Query Match 45.9%; Score 122.5; DB 2; Length 4845;  
Best Local Similarity 49.0%; Pred. No. 2.1e-06;  
Matches 24; Conservative 3; Mismatches 19; Indels 3; Gaps 1;

QY 1 LAKAGFYI--IGPGRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 46  
DB 284 MAAGFYIHQPASSGDDRRACFTCSVLCVNEPTEPWSHERHSPKCP 332

RESULT 13  
JC7568  
Kidney inhibitor of apoptosis protein - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001  
C:Accession: JC7568  
R:Lin, J.H.; Deng, G.; Morser, J.  
Biochem. Biophys. Res. Commun. 279, 820-831, 2000  
A:Title: KIP1, a novel member of the inhibitor of apoptosis protein family.  
A:Reference number: JC7568; MUID: 21092523; PMID:11162455  
A:Contents: Fetal kidney  
A:Accession: JC7568  
A:Molecule type: mRNA  
A:Residues: 1-298 <LIN>  
C:Comment: This protein, a new member of the inhibitor of apoptosis protein family, play  
C:Genetics:  
A:Gene: klap  
A:Map position: 20q13.3  
C:Keywords: apoptosis

Query Match 45.3%; Score 121; DB 2; Length 298;  
Best Local Similarity 45.7%; Pred. No. 2.3e-07;  
Matches 21; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 LAKAGFYI--IGPGRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 46  
DB 108 LAAAGFYHGHODKVCFCYCGSLQSMKRGDDPWEHAKWFI 153

RESULT 14  
T03183  
probable apoptosis inhibitor - Chilo iridescent virus  
C:Species: Chilo iridescent virus  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 02-Sep-2000  
C:Accession: T03183  
R:Bahr, U.; Tlodon, C.A.; Daral, G.  
Virus Genes 15, 235-245, 1997  
A:Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101  
A:Reference number: Z14834; MUID:98141693; PMID:9482389  
A:Accession: T03183  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-208 <BAH>  
A:Cross-References: EMBL:AF003534; NID:g2738385; PIDN:AA894481.1; PID:g2738454  
C:Superfamily: RING finger homology  
F:159-202/Domain: RING finger homology <RRN>

Query Match 41.9%; Score 112; DB 2; Length 208;

Best Local Similarity 47.5%; Pred. No. 2.1e-06;  
Matches 19; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 LAKAGFYI--IGPGRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 40  
DB 58 LSRAGFYI--INIGDQVOCFCYCDLKLKEMKRSNDPFEHKKH 97

RESULT 15  
T43523  
cut17 protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 02-Jun-2000  
C:Accession: T43523; T41649; T41700  
R:Moriishi, J.; Matsusaka, T.; Yanagida, M.  
submitted to the EMBL Data Library, August 1999  
A:Description: Fission yeast cut17 is required for chromosome segregation.  
A:Reference number: Z22536  
A:Accession: T43523  
A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-997 <MOR>  
A:Cross-References: EMBL:AB031034; PIDN:BA83415.1

R:Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, August 1998  
A:Reference number: Z22007  
A:Accession: T41649

A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-997 <HAR>

A:Cross-References: EMBL:AL031323; PIDN:CAA20434.1; GSPDB:GN00066; SPDB:SPCC962.02c  
A:Experimental source: strain 972h; cosmid c962  
R:Medler, H.; Diesterhoef, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1999  
A:Reference number: Z22010  
A:Accession: T41700

A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 932-997 <MED>

A:Cross-References: EMBL:AL121859; PIDN:CAB58376.1; GSPDB:GN00068; SPDB:SPCP31B10.10c  
C:Genetics:  
A:Gene: cut17; SPCC962.02c; SPDB:SPCP31B10.10c  
A:Map position: 3L  
A:introns: 43/3

Query Match 38.6%; Score 103; DB 2; Length 997;  
Best Local Similarity 37.0%; Pred. No. 0.00012;  
Matches 20; Conservative 6; Mismatches 20; Indels 8; Gaps 2;

QY 1 LAKAGFYI--IGPGRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 46  
DB 44 LATVGFYINPISBSNSEERLDNVTCTMCYKSPFYDWDDEDDPLKHTHTSPSCPW 97

Search completed: May 5, 2003, 16:08:11  
Job time: 7.03456 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:57:12 ; Search time 11.235 Seconds

(without alignments)  
843.627 Million cell updates/sec

Title: US-08-569-749-8

Perfect score: 267  
Sequence: 1 LAKAGFYITIGPDRAVACFAC.....WEPRDNAMSEHLRHPKCP 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

SPTRMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	235	88.0	374	11	Q921N0 mus musculus
2	232	86.9	589	11	Q9ESE8
3	232	86.9	589	11	Q9QZC6
4	226	84.6	602	11	Q9ESE9
5	223	83.5	195	13	Q91A70
6	223	83.5	195	13	Q91A69
7	223	83.5	324	13	Q9DDN2
8	223	83.5	610	13	Q57319
9	217	81.3	224	11	Q88642
10	195	73.0	628	13	Q8UWD2
11	194	72.7	493	13	Q8UYF8
12	175	65.5	496	11	Q9ESF0
13	175	65.5	501	11	Q9EQ05
14	175	65.5	501	11	Q9EQ04
15	152	56.9	403	5	Q8MRD9
16	145	54.3	236	4	Q96RWS

17	145	54.3	236	4	Q96P09	Q96P09 homo sapien
18	145	54.3	236	6	Q95M72	Q95M72 pan troglod
19	145	54.3	498	5	Q960U3	Q960U3 drosophila
20	144	53.9	236	6	Q95M71	Q95M71 gorilla gor
21	144	53.9	402	5	Q8R621	Q8R621 aedes albop
22	142	53.2	405	13	Q8UWH2	Q8UWH2 brachydanio
23	141	52.8	597	11	Q9R015	Q9R015 mus musculu
24	141	52.8	1160	4	Q8TD4	Q8TD4 homo sapien
25	133.5	50.0	153	5	Q9VEM2	Q9VEM2 drosophila
26	131	49.1	106	4	Q96RW6	Q96RW6 homo sapien
27	131	49.1	517	11	Q8R4U8	Q8R4U8 rattus norv
28	130	48.7	264	12	Q9EN27	Q9EN27 ansacta moo
29	129	48.3	438	5	Q9VUX5	Q9VUX5 drosophila
30	127	47.6	346	5	Q968T8	Q968T8 bombyx mori
31	126	47.2	377	5	Q9NJ07	Q9NJ07 spodoptera
32	126	47.2	379	5	Q9U492	Q9U492 trichoplusi
33	124	46.4	276	12	Q8QJ95	Q8QJ95 mamestra co
34	124	46.4	281	12	Q9YND8	Q9YND8 choristoneu
35	122.5	45.9	4845	11	Q88738	Q88738 mus musculu
36	121	45.3	261	12	Q9QES9	Q9QES9 epiphyas po
37	121	45.3	280	4	Q9HAP7	Q9HAP7 homo sapien
38	121	45.3	298	4	Q9H2A8	Q9H2A8 homo sapien
39	121	45.3	298	4	Q96CA5	Q96CA5 homo sapien
40	120	44.9	313	12	Q9J827	Q9J827 spodoptera
41	118	44.2	276	12	Q89744	Q89744 buzura supp
42	116	43.4	268	12	Q9IF18	Q9IF18 helioverpa
43	116	43.4	268	12	Q9E232	Q9E232 helioverpa
44	112	41.9	109	6	Q8RMV4	Q8RMV4 bos taurus
45	112	41.9	208	12	Q55770	Q55770 chilio lride

## ALIGNMENTS

## RESULT 1

Q921N0 PRELIMINARY; PRT; 374 AA.

AC Q921N0:

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Similar to baculoviral IAP repeat-containing 2.

GN BIRC2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC011338; AAH1338.1; -

DR MGD; MGI:1197007; BIRC2.

DR InterPro: IPR001370; BIR.

DR Pfam; PF00653; BIR; 3.

DR PROSITE; PS01282; BIR\_REPEAT\_1; UNKNOWN\_3.

DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.

SQ SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7E46F3 CRC64;

Query Match 88.0%; Score 235; DB 11; Length 374;  
Best Local Similarity 89.1%; Pred. NO. 6.9e-23;  
Matches 41; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKAGFYITIGPDRAVACFACGKGLSNWEPRDNAMSEHLRHPKCP 46  
DB 167 LAKAGFYITIGPDRAVACFACGKGLSNWEPRDNAMSEHLRHPKCP 232

RESULT 2  
Q9ESE8 PRELIMINARY; PRT; 589 AA.  
AC Q9ESE8:  
DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Inhibitor of apoptosis protein 2.	DE	Inhibitor of apoptosis protein 2.
OS	Rattus norvegicus (Rat).	OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
XX	NCBI_TaxID=10116;	XX	NCBI_TaxID=10116;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RA	Holcik M., Lefebvre C.A., Hicks R., Korneluk R.G.;	RA	Holcik M., Lefebvre C.A., Hicks R., Korneluk R.G.;
RT	"Cloning and Characterization of the Rat Homologs of the Inhibitor of	RT	"Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT	Apoptosis Protein 1, 2, and 3 Genes."	RT	Apoptosis Protein 1, 2, and 3 Genes."
RL	Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.	RL	Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR	EMBL; AF183431; AAC22971.1; "	DR	EMBL; AF183431; AAC22971.1; "
DR	HSSP; Q13490; 10BH.	DR	HSSP; Q13490; 10BH.
DR	InterPro; IPR001370; BIR.	DR	InterPro; IPR001370; BIR.
DR	InterPro; IPR001315; CARD.	DR	InterPro; IPR001315; CARD.
DR	InterPro; IPR001841; Znf_fing.	DR	InterPro; IPR001841; Znf_fing.
DR	Pfam; PF00653; BIR; 3.	DR	Pfam; PF00653; BIR; 3.
DR	Pfam; PF00619; CARD; 1.	DR	Pfam; PF00619; CARD; 1.
DR	Pfam; PF00097; zf-C3HC4; 1.	DR	Pfam; PF00097; zf-C3HC4; 1.
DR	SMART; SM00238; BIR; 3.	DR	SMART; SM00238; BIR; 3.
DR	SMART; SM00114; CARD; 1.	DR	SMART; SM00114; CARD; 1.
DR	SMART; SM00184; RING; 1.	DR	SMART; SM00184; RING; 1.
DR	PROSITE; PS01282; BIR_REPEAT_1; 2.	DR	PROSITE; PS01282; BIR_REPEAT_1; 2.
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.	DR	PROSITE; PS50143; BIR_REPEAT_2; 3.
DR	PROSITE; PS50209; CARD; 1.	DR	PROSITE; PS50209; CARD; 1.
KW	Zinc-finger.	KW	Zinc-finger.
SO	SEQUENCE 589 AA; 66750 MW; BA4F7089BD7CD285B CRC64;	SO	SEQUENCE 589 AA; 66750 MW; BA4F7089BD7CD285B CRC64;
Query Match	86.9%; Score 232; DB 1; Length 589;	Query Match	86.9%; Score 232; DB 1; Length 589;
Best Local Similarity	84.8%; Pred. No. 2.8e-23;	Best Local Similarity	84.8%; Pred. No. 2.8e-23;
Matches 39; Conservative 2; Mismatches 5; Indels 0; Gaps 0		Matches 39; Conservative 2; Mismatches 5; Indels 0; Gaps 0	
Oy	1 LAKAEFYIGPEDRYACFACGKSLNWEKXNANSEHRLRHPKCP 46	Oy	1 LAKAEFYIGPEDRYACFACGKSLNWEKXNANSEHRLRHPKCP 46
Db	176 LAKAEFYTGEDRYACFACGKSLNWEKXNANSEHRLRHPKCP 221	Db	176 LAKAEFYTGEDRYACFACGKSLNWEKXNANSEHRLRHPKCP 221
RESULT 3		RESULT 3	
09QZC6	PRELIMINARY; PRT; 589 AA.	09QZC6	PRELIMINARY; PRT; 589 AA.
AC	09QZC6.	AC	09QZC6.
DT	01-MAY-2000 (TREMBLrel. 13, Created)	DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Inhibitor of apoptosis protein 2.	DE	Inhibitor of apoptosis protein 2.
OS	Rattus norvegicus (Rat).	OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
XX	NCBI_TaxID=10116;	XX	NCBI_TaxID=10116;
RN	[1]	RN	[1]
RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RP	TISSUE=KIDNEY;	RP	TISSUE=KIDNEY;
RC	Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.;	RC	Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.;
RT	"Cloning of cDNA for rat inhibitor of apoptosis protein 2.;"	RT	"Cloning of cDNA for rat inhibitor of apoptosis protein 2.;"
RL	Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.	RL	Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR	EMBL; AF190020; AA04585.1; "	DR	EMBL; AF190020; AA04585.1; "
DR	HSSP; Q13490; 10BH.	DR	HSSP; Q13490; 10BH.
DR	InterPro; IPR001370; BIR.	DR	InterPro; IPR001370; BIR.
DR	InterPro; IPR001315; CARD.	DR	InterPro; IPR001315; CARD.
DR	InterPro; IPR001841; Znf_fing.	DR	InterPro; IPR001841; Znf_fing.
DR	Pfam; PF00653; BIR; 3.	DR	Pfam; PF00653; BIR; 3.
DR	Pfam; PF00619; CARD; 1.	DR	Pfam; PF00619; CARD; 1.
DR	Pfam; PF00097; zf-C3HC4; 1.	DR	Pfam; PF00097; zf-C3HC4; 1.
DR	SMART; SM00238; BIR; 3.	DR	SMART; SM00238; BIR; 3.
DR	SMART; SM00114; CARD; 1.	DR	SMART; SM00114; CARD; 1.
DR	SMART; SM00184; RING; 1.	DR	SMART; SM00184; RING; 1.
DR	PROSITE; PS01282; BIR_REPEAT_1; 3.	DR	PROSITE; PS01282; BIR_REPEAT_1; 3.
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.		

SQ	Zinc-finger.
ID	SEQUENCE
AA:	589 AA; 66777 MM; E6B12FEE3EA34142 CXC64;
Query Match	86.9%; Score 232; DB 11; Length 589;
Best Local Similarity	84.8%; Pred. No. 2.8e-22;
Matches 39; Conservative	2; Mismatches 5; Indels 0; Gaps 0;
OY	1 LAKAGFYITGPDRAVACFACGKGLSNMPEKDAMSEHLRHPKC PF 46                         :             Db 176 LAKAGFYITGPDRAVACFACGKGLSNMPEKDPLSEHRRHFPCPF 221
RESULT 4	
OQESES9	PRELIMINARY; PRT; 602 AA.
ID OQESES9	
DT 01-MAR-2001 (TREMBLrel. 16, Created)	
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)	
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE Inhibitor of apoptosis protein 1.	
OS Rattus norvegicus (Rat).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; CX NCBI_Taxid=10116. RN [1] RP SEQUENCE FROM N.A. RT "Cloning and Characterization of the Rat Homologues of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes"; RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases. CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER. DR EMBL; AF183450; ABG22970.1; -. DR HSSP; Q13490; IOBH. DR InterPro; IPR001370; BIR. DR InterPro; IPR001315; CARD. DR InterPro; IPR001841; Zn_f_ring. DR Pfam; PF00653; BIR_3. DR Pfam; PF00619; CARD_1. DR Pfam; PF00097; zf-C3HC4_1. DR SMART; SM00238; BIR_3. DR SMART; SM00114; CARD_1. DR SMART; SM00184; RING_1. DR PROSITE; PS01283; BIR_REPEAT_1; 2. DR PROSITE; PS50143; BIR_REPEAT_2; 3. DR PROSITE; PSS0209; CARD_1. KW Zinc-finger. SQ SEQUENCE 602 AA; 67326 MM; CC91385EBAZ2D5A CRC64;	
Query Match	84.6%; Score 226; DB 11; Length 602;
Best Local Similarity	82.6%; Pred. NO. 1.8e-21;
Matches 36; Conservative	3; Mismatches 5; Indels 0; Gaps 0;
OY	1 LAKAGFYITGPDRAVACFACGKGLSNMPEKDAMSEHLRHPKC PF 46                         :             Db 189 LAKAGFYITGPDRAVACFACGKGLSNMPDKDDPLSEHRRHFPCSF 234
RESULT 5	
OQIAI70	PRELIMINARY; PRT; 195 AA.
ID OQIAI70	
AC OQIAI70;	
DT 01-OCT-2000 (TREMBlrel. 15, Created)	
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)	
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)	
DS Inhibitor of apoptosis 1 (Fragment).	
OS Gallus gallus (Chicken).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CC Archaeosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; CX NCBI_Taxid=9031; RN [1] RP SEQUENCE FROM N.A. STRAIN-BREED LECHORN; TISSUE=SPLEEN; CC	

[illegible]

	DE	Apopotosis inhibitor ch-IAPI (Fragment).
	OS	Gallus gallus (Chicken)
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	CC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
	GC	Gallus.
--OX	NCHI_TaxID=9031;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Pendleton C.N., Bargmann W.J., Varadarajan J., Bose H.R. Jr.;	
RT	"the apoptosis inhibitor ch-IAPI is a direct transcriptional target of	
RL	v-rel and c-rel";	
DR	Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF311289; AACG42316.1; -	
DR	HSSP; Q13490; IOBH.	
DR	InterPro; IPR001370; BIR.	
DR	Pfam; PF00653; BIR_3	
DR	SMART; SMO0238; BIR_3	
DR	PROSITE; PS01282; BIR_REPEAT_1; 1.	
DR	PROSITE; PSS0143; BIR_REPEAT_2; 3.	
FT	NON_TER 324        324	
SQ	SEQUENCE       324 AA;    5E2B89DEAE373F3 CRC64;	
	Query Match             83.5%; Score 223; DB 13; Length 324; Best Local Similarity     80.4%; Fred. No. 2.3e-21; Matches     37; Conservative     3; Mismatches     6; Indels     0; Gaps     0;	
OY	1 LAKAGFYIIGPDRIVACFCACGGKLTNNMEPKDNAMEHLHFPCPF 46	:  :
Db	196 LAKAGLYYLGTADKYVCATCGQSGLSNWEKDAMENHRHFNCF 241	:  :
	RESULT 8	
ID	057319	PRELIMINARY; PRT; 610 AA.
AC	057319;	
DT	01-JUN-1998 (Tremblrel. 06, Created)	
DI	01-JUN-1998 (Tremblrel. 06, Last sequence update)	
Dt	01-JUN-2001 (Tremblrel. 17, last annotation update)	
De	Inhibitor of apoptosis protein 1 (IAP) (Inhibitor of T cell apoptosis	
GN	PROTEIN).	
IAP1.		
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
GC	Gallus.	
OK	NCHI_TaxID=9031;	
XN	[1]	
RP	SEQUENCE FROM N.A.	
RA	STRAIN-WHITE LEGORN; TISSUE-EMBRYONIC FIBROBLAST;	
RX	MELINDA-98038801; PubMed-9372964;	
RA	You M., Ku P.-T., Hidlickova R., Bose H.R. Jr.;	
RT	"Ch-IAPI, a member of the Inhibitor-of-apoptosis protein family, is a	
RL	mediator of the antiapoptotic activity of the v-rel oncprotein.";	
JMol. Cell. Biol.	17(7);328-341(1997).	
-1-	FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED CELLS.	
-1-	SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF THE V-REL-TRANSFORMED CELLS.	
-1-	TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE SPLEEN, THYMUS, BUCCA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS IN TESTES, BRAIN, AND SKLETAL MUSCLE.	
-1-	INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION PROCESS.	
-1-	DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTI-APOPTOTIC EFFECT.	
-1-	SIMILARITY: MEMBER OF THE IAP FAMILY.	
-1-	SIMILARITY: CONTAINS 3 BIR DOMAINS (BAKUOVIRAL INHIBITION OF APOPTOSIS PROTEIN REPEAT).	
-1-	SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.	
EMBL:	AF008592; AAB88044.1; -	
HSP:	Q13490; IOBH	
Interpro:	IPR001370; BIR.	
Interpro:	IPR001315; CARD.	
Interpro:	IPR001841; Zn_fing.	

DR Pfam; PF00653; BIR; 3.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00238; BIR; 3.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS50209; CARD; 1.  
 KW Apoptosis; Zinc-finger; Repeat.  
 FT REPEAT 30 97 BIR\_REPEAT\_1.  
 FT REPEAT 176 242 BIR\_REPEAT\_2.  
 FT REPEAT 262 329 BIR\_REPEAT\_3.  
 FT ZN\_RING 563 597 C3HC4-TYPE.  
 SQ SEQUENCE 610 AA; 68924 MW; ADF47619650B4A6 CRC64;

Query Match 83.5%; Score 223; DB 13; Length 610;  
 Best Local Similarity 80.4%; Pred. No. 4,5e-11;  
 Matches 37; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 LAKAGFYTGPDRAVACFCAGGKLSWEPKDNMSHRLHFPKCP 46  
 DB 196 LAKAGLYTGPDRAVACFCAGGKLSWEPKDNMSHRLHFPKCP 241

RESULT 9  
 O88642 PRELIMINARY; PRT; 224 AA.  
 AC O88642;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Inhibitor of apoptosis protein (Fragment).  
 GN RIAP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WISTAR; TISSUE=OVARY;  
 RA Bradley C.R., Lareu R.R., Dharmarajan A.M.;  
 RT "Cloning and characterisation of an inhibitor of apoptosis protein  
 (IAP) in the rat corpus luteum."; PubMed (Aug-1998) to the EMBL/Genbank/DBJ databases.  
 RL EMBL; AF081503; AAC32497.1; -  
 DR HSP; Q13490; IQBH.  
 DR InterPro; IPR001370; BIR.  
 DR Pfam; PF00653; BIR; 3.  
 DR SMART; SM00238; BIR; 2.  
 DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
 FT NON\_TER 1 1  
 FT NON\_TER 224 224  
 SQ SEQUENCE 224 AA; 25209 MW; 213A52534D5EB56A CRC64;

Query Match 81.3%; Score 217; DB 11; Length 224;  
 Best Local Similarity 78.3%; Pred. No. 9,5e-21;  
 Matches 36; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 LAKAGFYTGPDRAVACFCAGGKLSWEPKDNMSHRLHFPKCP 46  
 DB 105 LGAAGFYTGPDRAVACFCAGGKLSWEPKDNMSHRLHFPKCP 150

RESULT 10  
 O88642 PRELIMINARY; PRT; 628 AA.  
 AC O88642;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Iap1.  
 GN IAP1.

OS Brachydanio rerio (zebrafish) (Zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20373792; PubMed=10917738;  
 RA Inohara N., Nunez G.;  
 RT "Genes with homology to mammalian apoptosis regulators identified in  
 zebrafish";  
 RN Cell Death Differ. 7:509-510(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Inohara N., Nunez G.;  
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF442500; AAL33679.1; -  
 DR InterPro; IPR001370; BIR.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR001841; znf\_ring.  
 DR Pfam; PF00653; BIR; 3.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00238; BIR; 3.  
 DR SMART; SM00114; CARD; 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; UNKNOWN\_2.  
 DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS50089; zf\_RING\_2; 1.  
 SQ SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87C8A95 CRC64;

Query Match 73.0%; Score 195; DB 13; Length 628;  
 Best Local Similarity 69.6%; Pred. No. 2,3e-17;  
 Matches 32; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 1 LAKAGFYTGPDRAVACFCAGGKLSWEPKDNMSHRLHFPKCP 46  
 DB 207 LAKAGLYTGPDRAVACFCAGGKLSWEPKDNMSHRLHFPKCP 252

RESULT 11  
 O88642 PRELIMINARY; PRT; 493 AA.  
 AC O88642;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Inhibitor of apoptosis protein 3.  
 GN IAP3.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Brigham J.T., Johnson A.L.;  
 RT "Identification of chicken inhibitor of apoptosis protein XIAP  
 (IAP3).";  
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF451854; AAL47170.1; -  
 DR InterPro; IPR001370; BIR.  
 DR InterPro; IPR001841; znf\_ring.  
 DR Pfam; PF00653; BIR; 3.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00238; BIR; 3.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; UNKNOWN\_2.  
 DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS50089; zf\_RING\_2; 1.  
 SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;



Query Match	56.9%	Score 153	DB 5	Length 403
Best Local Similarity	55.6%	Pred. NO. 7e-12		
Matches 25, Conservative	6	Mismatches	14	Indels 0; Gaps 0

QY	1	LAKAGFTYIGPGRVACACGGKLSNWEPEKDNASEHTRHFP	45
Db	59	LARYGFTYVGPNDMAKCYFCRVEIGLWEPNDNVLSEHTRWSP <td>103</td>	103

Search completed: May 5, 2003, 16:06:26  
Job time : 11.235 secs